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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:59 ; Search time 18 seconds
(without alignments)
1638.376 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651

Sequence: 1 MLFCGALLLAANTARALEV.....QNNYENPTKFFPHOMKK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 423:0858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCFUS-COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	3651	100.0	697	4 US-09-548-372D-16 Sequence 16, Appl
2	3651	100.0	697	4 US-09-548-367D-16 Sequence 16, Appl
3	3651	100.0	697	4 US-09-551-853D-16 Sequence 16, Appl
4	3646	99.9	697	4 US-09-548-372D-20 Sequence 20, Appl
5	3646	99.9	697	4 US-09-548-367D-20 Sequence 20, Appl
6	3646	99.9	697	4 US-09-551-853D-20 Sequence 20, Appl
7	3643	99.8	697	4 US-09-548-372D-18 Sequence 18, Appl
8	3643	99.8	697	4 US-09-548-367D-18 Sequence 18, Appl
9	3643	99.8	697	4 US-09-551-853D-18 Sequence 18, Appl
10	3641	99.7	695	2 US-08-123-702-2 Sequence 2, Appl
11	3641	99.7	695	2 US-08-104-165-1 Sequence 1, Appl
12	3641	99.7	695	3 US-08-464-250-1 Sequence 1, Appl
13	3641	99.7	695	4 US-08-464-250-1 Sequence 1, Appl
14	3641	99.7	695	4 US-09-458-481B-7 Sequence 7, Appl
15	3641	99.7	695	4 US-09-458-481B-8 Sequence 8, Appl
16	3641	99.7	695	4 US-09-548-372D-10 Sequence 10, Appl
17	3641	99.7	695	4 US-09-548-367D-10 Sequence 10, Appl
18	3641	99.7	695	4 US-09-551-853D-10 Sequence 10, Appl
19	3641	99.7	695	6 5218:00-2 Patent No. 521800
20	3636	99.6	695	4 US-09-548-372D-14 Sequence 14, Appl
21	3636	99.6	695	4 US-09-548-367D-14 Sequence 14, Appl
22	3636	99.6	695	4 US-09-551-853D-14 Sequence 14, Appl
23	3635	99.6	694	1 US-08-339-152A-18 Sequence 18, Appl
24	3635	99.6	694	2 US-08-007-999B-5 Sequence 5, Appl
25	3635	99.6	694	2 US-08-689-276A-5 Sequence 5, Appl
26	3633	99.5	695	4 US-09-548-372D-12 Sequence 12, Appl
27	3633	99.5	695	4 US-09-548-367D-12 Sequence 12, Appl

10/2

3633 59.5 695 4 US-09-551-853D-12 Sequence 12, Appl
3629 59.4 695 1 US-08-371-930-27 Sequence 27, Appl
3629 59.4 695 5 PCT-US94-01712-27 Sequence 27, Appl
3617 59.1 695 1 US-08-339-152A-30 Sequence 30, Appl
3612 98.9 753 4 US-09-548-372D-61 Sequence 61, Appl
3612 98.9 753 4 US-09-548-367D-61 Sequence 61, Appl
3612 98.9 753 4 US-09-551-853D-61 Sequence 61, Appl
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3602 98.7 751 2 US-08-104-165-2 Sequence 2, Appl
3602 98.7 751 2 US-08-422-333-2 Sequence 2, Appl
3602 98.7 751 3 US-08-422-333-21 Sequence 21, Appl
3602 98.7 751 3 US-08-464-250-2 Sequence 2, Appl
3602 98.7 751 4 US-08-464-250-2 Sequence 2, Appl
3602 98.7 751 4 US-08-832-867-5 Sequence 5, Appl
3602 98.7 751 4 US-09-548-372D-57 Sequence 57, Appl
3602 98.7 751 4 US-09-548-367D-57 Sequence 57, Appl
3602 98.7 751 4 US-09-551-853D-57 Sequence 57, Appl
3602 98.7 751 6 5187153-2 Patent No. 5187153

ALIGNMENTS

RESULT 1
US-09-548-372D-16
; Sequence 16, Application US/09548372D
; Patent No. 6420534

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND

; FILE OF INVENTION: THEREOF

; CURRENT APPLICATION NUMBER: US/09/548,372D

; CURRENT FILING DATE: 2000-04-12

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 16

; LENGTH: 697

; TYPE: PR

; ORGANISM: Homo sapiens

US-09-548-372D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLFCGALLLAANTARALEVPTDGNAGLLAEPOJAMPCGRLNMHMNVQSKWSDPSGTX 60
QY 61 TCIDTREGILQYCOEYVPELOITNVYVANOPTVIONMCKRCKOCTHPIVPIYRCLVG 120
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Db 121 EFVSDALLVPDKCKFLHQRERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
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Db 181 GFVFCVCPAAEESNDVDSADAEEDSDVWVGADTDYADGSEKVVVEAEVEEVEE 240
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DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRRHHVFNMLK 420
QY 421 KYVRAEQDKRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPAYA 480
DB 421 KYVRAEQDKRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPAYA 480
QY 481 BEIQDEVDELLOKQKONSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
DB 481 BEIQDEVDELLOKQKONSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
QY 541 DDLQPMHSGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNKTETISEVKKMDAEF 600
DB 541 DDLQPMHSGADSVANTENEVEPVDARPAADRGLTTRPGSGLTNKTETISEVKKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVITVLMKKKQYTSIHGCV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVITVLMKKKQYTSIHGCV 660
QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697

RESULT 2

US-09-548-367D-16
; Sequence 16, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 2915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TCIDTKEGILQYCOEYVPELOJITNNVEANQPVTIONCKRGRKQCKTHPHFVYPCVLG 120
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DB 121 EFVSDALLVPCKEKLHQRMDVOCETHLHWHTVAKETCSKSNLHDIYGMLLPCGIDKFR 180

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DB 181 GVFEVCCPLAEESDNDVSADAEEDSDVVMGGADTDYADGSEDKVYVEVAEEVAEVEE 240
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DB 301 DKYLETPGDNEHAHFQKAKERLRAKRRMSQVMPREWEAFQAKNLPKAKKAVIQHF 360
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DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRRHHVFNMLK 420
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DB 421 KYVRAEQDKRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLYNVPAYA 480
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DB 481 BEIQDEVDELLOKQKONSDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
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RESULT 3

US-09-551-953D-16
; Sequence 16, Application US/09551953D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 2915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,953D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-953D-16

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.6e-264;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 TCIDTKGILQCYQEVYPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCVLG 120
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Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 130
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Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKXVVEAEFEAEVEE 240
QY 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
Db 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
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Db 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVREMEAEERQAKNLPKADKAVIOHP 360
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Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVIFRMSQSLSLYNNPVA 480
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Db 481 EBIQDEVDELLQKEQNSCDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFS 540
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Db 601 RHDSEYEVHOKLVFFAEVGSNGKAIIGLMVGGVYATVITVITLMLKKKQYTSIHGV 660
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Db 661 VEVDAAVTPEERHLSKMOONGYENPTYKFEQMNKK 697

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RESULT 4

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US-09-548-372D-20
; Sequence 20, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-20

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Query Match 99.9% Score 3646; DB 4; length 697;
Best Local Similarity 99.9% Pred. NO. 3.7e-264;

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Db 1 MLPGLALLLAAWTAARALEVPTDGNAGLLARPOIAMFCGRNLNMHNVONGKWDSPSGTK 60
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Db 61 TCIDTKGILQCYQEVYPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKXVVEAEFEAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKXVVEAEFEAEVEE 240
QY 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
Db 241 EADDDDDDDGDEVEBEAEPEYEAETERTTS:ATTTTITTESVEVVRVPTTAASTPDV 300
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Db 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVREMEAEERQAKNLPKADKAVIOHP 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMK 420
Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVIFRMSQSLSLYNNPVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRVMDPKKAAQIRSOVMTHLRVIFRMSQSLSLYNNPVA 480
QY 481 EBIQDEVDELLQKEQNSCDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFS 540
Db 481 EBIQDEVDELLQKEQNSCDVLANMISEPRIISYNDALMPSLTETKTIVELLPVNGEFS 540
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Db 541 DDLQPHWSFGADSVDPANTENEVEVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAE 600
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Db 661 VEVDAAVTPEERHLSKMOONGYENPTYKFEQMNKK 697

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RESULT 5

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US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20

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; LENGTH: 697
; TYPE: Prt
; ORGANISM: Homo sapiens
; PRIOR APPLICATION NUMBER: US 09/551-853D-20
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: Prt
; ORGANISM: Homo sapiens
; US-09-551-853D-20

Query Match      99.9%   Score 3646;   DB 4;   Length 697;
Best Local Similarity 99.9%   Pred. No. 3,7e-264;
Matches 696;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNLMHNVQNGKWDSDSGTK 60
DB 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNLMHNVQNGKWDSDSGTK 60
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DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEAEQAKNPKADKAVIOHF 360
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QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVITVLMKKKQVTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVITVLMKKKQVTSIHGV 660
QY 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697

RESULT 6
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 299/5/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 03/404,133
; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: Prt
; ORGANISM: Homo sapiens
; US-09-551-853D-20

Query Match      99.9%   Score 3646;   DB 4;   Length 697;
Best Local Similarity 99.9%   Pred. No. 3,7e-264;
Matches 696;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNLMHNVQNGKWDSDSGTK 60
DB 1 MLPLGALLLAANTARALEVPTDGNAGLLAEPOIAFCGLNLMHNVQNGKWDSDSGTK 60
QY 61 TCIDTKEGILQYCOEYYPE-QITNVVEANOPVTIQNCKRGRKQCKTHPHFVYPCVLG 120
DB 61 TCIDTKEGILQYCOEYYPE-QITNVVEANOPVTIQNCKRGRKQCKTHPHFVYPCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSKSTNLHDYGMCLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHWHTVAKETCSKSTNLHDYGMCLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEEVEE 240
QY 241 EADDEDDGDEVEEAEPEEATERTISATTTTTSVEEVVVRVPTTAASPDVAV 300
DB 241 EADDEDDGDEVEEAEPEEATERTISATTTTTSVEEVVVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEAEQAKNPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEAEQAKNPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKROHTLKHFHVRMYDPKKAQIRSOVMTHLRVIVERNOSLSLLYNVFAVA 480
DB 421 KYVRAEQKROHTLKHFHVRMYDPKKAQIRSOVMTHLRVIVERNOSLSLLYNVFAVA 480
QY 481 EEIQDEVDLQKEQNYSDVLANMISEPRIISYGNDAIMPSTETKTIVELLVNGEFSL 540
DB 481 EEIQDEVDLQKEQNYSDVLANMISEPRIISYGNDAIMPSTETKTIVELLVNGEFSL 540
QY 541 DDLCQPHSFAGDSVPANTENEVEPVDAARPAADRGLTTRPGSGLTNKTETELSEVKMDAEF 600
DB 541 DDLCQPHSFAGDSVPANTENEVEPVDAARPAADRGLTTRPGSGLTNKTETELSEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVITVLMKKKQVTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVITVLMKKKQVTSIHGV 660
QY 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLKSKMQQNGYENPTYKFFEQMONKK 697

RESULT 7
US-09-548-372D-18
; Sequence 18, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF

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Qy	661	VEVDAAVTPERHLKSMQCNQYENPTYKFFEQMKNK	697
Db	661	VEVDAAVTPERHLKSMQCNQYENPTYKFFEQMKNK	697
RESULT 9			
US-09-551-853D-18			
: Sequence 18, Application US/09551853D			
: Patent No. 6500667			
: GENERAL INFORMATION:			
: APPLICANT: GURNEY ET AL			
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES			
: TITLE OF INVENTION: THEREOF			
: FILE REFERENCE: 29915/5290L			
: CURRENT APPLICATION NUMBER: US/09/551,853D			
: CURRENT FILING DATE: 2000-04-18			
: PRIOR APPLICATION NUMBER: US 60/155,493			
: PRIOR FILING DATE: 1999-09-23			
: PRIOR APPLICATION NUMBER: US 09/404,133			
: PRIOR FILING DATE: 1999-09-23			
: PRIOR APPLICATION NUMBER: PCT/US99/20881			
: PRIOR FILING DATE: 1999-09-23			
: PRIOR APPLICATION NUMBER: US 60/101,594			
: PRIOR FILING DATE: 1998-09-24			
: NUMBER OF SEQ ID NOS: 73			
: SOFTWARE: PatentIn version 3.1			
: SEQ ID NO 18			
: LENGTH: 697			
: TYPE: PR1			
: ORGANISM: Homo sapiens			
US-09-551-853D-18			
Query Match 99.8%; Score 3643; DB 4; Length 697;			
Best Local Similarity 99.7%; Pred. No. 6.2e-264;			
Matches 695; Conservative i; Mismatches 1; Indels 0; Gaps 0;			
Qy	1	MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFGRLLNMHNVONGKWDSPGSK	63
Db	1	MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFGRLLNMHNVONGKWDSPGSK	63
Qy	61	TCIDTREGILQYCEVYPELOITNVVEANGPVITCNCKRGRKCKTHPHEVITYRGLVG	120
Db	61	TCIDTREGILQYCEVYPELOITNVVEANGPVITCNCKRGRKCKTHPHEVITYRGLVG	120
Qy	121	EFVSDALLVPDKCKFLHQGRMDVCKTHLHWFTVAKETCSKSTNLHDYGMGLPGIDPKR	189
Db	121	EFVSDALLVPDKCKFLHQGRMDVCKTHLHWFTVAKETCSKSTNLHDYGMGLPGIDPKR	189
Qy	181	GVFVCCPLAESDNVDSAPAEEDSDVWVGGAOTDYADGSDCKVVEVAPEEEVAEVEE	243
Db	181	GVFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSDCKVVEVAPEEEVAEVEE	243
Qy	241	EADDDDEDDGDEVEEAEAEPIEAEIERTSTA:TTTTTTSVEVVEVPVITASTDAY	300
Db	241	EADDDDEDDGDEVEEAEAEPIEAEIERTSTA:TTTTTTSVEVVEVPVITASTDAY	300
Qy	301	DKYLETPGDNENHAHFQAKERLEAKHIREMSQVMEAEERCAKNLPKAKKAV:CHF	369
Db	301	DKYLETPGDNENHAHFQAKERLEAKHIREMSQVMEAEERCAKNLPKAKKAV:CHF	369
Qy	361	OEKVSELEGAANFRQOLVETHMARVEAMLNDRRLALENYITLQAVPPRPREFVFNMLK	420
Db	361	OEKVSELEGAANFRQOLVETHMARVEAMLNDRRLALENYITLQAVPPRPREFVFNMLK	420
Qy	421	KYVRAEQKORHTLKHFEHVRVMDPKAAQIRSOVWTHLRVIYERMGNSILLNVNVA	480
Db	421	KYVRAEQKORHTLKHFEHVRVMDPKAAQIRSOVWTHLRVIYERMGNSILLNVNVA	480
Qy	481	EEIQDEVEDELLOKEQNSDVLANNISPEPRISYGNDAIMPSTETKTVELPYNGFSL	540
Db	481	EEIQDEVEDELLOKEQNSDVLANNISPEPRISYGNDAIMPSTETKTVELPYNGFSL	540

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541 DLQPHSFGADSVPANTENEVEVDARPAADRGLTTRPGSGLTNKTTEE1SEVVKMDAEF 600
541 DLQPHSFGADSVPANTENEVEVDARPAADRGLTTRPGSGLTNKTTEE1SEVNI.DAEF 500
601 RDHSGYEVHHOKLYFFAEVDGNSKGALIGLMVGGVVIATVIVITLYMLKKKQYTSIRHGV 660
601 RDHSGYEVHHOKLYFFAEVDGNSKGALIGLMVGGVVIATVIVITLYMLKKKQYTSIRHGV 660
661 VEVDAAVTPFEERHLSKMOONGYENPTYKFFEOMONKK 697
661 VEVDAAVTPFEERHLSKMOONGYENPTYKFFEOMONKK 697

RESULT 10
US-08-123-702-2
? Sequence 2, Application US/08123702
? Patent No. 5604131
? GENERAL INFORMATION:
? APPLICANT: Wadsworth, Samuel
? APPLICANT: Snyder, Benjamin
? APPLICANT: Reddy, Veermuri, B.
? APPLICANT: Wei, Chamer
? TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding Ap770
? Patent No. 5604131
? TIME OF INVENTION: Containing a Genomic DNA Insert of the XI and OX-2 Regio
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Patricia L. Pabst
? STREET: 2800 One Atlantic Center
? STREET: 1201 West Peachtree Street
? CITY: Atlanta
? STATE: GA
? COUNTRY: USA
? ZIP: 30309-3450
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/123.702
? FILING DATE: 17-SEPT-1993
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Pabst, Patrea L.
? REGISTRATION NUMBER: 31,284
? REFERENCE/DOCKET NUMBER: TS1121
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (404)-873-8794
? TELEFAX: (404)-873-8795
? INFORMATION FOR SEQ ID NO. 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 695 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
US-08-123-702-2

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Query Match.	99.7%	Score 3641	DB 1	Length 695
Best Local Similarity	100.0%	Pred. No. 8.7e-264		
Matches	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0

Qy	1	M L P G L A L L L A A W T A R A L E V P T D G N A G L L A E P Q I A M F C G R L N N H M V Q N G K K W D S O P S G T K	60
Db	1	M L P G T A L L L A A W T A R A L E V P T D G N A G L L A E P Q I A M F C G R L N N H M V Q N G K K W D S O P S G T K	60
Qy	61	T C I D T K E G I L Q Y C Q E Y V P E L Q I T T N V V E A N P V T I Q N W C K K R G R K C Q K T H P H F V I P Y C L V G	120
Db	61	T C I D T K E G I L Q Y C Q E Y V P E L Q I T T N V V E A N P V T I Q N W C K K R G R K C Q K T H P H F V I P Y C L V G	120
Qy	121	E F V S D A L L V P D K C K L H Q E R M D V C E T H L H W H T V A K E T S E K S T N L H D Y G M L P C G I D K F R	180
Db	121	E F V S D A L L V P D K C K L H Q E R M D V C E T H L H W H T V A K E T S E K S T N L H D Y G M L P C G I D K F R	180

181 GVEFYCCPLAEEJNDVSDAEDDDSDVMGGAOTDYADGSEDKVVVEVAEEAEVEEE 240
181 GVEFYCCPLAEEJNDVSDAEDDDSDVMGGAOTDYADGSEDKVVVEVAEEAEVEEE 240
241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTSSVEEUVVPTTAASTPDV 300
241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTSSVEEUVVPTTAASTPDV 300
301 DKYLETGPDGNEHAHFQAKERLEAKHREMSQVMEAEERQAKNLPKADKAVIQHF 360
301 DKYLETGPDGNEHAHFQAKERLEAKHREMSQVMEAEERQAKNLPKADKAVIQHF 360
361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVFNK 420
361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVFNK 420
421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMMQSLSLYNVPA 480
421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMMQSLSLYNVPA 480
461 EEIQDEVDDELLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGE 540
461 EEIQDEVDDELLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGE 540
541 DDLOPHWSPGADSVDPANTENEVEPVDARPAADRGITTRPGSGITNKTETSEVKMDAE 600
541 DDLOPHWSPGADSVDPANTENEVEPVDARPAADRGITTRPGSGITNKTETSEVKMDAE 600
601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIAIVITLVMKKQYTSIHGV 660
601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIAIVITLVMKKQYTSIHGV 660
661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQM 695
661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQM 695

RESULT 11

US-08-104-165-1
Sequence 1, Application US/08104165
Patent No. 5877015
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GORTE, Alison Mary
APPLICANT: MOLLAN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104.165
FILING DATE: 21-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9101:07.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 911845.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 16163-000100
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-165-1

Query Match 99.7%; Score 3641; DB 2: Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHVYONGKWDSPGSK 60
DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNHMHVYONGKWDSPGSK 60
QY 61 TCIDTKESILQYCOEYVPELQITNVVEANQVPTIONCKKGRKCKTTPHFVPIPRCLVG 120
DB 61 TCIDTKESILQYCOEYVPELQITNVVEANQVPTIONCKKGRKCKTTPHFVPIPRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESQVDSADAEEDSDVMGGAOTDYADGSEDKVVVEVAEEAEVEEE 240
DB 181 GVEFVCCPLAEESQVDSADAEEDSDVMGGAOTDYADGSEDKVVVEVAEEAEVEEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTTESVEEUVVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTTESVEEUVVPTTAASTPDV 300
QY 301 DKYLETGPDGNEHAHFQAKERLEAKHREMSQVMEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETGPDGNEHAHFQAKERLEAKHREMSQVMEAEERQAKNLPKADKAVIQHF 360
QY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVFNK 420
DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHRVFNK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMMQSLSLYNVPA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMMQSLSLYNVPA 480
QY 481 EEIQDEVDDELLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGE 540
DB 481 EEIQDEVDDELLOKEQNYSDVLANMISEPRISYGNCAIMFSLTETKTIVVELLPVNGE 540
QY 541 DDLOPHWSPGADSVDPANTENEVEPVDARPAADRGITTRPGSGITNKTETSEVKMDAE 600
DB 541 DDLOPHWSPGADSVDPANTENEVEPVDARPAADRGITTRPGSGITNKTETSEVKMDAE 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIAIVITLVMKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIAIVITLVMKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQM 695
DB 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQM 695

RESULT 12

US-08-464-250-1
Sequence 1, Application US/08464250
Patent No. 6107542
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GORTE, Alison Mary

APPLICANT: MULLAN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
CS-08-464-250-1

Query Match 99.7% Score 3641; DH 3; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-244;
Matches 595; Conservative 0; Mismatches 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQTAMFCGRINMIMNYONGKWSDPGSK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQTAMFCGRINMIMNYONGKWSDPGSK 60
QY 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTQNNCKRGKCKCKTHPHFVYRCVLG 120
DB 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTQNNCKRGKCKCKTHPHFVYRCVLG 120
QY 121 EFVSDALLVPCKFLHQRMDVCEHLHWHIVAKESCKSEKSTNLHDYGMILPCKGICKFR 180
DB 121 EFVSDALLVPCKFLHQRMDVCEHLHWHIVAKESCKSEKSTNLHDYGMILPCKGICKFR 180
QY 181 GVEFVCCPLAESQNVDSADAEEDSDVWKGADIDVADGSEDVWVAEEEEVAEEES 240
DB 181 GVEFVCCPLAESQNVDSADAEEDSDVWKGADIDVADGSEDVWVAEEEEVAEEES 240
QY 241 EADDEDEDGDEVEEEAEPEYERATERTTSIATTTTTSVEVEVVRVPTTAASTPDAY 300
DB 241 EADDEDEDGDEVEEEAEPEYERATERTTSIATTTTTSVEVEVVRVPTTAASTPDAY 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVWREWEAEAKKLPKADKKAVICHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVWREWEAEAKKLPKADKKAVICHF 360
QY 361 QEKVESLFOEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMK 420

DE 361 QEKVESLFOEAAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNOSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNOSLSLLYNVPAVA 480
QY 481 EEIQDEVELLQKEQYSDDVLANMISBPRIISYGNDAIMPSTLTKTTVFLLPVNGEESL 540
DB 481 EEIQDEVELLQKEQYSDDVLANMISBPRIISYGNDAIMPSTLTKTTVFLLPVNGEESL 540
QY 541 DDLQPMHSGADSVFANTFNEVEPYDARFAADRGILITRPGSLTNKITEEISEVKMDAEF 600
DB 541 DDLQPMHSGADSVFANTFNEVEPYDARFAADRGILITRPGSLTNKITEEISEVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEDVGSNGKGAIGLVMGVVYATVIVITLVMKKKQYTSIRHGV 660
DB 601 RHDSGYEVHHQKLVFFAEDVGSNGKGAIGLVMGVVYATVIVITLVMKKKQYTSIRHGV 660
QY 661 VEYDAAVTPERHLSKMOONGYENETKYKFFEQKN 695
DB 661 VEYDAAVTPERHLSKMOONGYENETKYKFFEQKN 695

RESULT 13
US-08-464-250-1
Sequence 1, Application US/08464250
Patent No. 6300540
GENERAL INFORMATION:
APPLICANT: GOATE, John Anthony
MULLAN, Michael John
CHARTIER-HARLIN, Marie-Christine
OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 695 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-464-250-1

Query Match 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
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DB 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGKCKTTHPHFVTPYRCLVG 120
QY 121 EFVSUALLVPCKFLHGERMDVCETHLHWHITVAKETCSEKSTNHLHGYMLLPCGIDKFR 180
DB 121 EFVSUALLVPCKFLHGERMDVCETHLHWHITVAKETCSEKSTNHLHGYMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAAVEEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAAVEEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTESVEEVVAVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTESVEEVVAVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNQSLSLYNVPAVA 480
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QY 481 EIQDEVDLLOKEQNYSDVLANNMISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
DB 481 EIQDEVDLLOKEQNYSDVLANNMISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
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DB 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVKMDAEF 600
QY 601 RHDGSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIIHGV 660
DB 601 RHDGSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 14
US-09-458-481B-7
; Sequence 7, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
; APPLICANT: KUMAR, Vijaya B.
; TITLE OF INVENTION: ANTI-SENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
; FILE REFERENCE: 16153-9250
; CURRENT APPLICATION NUMBER: US/09/458,481B
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Monkey
US-09-458-481B-7

Query Match 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Rest Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGKCKTTHPHFVTPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNNVEANQPVTONMCKRGKCKTTHPHFVTPYRCLVG 120
QY 121 EFVSUALLVPCKFLHGERMDVCETHLHWHITVAKETCSEKSTNHLHGYMLLPCGIDKFR 180
DB 121 EFVSUALLVPCKFLHGERMDVCETHLHWHITVAKETCSEKSTNHLHGYMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAAVEEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSDKVVVEAEFEVAAVEEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTESVEEVVAVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTTESVEEVVAVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYIERMNQSLSLYNVPAVA 480
QY 481 EIQDEVDLLOKEQNYSDVLANNMISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
DB 481 EIQDEVDLLOKEQNYSDVLANNMISEPRISYNDALMPSLTETKTITVELLPVNGEESL 540
QY 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVKMDAEF 600
DB 541 DDLQPHSFAGDSVPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVKMDAEF 600
QY 601 RHDGSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIIHGV 660
DB 601 RHDGSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
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RESULT 15
US-09-458-481B-8
; Sequence 8, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
; APPLICANT: KUMAR, Vijaya B.
; TITLE OF INVENTION: ANTI-SENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
; FILE REFERENCE: 16153-9250
; CURRENT APPLICATION NUMBER: US/09/458,481B
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-458-481B-8

Query Match 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 8.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TCIDTKEGILQYCOEVYPELOITNVVEANQPVTTIONCKKGRKCKTHPHFVIFYRCJVG 120
QY 121 EFVSDALLVPCKCFELHGRMDVCETHLHHTVAKETCSKSTNLDPYGMILFQGIKFR 180
DB 121 EFVSDALLVPCKCFELHGRMDVCETHLHHTVAKETCSKSTNLDPYGMILFQGIKFR 180
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DB 181 GVEFVCCPLAESDNVSDADAEEDSDVWKGCCADTDYADGSEDKVVEVAKEEVEAEVEE 240
QY 241 EADDDDEDDEDEVEEAEPEYEATERTTSIATTTTTSVEEVYVVTAASTPCAV 300
DB 241 EADDDDEDDEDEVEEAEPEYEATERTTSIATTTTTSVEEVYVVTAASTPCAV 300
QY 301 DKYLETPGDENEHAFKAKERLEAKHREMSQVMREWEAEEROAKNLPKADKKAVIOHF 360
DB 301 DKYLETPGDENEHAFKAKERLEAKHREMSQVMREWEAEEROAKNLPKADKKAVIOHF 360
QY 361 QEKVESLEQEAANROQLVETHMARVEAMLNDRRLALENYITALOAVPPRPHVFNKJK 420
DB 361 QEKVESLEQEAANROQLVETHMARVEAMLNDRRLALENYITALOAVPPRPHVFNKJK 420
QY 421 KYVRAEQKDRQHTLKHFEFVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEFVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNVPAVA 480
QY 481 EEIODEVDEILQKQNSDVLANNISEPRISYNDALMPSLITETKTVEELLPVNGEFSI 540
DB 481 EEIODEVDEILQKQNSDVLANNISEPRISYNDALMPSLITETKTVEELLPVNGEFSI 540
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DB 541 DDLOPWHSEFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVIAIVIVITVLMKKKQYTSIHGGV 660
DB 601 RHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVIAIVIVITVLMKKKQYTSIHGGV 660
QY 661 VEVDAAVTPEERHLSKMCNGENPTYKFFQOMQ 695
DB 661 VEVDAAVTPEERHLSKMCNGENPTYKFFQOMQ 695

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Search completed: October 2, 2003, 14:03:34
 Job time : 20 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:09 ; Search time 38.3333 Seconds
(without alignments)
2886.663 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651
Sequence: 1 MLCGLALLLAAMTARALEV.....QQNGYENPTYKFFEQMNKX 697

Scoring table:

BLOSUM62
Gapcp 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158725573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3651	100.0	697	21	AA198428 Human APP696-KK am
2	3651	100.0	697	22	AAE10635 Human amyloid prot
3	3651	100.0	697	22	AAE06865 Human amyloid prec
4	3651	100.0	697	22	AAU06609 Human Amyloid prec
5	3651	100.0	697	22	AAU07206 Human beta-amyloid
6	3651	100.0	697	22	AAE02587 Human amyloid prec
7	3651	100.0	697	23	ABB78596 Human APP695-KK pr
8	3646	99.9	697	21	AA198430 Human APP695-VF-KK
9	3646	99.9	697	22	AAE10637 Human amyloid prot

10	3646	99.9	697	22	AAE06867 Human amyloid prec
11	3646	99.9	697	22	AAU06611 Human amyloid prec
12	3646	99.9	697	22	AAU07210 Human beta-amyloid
13	3646	99.9	697	22	AAE02589 Human amyloid prec
14	3646	99.9	697	23	ABB78598 Human APP695-VF-KK
15	3643	99.8	697	21	AA198429 Human APPSW-KK am
16	3643	99.8	697	22	AAE10636 Human amyloid prec
17	3643	99.8	697	22	AAE06866 Human amyloid prec
18	3643	99.8	697	22	AAU06610 Human Amyloid prec
19	3643	99.8	697	22	AAU07209 Human beta-amyloid
20	3643	99.8	697	22	AAE02588 Human amyloid prec
21	3643	99.8	697	23	ABB78597 Human APP695-SW-KK
22	3641	99.7	695	9	AA1981692 Sequence of human APP695. Homo sapi
23	3641	99.7	695	13	AAE26338 Human beta-amyloid
24	3641	99.7	695	19	AA192033 Amyloid precursor
25	3641	99.7	695	20	AA197221 Human APP695 amino
26	3641	99.7	695	21	AA198434 Human beta amyloid
27	3641	99.7	695	21	AA194705 Human wild-type am
28	3641	99.7	695	22	AAE10632 Human amyloid prec
29	3641	99.7	695	22	AAE06862 Human wild-type am
30	3641	99.7	695	22	AAU06606 Human amyloid prec
31	3641	99.7	695	22	AAE02584 Human amyloid prec
32	3641	99.7	695	23	ABG32721 Human amyloid prec
33	3641	99.7	695	23	ABB78593 Human APP695 prote
34	3641	99.7	695	23	AAE68315 Human amyloid prec
35	3641	99.7	695	24	ABH99604 Amino acid sequenc
36	3638	99.5	695	20	AA194950 Human beta amyloid
37	3636	99.5	695	18	AA19498 APP695 mutant A-be
38	3636	99.5	695	18	AA19484 APP695 mutant A-be
39	3636	99.5	695	18	AA19495 APP695 mutant A-be
40	3636	99.6	695	18	AA19481 APP695 mutant A-be
41	3636	99.6	695	21	AA188436 Human APP695-VF am
42	3636	99.6	695	22	AAE10634 Human amyloid prot
43	3636	99.6	695	22	AAE06864 Human amyloid prec
44	3636	99.6	695	22	AAU06608 Human Amyloid prec
45	3636	99.6	695	22	AAU07207 Human: beta-amyloid

ALIGNMENTS

RESULT 1
AA198428
10 AA198428 standard; Protein: 697 AA.
XX
XX AA198428;
XX
XX 03-AUG-2000 (first entry)
XX
XX Human APP696-KK amino acid sequence.
DE
XX Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
KW Alzheimer's disease; beta secretase site; APP696-KK.
XX
XX Homo sapiens.
XX
XX WO2000i7369-A2.
XX
XX 30-MAR-2000.
XX
XX 23-SEP-1999; 99WO-US20881.
XX
XX 24-SEP-1998; 98US-0101594.
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Gurney ME, Bienkowski MJ, Heinrikson RL, Zarodi LA, Yan R;
XX
XX WPI; 2000-303205/26.
XX
XX N-PSDB; AAA15665.
XX
XX New enzyme designated human aspartase useful in research into
XX Alzheimer's Disease is capable of cleaving amyloid protein precursor at

the beta secretase site to produce amyloid beta peptide

Claim 132: Page 137-141: 183pp; English.

This sequence represents a modified version of the human amyloid precursor protein (APP) amino acid sequence. The sequence is used in an example of the method of the invention, to show that modification of APP increases beta amyloid protein processing. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DSG or LTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal trans-membrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.

Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 21; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.7e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPLQAFCGRLNHHMNVQNGKWDSPSGTK	60
DB	1	MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPLQAFCGRLNHHMNVQNGKWDSPSGTK	60
QY	61	TCIDTKREGILOVCOEYVPELOIINVEANQPVTTIONMCKRGRKCKTHPHFVPIYRCVAG	120
DB	61	TCIDTKREGILOVCOEYVPELOIINVEANQPVTTIONMCKRGRKCKTHPHFVPIYRCVAG	120
QY	121	EFVSDALLVPCKEFLHGRMDVCEHLLHWHVAKETCSKSTNLHDYGMILPGCIDKFR	180
DB	121	EFVSDALLVPCKEFLHGRMDVCEHLLHWHVAKETCSKSTNLHDYGMILPGCIDKFR	180
QY	181	GVEFVCCPLAESDNVDSDADAEEDSDVWVGADTDYAKSDKVVVEVAEEVEAEVEE	240
DB	181	GVEFVCCPLAESDNVDSDADAEEDSDVWVGADTDYAKSDKVVVEVAEEVEAEVEE	240
QY	241	EADDDDEDGDEVEEAESEYEATERITTSATITTTTTSVEEVVVPVPTTAASPTDVA	300
DB	241	EADDDDEDGDEVEEAESEYEATERITTSATITTTTTSVEEVVVPVPTTAASPTDVA	300
QY	301	DKYLETPGDENEHAFKAKERLEAKHREMSQVNRWEAEAFROAKNLPKADKKAVTCHF	360
DB	301	DKYLETPGDENEHAFKAKERLEAKHREMSQVNRWEAEAFROAKNLPKADKKAVTCHF	360
QY	361	QEKVSLFOEANEQQQLVETHMARVEAMUNDRRLALENYITAJQAVPPRPFRVFNMLK	420
DB	361	QEKVSLFOEANEQQQLVETHMARVEAMUNDRRLALENYITAJQAVPPRPFRVFNMLK	420
QY	421	KVRAEQDQROHTLKHFEHVRWDPKKAQIRSOVNTHLRVYIERMNGSLSLNYPAVA	480
DB	421	KVRAEQDQROHTLKHFEHVRWDPKKAQIRSOVNTHLRVYIERMNGSLSLNYPAVA	480
QY	481	BEIQEVDDELLOKEONYSDDVLANMISUPRISYGNDAIMPSTTKTIVELLPNNGEFSL	540
DB	481	BEIQEVDDELLOKEONYSDDVLANMISUPRISYGNDAIMPSTTKTIVELLPNNGEFSL	540
QY	541	DLQLPWHSFGADSVPAENTENEVPVDARPAADRLGTLTPQSGSLTNKTEELSEVKMAEF	600
DB	541	DLQLPWHSFGADSVPAENTENEVPVDARPAADRLGTLTPQSGSLTNKTEELSEVKMAEF	600
QY	601	RHDSGYEVHHOKLVFAEDVGSNKGAIIGCMVGWVATVIVFLVMLKKQVTSIHGGV	660
DB	601	RHDSGYEVHHOKLVFAEDVGSNKGAIIGCMVGWVATVIVFLVMLKKQVTSIHGGV	660

QY	661	VEVDAAVTPERHLSKMOQNGYENPTYKFFEQMONKK	697
DB	661	VEVDAAVTPERHLSKMOQNGYENPTYKFFEQMONKK	697

RFSULI 2
AAE10635
AAE10635 standard; Protein: 697 AA.

XX	AC	AAE10635;
XX	CT	10-DEC-2001 (first entry)
XX	DE	Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX	KW	Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP695-KK;
XX	KW	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
XX	KW	amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective.
XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	PK	GD2357767-A.
XX	XX	
XX	PD	04-JUL-2001.
XX	XX	
XX	PF	22-SEP-2000; 2000GR-0023315.
XX	XX	
XX	PR	23-SEP-1999; 99US-0155493.
XX	PR	23-SEP-1999; 99US-0404133.
XX	PR	23-SEP-1999; 99WC-US20681.
XX	PR	13-OCT-1999; 99US-0416901.
XX	PR	06-DEC-1999; 99US-0169232.
XX	XX	
XX	PA	(PHAA) PHARMACIA & UPJOHN CO.
XX	XX	
XX	P1	BienKowkski MJ, Gurney M;
XX	XX	
XX	W21	2001-444208/48.
XX	DR	N-PSDB; AADI7871.
XX	XX	

Polypeptide comprising fragments of human aspartyl protease with amyloid precursor protein processing activity and alpha-secretase activity, for identifying modulators useful in treating Alzheimer's disease.

Example 6: Page 114-116: 187pp; English.

The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1 proteins which lack transmembrane domain or amino terminal domain or cytoplasmic domain and retains alpha-secretase activity and amyloid protein precursor (APP) processing activity. The proteins of the invention are useful for assaying hu-Asp1 alpha-secretase activity, which in turn is useful for identifying modulators of hu-Asp1 alpha-secretase activity, where modulators that increase hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's disease (AD) which causes progressive dementia with consequent formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with the substrate under acidic conditions and determining the level of hu-Asp1 proteolytic activity. The present sequence is human amyloid protein precursor 695-KK (APP695-KK) isoform which is obtained by the addition of two lys residues (KK motif) at the C-terminus of APP695 protein.

Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.7e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPLQAFCGRLNHHMNVQNGKWDSPSGTK 60

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DB 1 MLPGALLLLAAWTARALEVPTDGNAGLLASQIMFCGRNLNMHNMVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVYPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120
DB 61 TCIDTKEGILQYCOEVYPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120
QY 121 EFVSDALLVPCKCFLHOERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPCKCFLHOERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVVRVP:TAASIPDAV 300
DB 241 EADDEDEDEGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVVRVP:TAASIPDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAQVQH 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAQVQH 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSQLLYNVFAVA 480
DB 421 KYVRAEQKDRHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSQLLYNVFAVA 480
QY 481 BEIGDEVDLQKQNSYSDVLANK:SEPR:SYGNDALMPSLITETKTIVELVPNGEFSL 540
DB 481 BEIGDEVDLQKQNSYSDVLANK:SEPR:SYGNDALMPSLITETKTIVELVPNGEFSL 540
QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGITRPGSLNKTTEESEVKMAAEF 600
DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGITRPGSLNKTTEESEVKMAAEF 600
QY 601 RHDSGYEVHHOKLVFFAEEDVGSNGKAGLIGLVGGVVIATVITLVMLKKQYTSIHGGV 660
DB 601 RHDSGYEVHHOKLVFFAEEDVGSNGKAGLIGLVGGVVIATVITLVMLKKQYTSIHGGV 660
QY 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMONKK 697

```

RESULT 3

AAE06855

XX AAE06865 standard; Protein: 697 AA.

XX AC AAE06865;

XX DT 23-Oct-2001 (first entry)

XX DE Human amyloid precursor protein 695-KK (APP695-KK) isoform.

XX KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
 KW neuroprotective; antisense therapy; gene therapy; APP695-KK; mutant;
 KW mutin.

XX OS Homo sapiens.

XX PN WC200150829-A2.

XX XX 19-JUL-2001.

XX XX 09-MAY-2001; 2001WO-IB00799.

XX XX 09-MAY-2001; 2001WO-IB00799.

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XX PA (BIEN/) BIENKOWSKI M J.
PA (GJRN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX BIenkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI: 2001-483072/52.
XX N-PSDB: AAD13027.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity.
XX
XX Example 6: Page 144-146; 185pp; English.
XX
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease.
XX dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
XX and neuronal loss. APP isoforms are also used in methods for identifying
XX inhibitors and modulators of human Asp2 activity. The invention relates
XX to a method for identifying agents that modulate the activity of human
XX aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
XX as a means to screen in cellular assays for the inhibitors of beta- and
XX gamma-secretase. Hu-Asp DNA fragments are useful as probes or primers in
XX polymerase chain reactions (PCR). The probes are useful for detecting
XX Hu-Asp nucleic acids in vitro assays and in Northern and Southern
XX blots. The present sequence is modified human amyloid precursor
XX protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
XX addition of two Lys residues (KK motif) at the C-terminal end of APP695
XX isoform.
XX
XX SQ Sequence 697 AA;

```

Query Match 100.0%; Score 3651; DB 22; Length 697;

Best local similarity 100.0%; Pred. No. 1.7e-256;

Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLASQIMFCGRNLNMHNMVQNGKWDSPSGTK 60
 DB 1 MLPGALLLLAAWTARALEVPTDGNAGLLASQIMFCGRNLNMHNMVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEVYPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120
 DB 61 TCIDTKEGILQYCOEVYPELQITNVVEANQPVTIONMCKRGKQCKTHPHFVPIYRCIVG 120

QY 121 EFVSDALLVPCKCFLHOERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180
 DB 121 EFVSDALLVPCKCFLHOERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240

QY 241 EADDEDEDEGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVVRVP:TAASIPDAV 300
 DB 241 EADDEDEDEGDEVEEAEPEYEAERTTSIATTTTTTTSVEEVVRVP:TAASIPDAV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAQVQH 360
 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAQVQH 360

QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420

QY 421 KYVRAEQKQKQHTLKHFEHVRMVDPKAAQKRSQWHLHLEVYERMGSLSLYNVPAVA 480
 DB 421 KYVRAEQKQKQHTLKHFEHVRMVDPKAAQKRSQWHLHLEVYERMGSLSLYNVPAVA 480
 QY 481 EETODEVDELLQEQNYSCDVLANNISEPRISVGNDAIMPSTLTKTIVELLPVNGHESL 540
 DB 481 EETODEVDELLQEQNYSCDVLANNISEPRISVGNDAIMPSTLTKTIVELLPVNGHESL 540
 QY 541 DQ-LQPHSEFCADSVDPANTENEVEPVDPARPAADRGGLTRPGSGITNLTKEISEVKNDAEF 600
 DB 541 DQ-LQPHSEFCADSVDPANTENEVEPVDPARPAADRGGLTRPGSGITNLTKEISEVKNDAEF 600
 QY 601 RHDSGVEVHHQKLVFFADHVGSKNGALGLMVGCVVIAIVITIVMLKKKTYTSHHGV 660
 DB 601 RHDSGVEVHHQKLVFFADHVGSKNGALGLMVGCVVIAIVITIVMLKKKTYTSHHGV 660
 QY 661 VEYDAVTPTEERHLSKMGQNGYENPTYKFFEQMONKK 697
 DB 661 VEYDAVTPTEERHLSKMGQNGYENPTYKFFEQMONKK 697
 RESULT 4
 AAU06609
 ID AAU06609 standard; Protein: 697 AA.
 XX
 AC AAU06609;
 XX
 XT 24-OCT-2001 (first entry)
 XX
 DE Human Amyloid precursor protein mutant, APP695-KK.
 XX
 KW Human: Aspartyl protease; Asp2b; beta-secretase; nototropic;
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 KW amyloid-beta; Abeta; APP695-KK; mutant; muten.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 696..697
 FT /note="2 Extra Lys residues added compared to
 FT wild-type APP695"
 XX
 PN WO200149098-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-1B00798.
 XX
 PK 09-MAY-2001; 2001WO-1B00798.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R.
 XX
 UR WPI: 2001-502549/55.
 DR N-PSDB: AAS11523.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity
 XX
 PS Example 6: Page 144-146; 185pp; English.
 XX
 CC The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp

CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the App-Sw-beta-secretase peptide sequence (NLDA), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC Asp oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is the human
 CC APP695 mutant, APP695-KK which has 2 extra Lys residues added at
 CC the C-terminus compared to the wild-type APP695. The mutation alters the
 CC specificity of the APP gamma-secretase activity and increases the rate
 CC of processing of the amyloid Abeta peptide.

Sequence 697 AA;
 Query Match 100.0%; Score 3651; DB 22; Length 697;
 Best Local Similarity 100.0%; Pred. No. 1,7e-256;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRNLNMMNVQNGKWDSDSGTK 60
 DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRNLNMMNVQNGKWDSDSGTK 60
 QY 61 TCIDTKEGILQYCOEVYPELQITNVVEANQPVITQNMCKRGRKQCKTHPHFVYRCLVG 120
 DB 61 TCIDTKEGILQYCOEVYPELQITNVVEANQPVITQNMCKRGRKQCKTHPHFVYRCLVG 120
 QY 121 EFVSDALIVPCKCKFLHOERMDVCETHLHMHTVAKFTCSKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALIVPCKCKFLHOERMDVCETHLHMHTVAKFTCSKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIAITTTTTTESVEEVVVRPTTAASPTDVA 300
 DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIAITTTTTTESVEEVVVRPTTAASPTDVA 300
 QY 301 DKYLETPGDENEHAIFOKAKERLEAKHREMSVOMREWEAEERQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDENEHAIFOKAKERLEAKHREMSVOMREWEAEERQAKNLPKADKKAVIQHF 360
 QY 361 QEKVESLEQEAANEKQQLVETHMARVEAMLNDRKRLALENYITALQAVPPRPHVNMUK 420
 DB 361 QEKVESLEQEAANEKQQLVETHMARVEAMLNDRKRLALENYITALQAVPPRPHVNMUK 420
 QY 421 KYVRAEQKQKQHTLKHFEHVRMVDPKAAQKRSQWHLHLEVYERMGSLSLYNVPAVA 480
 DB 421 KYVRAEQKQKQHTLKHFEHVRMVDPKAAQKRSQWHLHLEVYERMGSLSLYNVPAVA 480
 QY 481 EETODEVDELLQEQNYSCDVLANNISEPRISVGNDAIMPSTLTKTIVELLPVNGHESL 540
 DB 481 EETODEVDELLQEQNYSCDVLANNISEPRISVGNDAIMPSTLTKTIVELLPVNGHESL 540
 QY 541 DQ-LQPHSEFCADSVDPANTENEVEPVDPARPAADRGGLTRPGSGITNLTKEISEVKNDAEF 600
 DB 541 DQ-LQPHSEFCADSVDPANTENEVEPVDPARPAADRGGLTRPGSGITNLTKEISEVKNDAEF 600
 QY 601 RHDSGVEVHHQKLVFFADHVGSKNGALGLMVGCVVIAIVITIVMLKKKTYTSHHGV 660
 DB 601 RHDSGVEVHHQKLVFFADHVGSKNGALGLMVGCVVIAIVITIVMLKKKTYTSHHGV 660

Qy 661 VEYDAAVTPPEERHLSKMQNGYENPTYKFFEQMNKK 697
 ID AAU07208
 AC AAU07208
 XX AAU07208
 XX AAU07208

RESULT 5
 ID AAU07208 standard; Protein: 697 AA.

DT 24-OCT-2001 (first entry)

DE Human: beta-amyloid protein precursor, APP695-KK.

XX Human: aspartyl protease 1; Asp1; nootropic; neuroprotective;

XX aspartyl protease 2; Asp2; amyloid protein precursor; APP;

XX beta-secretase; Alzheimer's disease; APP695-KK.

XX Homo sapiens.

OS WO200149097-A2.

PN 12-JUL-2001.

PD 09-MAY-2001; 2001WO-IB00797.

PF 09-MAY-2001; 2001WO-IB00797.

PR (BIEN/) BIENKOWSKI M J.

XX (GURNEY/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARODI/) PARODI L A.

PA (YANR/) YAN R.

XX Blenkowski M, Gurney ME, Heinrikson RL, Parodi LA, Yan R.

PI WPI: 2001-502548/55.

DR N-PSDB: AAS1708.

XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 protease 2, lacking Asp2 transmembrane domain and retaining beta
 secretase activity of Asp2 useful for identifying inhibitors of Asp2
 activity

PS Example 6: Page 144-146; 185pp; English.

XX The invention relates to a novel purified polypeptide comprising a
 fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 and the fragment retain the beta-secretase activity of the mammalian Asp2
 protein. Also included is an isoform of amyloid protein precursor (APP)
 comprising the amino acid sequence of a APP or its fragment containing
 an APP cleavage site recognizable by a mammalian beta-secretase, and
 further comprising two lysine residues at the carboxyl terminus of the
 amino acid sequence of the mammalian APP or APP fragment. The
 polypeptides are used for assaying for modulators of beta-secretase
 activity; identifying agents that inhibit the APP processing activity
 of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 modulate the activity of Asp2; and for reducing cellular production of
 amyloid beta (Aβ) from APP. Agents identified by the above methods
 are useful for treating Alzheimer's disease; and for identifying
 modulators of amyloid-beta (Aβ) peptide production, for use in
 designing therapeutics for the treatment or prevention of Alzheimer's
 disease. Probes and primers derived from Asp nucleic acid sequences
 are useful for detecting Hu-Asp nucleic acids in vitro assays and in
 Northern and Southern blots. The present sequence represents the
 amino acid sequence of human amyloid protein precursor, APP695-KK,
 used in the method of the invention.

XX Sequence 697 AA;

Query Match

100.0%; Score 3651; DB 22; Length 697;

Best Local Similarity 100.0%; Pred. No. 1.7e-256;		Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAFMFCGRLLNHNWQNGKWDSPSGTK	60
Db	1	MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAFMFCGRLLNHNWQNGKWDSPSGIK	60
Qy	61	TCIDTKEGILQYCOEYVPELOITNVVEANOPTVIONWCKRGKCKTHPHFVPIYRCVLVG	120
Db	61	TCIDTKEGILQYCOEYVPELOITNVVEANOPTVIONWCKRGKCKTHPHFVPIYRCVLVG	120
Qy	121	EFVSDALLVPDKCKFLHQRMDVCEHLHWHVYAKETSEKSTINLHDXGMLLPCGIDKFR	180
Db	121	EFVSDALLVPDKCKFLHQRMDVCEHLHWHVYAKETSEKSTINLHDXGMLLPCGIDKFR	180
Qy	161	GVEFVCCPLARESDNVDADAEEDSDVMWGADTDYADGSDKVVEVAEREVEAEVEE	240
Db	161	GVEFVCCPLARESDNVDADAEEDSDVMWGADTDYADGSDKVVEVAEREVEAEVEE	240
Qy	241	EADDDDEDDGDFEPEAEPEYEEATEITISATTTTTSVEEVRVPTTAASTPDV	300
Db	241	EADDDDEDDGDFEPEAEPEYEEATEITISATTTTTSVEEVRVPTTAASTPDV	300
Qy	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSQVREWEAEERQAKNLPKADKKAVIQHF	360
Db	301	DKYLETPGDENEHAHFQKAKERLEAKHREMSQVREWEAEERQAKNLPKADKKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPRPHVFNMLK	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPRPHVFNMLK	420
Qy	421	KYVRAEQDKRQHTLKHFEHVRMVDPKKAAQIRSQVYTHLRVYERMNGLSLLYNPAVA	480
Db	421	KYVRAEQDKRQHTLKHFEHVRMVDPKKAAQIRSQVYTHLRVYERMNGLSLLYNPAVA	480
Qy	481	BEIQDEVDELLOKEQNSDDVLANNISEPRISYGNALMPSLTETKTVELLPVNGEESL	540
Db	481	BEIQDEVDELLOKEQNSDDVLANNISEPRISYGNALMPSLTETKTVELLPVNGEESL	540
Qy	541	DLQPMHSPGADSVDPANTENEVEPYDARPAADRGLTTRPGSLTNIKTEEISEVKMDAEF	600
Db	541	DLQPMHSPGADSVDPANTENEVEPYDARPAADRGLTTRPGSLTNIKTEEISEVKMDAEF	600
Qy	601	RHDSGYEVHHQKLVFEAEEDVGSNKGAIIGLMVGGVVYATVITILVMLKKQYTSIHGV	660
Db	601	RHDSGYEVHHQKLVFEAEEDVGSNKGAIIGLMVGGVVYATVITILVMLKKQYTSIHGV	660
Qy	661	VEYDAAVTPPEERHLSKMQNGYENPTYKFFEQMNKK 697	
Db	661	VEYDAAVTPPEERHLSKMQNGYENPTYKFFEQMNKK 697	
RESULT 6			
AAE02587			
ID	AAE02587 standard; Protein: 697 AA.		
XX	AAE02587;		
XX	10-AUG-2001 (first entry)		
DE	Human amyloid precursor protein 695-KK (APP695-KK).		
XX	Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;		
XX	therapy; Alzheimer's disease; antialzheimer's.		
XX	Homo sapiens.		
XX	Synthetic.		
PN	WO200123533-A2.		
XX	05-APR-2001.		
XX	22-SEP-2000; 2000WO-US26080.		

XX PR 23-SEP-1999: 99US-0155493.
 XX PR 23-SEP-1999: 99US-0155493.
 XX PR 13-OCT-1999: 99US-0416901.
 XX PR 06-DEC-1999: 99US-0169232.
 XX PA (PRAA) PHARMACIA & UPJOHN CO.
 XX PI Gurney M, Bienkowski MJ;
 XX DR WP1: 2001-290516/30.
 XX DR N-PSDB: AAD36745.
 XX PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 XX PT protein, useful for the treatment of Alzheimer's disease -
 XX PS Example 6: Page 143-145; 189pp; English.
 XX CC The present invention relates to enzymes for cleaving the alpha-
 XX CC secretase site of the amyloid precursor protein (APP) and methods of
 XX CC identifying those enzymes. The methods may be used to identify enzymes
 XX CC that may be used to cleave the alpha-secretase cleavage site of the APP
 XX CC protein. The enzymes may be used to treat or modulate the progress of
 XX CC Alzheimer's disease. The present sequence is human APP695-KK. This
 XX CC sequence contains two carboxy-terminal lysine residues.
 XX SQ Sequence 597 AA;
 Query Match 100.0%; Score 3651; DB 22; Length 697;
 Best Local Similarity 100.0%; Pred No.: 7e-256;
 Matches 697; Conservative C; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLPLGALLLAAWTARAELVPTDGNAGLAEPLAMFCGRINMNMVQNGKWDSPSSTK 60
 Db 1 MLPLGALLLAAWTARAELVPTDGNAGLAEPLAMFCGRINMNMVQNGKWDSPSSTK 60
 Qy 61 TCIDTREGILOCOEYVPELOITNVVEANOPVTIONMKGRKCKTTPHPIVPECLVG 120
 Db 61 TCIDTREGILOCOEYVPELOITNVVEANOPVTIONMKGRKCKTTPHPIVPECLVG 120
 Qy 121 EFVSDALLVPDKCKFLHQFRMDVCEPHLHHTVAKFTCEKSLINLEYSMLLPSCIDKPR 180
 Db 121 EFVSDALLVPDKCKFLHQFRMDVCEPHLHHTVAKFTCEKSLINLEYSMLLPSCIDKPR 180
 Qy 181 GVEFVCCPLAESNDVSDADAEEDSDVWNGADTGYADSEKVFVEVAKHEVAVPEER 240
 Db 181 GVEFVCCPLAESNDVSDADAEEDSDVWNGADTGYADSEKVFVEVAKHEVAVPEER 240
 Qy 241 EADDDEDEDGDEVEFEAEPEPFEATERTTS-ATTTTITESVEEVVRYPTTAASPTAV 300
 Db 241 EADDDEDEDGDEVEFEAEPEPFEATERTTS-ATTTTITESVEEVVRYPTTAASPTAV 300
 Qy 301 DKYLETPGDENEHAFQKAKERLEAKHRRERMSOVKHEFESARQAKNLPKAKKAVIQHF 360
 Db 301 DKYLETPGDENEHAFQKAKERLEAKHRRERMSOVKHEFESARQAKNLPKAKKAVIQHF 360
 Qy 361 QEKVESDEQEAANERQOLVEIHMARVEAMLNDRRLALANY-TALQAVPPRPHVENMLK 420
 Db 361 QEKVESDEQEAANERQOLVEIHMARVEAMLNDRRLALANY-TALQAVPPRPHVENMLK 420
 Qy 421 KYVRAEQKQKHTLKFEHIVRMVDPKKAACISQVWTHLVRYERNQSLILYVPAVA 480
 Db 421 KYVRAEQKQKHTLKFEHIVRMVDPKKAACISQVWTHLVRYERNQSLILYVPAVA 480
 Qy 481 EEIQDEYDELLQXQNYSDVPLANNI-SEPRISYVGNALMPSTETPKITVELLPVNGEESL 540
 Db 481 EEIQDEYDELLQXQNYSDVPLANNI-SEPRISYVGNALMPSTETPKITVELLPVNGEESL 540
 Qy 541 DQAPWHSFGADSVPAANTENEVEFVDPARPAADRLTRPGSLINKIKTESEFVKMDAEF 600
 Db 541 DQAPWHSFGADSVPAANTENEVEFVDPARPAADRLTRPGSLINKIKTESEFVKMDAEF 600
 Qy 601 RHDSGYEVHQQKLVFAEDVGSNKGAIIGLMYGGVVIATVITLMLKKKQYTSIHGGV 660

Db 601 RHDSGYEVHQQKLVFAEDVGSNKGAIIGLMYGGVVIATVITLMLKKKQYTSIHGGV 660
 Qy 661 VEYDAAVTPERHESKMOONGYENPTYKFFEOMONKK 697
 Db 661 VEYDAAVTPERHESKMOONGYENPTYKFFEOMONKK 697
 RESULT 7
 ABB78596
 ID ASB78596 standard; Protein; 697 AA.
 XX AC ABB78596;
 XX PT 16-JUL-2002 (first entry)
 XX DE Human APP695-KK protein sequence SEQ ID NO:16.
 XX KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 XX KW proteolytic; amyloid precursor protein; APP.
 XX OS Homo sapiens.
 XX EN G82367060-A.
 XX XX 27-MAR-2002.
 XX PF 29-OCT-2001; 20JLGB-0025934.
 XX PR 23-SEP-1999; 99US-155493P.
 XX PR 23-SEP-1999; 99US-0404133.
 XX PR 23-SEP-1999; 99US-0404133.
 XX PR 13-OCT-1999; 99US-0416901.
 XX PR 06-DEC-1999; 99US-169232P.
 XX PR 22-SEP-2000; 2000GB-0023315.
 XX PA (PRAA) PHARMACIA & UPJOHN CO.
 XX PI Bienkowski MJ, Gurney M;
 XX DR WP1: 2002-396337/43.
 XX DR N-PSDB: ABL52463.
 XX PT Human aspartyl protease 1 substrates useful in assays to detect
 XX PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 XX PT Disease -
 XX PS Example 6: Page 114-116; 182pp; English.
 The present invention describes a human aspartyl protease 1 (hu-Asp1)
 substrate (1) which comprises a peptide of no more than 50 amino acids,
 and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 Ala-Pro. Also described are: (i) a method (II) for assaying hu-Asp1
 proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 (1) under acidic conditions; and (b) determining the level of hu-Asp1
 proteolytic activity; (2) a purified polynucleotide (III) comprising a
 nucleotide sequence that hybridises under stringent conditions to the
 non-coding strand complementary to a defined 1804 nucleotide sequence
 (see ABL52463) where the nucleotide sequence encodes a polypeptide having
 Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 domain; (3) a purified polynucleotide (III') comprising a sequence that
 hybridises under stringent conditions to (III) (the nucleotide sequence
 encodes a polypeptide further lacking a pro-peptide domain corresponding
 to amino acids 23-62 of hu-Asp1 (see ABB78596)); (4) a vector (IV)
 comprising (III) or (III') and (5) a host cell (V) transformed or
 transfected with (III), (III') and/or (IV). The hu-Asp1 protease or
 substrate (1) may be used as an enzyme substrate in assays to detect
 aspartyl protease activity, (II) and therefore diagnose diseases
 associated with aberrant hu-Asp1 expression and activity such as
 Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 sequence represents human amyloid precursor protein APP695-KK, which is
 given in an example from the present invention.

```
XX SQ Sequence 697 AA;
Query Match 100.0%; Score 3651; DB 23; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.7e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAMFCGRINMNMVQNGKWDSPSGTK 60
Db 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAMFCGRINMNMVQNGKWDSPSGTK 60
Qy 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTIONKCKRGRKCKTHPHEVPIYRCLVG 120
Db 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTIONKCKRGRKCKTHPHEVPIYRCLVG 120
Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVVEAEVEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVVEAEVEEVEE 240
Qy 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVVRVPTTAASTPDV 300
Db 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVVRVPTTAASTPDV 300
Qy 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Qy 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEOKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYERMNQSLSLLYNPFAVA 480
Db 421 KYVRAEOKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYERMNQSLSLLYNPFAVA 480
Qy 481 EELQYVDELLQKQNYSDVLANMISEPRISYNDALMPSLTKETVELLPVNGEFL 540
Db 481 EELQYVDELLQKQNYSDVLANMISEPRISYNDALMPSLTKETVELLPVNGEFL 540
Qy 541 DDLQPHWSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNKTIELSEVKMDAEF 600
Db 541 DDLQPHWSFGADSVPAANTENEVEVPDARPAADRGLTTRPGSGLTNKTIELSEVKMDAEF 600
Qy 601 RHDSGYEVHHQKLVFFAEEDVGSNGKGAIIIGLMVGQVIAIVITVIMLKKKQYTSIHGV 660
Db 601 RHDSGYEVHHQKLVFFAEEDVGSNGKGAIIIGLMVGQVIAIVITVIMLKKKQYTSIHGV 660
Qy 661 VEYDAAVTPPEERHLSKMQQNGYENPTYKFFQMQNKK 697
Db 661 VEYDAAVTPPEERHLSKMQQNGYENPTYKFFQMQNKK 697

RESULT 8
AAY88430
ID AAY88430 standard; Protein: 697 AA.
XX AC AAY88430;
XX DT 03-AUG-2000 (first entry)
XX DE Human APP695-VF-KK amino acid sequence.
XX KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
XX KW Alzheimer's disease; beta secretase site; APP695-VF-KK.
XX OS Homo sapiens.
XX PN WO200017369-A2.
XX
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PD 3C-MAR-2000.
XX 23-SEP-1999; 99MC-US20881.
XX 24-SEP-1998; 98US-0101594.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;
XX N-PSDB: AAAJ5667.
XX WPI: 2000-303269/26.
XX DR N-PSDB: AAAJ5667.
XX PT New enzyme designated human aspartase useful in research into
XX PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at
XX PT the beta secretase site to produce amyloid beta peptide -
XX PS Claim 133; Page 148-153; 183pp; English.
XX CC This sequence represents a modified version of the human amyloid
XX CC precursor protein (APP) amino acid sequence. The sequence is used in an
XX CC example of the method of the invention, to show that modification of APP
XX CC increases beta amyloid protein processing. The invention relates to a
XX CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
XX CC amyloid precursor protein (APP). The protease contains a sequence
XX CC encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
XX CC separated by 100-300 amino acids. When mutated the APP gene causes an
XX CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
XX CC surface membrane and have a single C-terminal transmembrane domain.
XX CC Proteolytic processing of APP produces the amyloid beta protein, which is
XX CC possibly very important in Alzheimer's disease. The invention includes a
XX CC nucleotide sequence encoding the protease, a vector containing the
XX CC screening for inhibitors of the protease, and a cell line comprising the vector. Methods for
XX CC screening for inhibitors of beta secretase activity are also given in the
XX CC invention. The human aspartase protein and nucleotide sequences and the
XX CC methods for identifying inhibitors of the protease, are useful in the
XX CC treatment of and research in to Alzheimer's disease.
XX SQ Sequence 697 AA;

Query Match 99.9%; Score 3646; DB 21; Length 697;
Best Local Similarity 99.9%; Pred. No. 4e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAMFCGRINMNMVQNGKWDSPSGTK 60
Db 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAMFCGRINMNMVQNGKWDSPSGTK 60
Qy 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTIONKCKRGRKCKTHPHEVPIYRCLVG 120
Db 61 TCIDTKGILQYCOEYVPELOITNVVEANQPVTIONKCKRGRKCKTHPHEVPIYRCLVG 120
Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVVEAEVEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVVEAEVEEVEE 240
Qy 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVVRVPTTAASTPDV 300
Db 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTTSVEEVVVRVPTTAASTPDV 300
Qy 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Qy 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEOKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYERMNQSLSLLYNPFAVA 480
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DB 421 KYVRAEOKDROHTLKHFHEHVMVDPKAAQIRSOVTHLRVYVERNMQSLSLYNPFAVA 480
 QY 481 EIIODEVDELLOKCNYSDDVLANMISEPRISYGNALMPSLTIETVTELLIPYNSEFSL 540
 DB 481 EIIODEVDELLOKCNYSDDVLANMISEPRISYGNALMPSLTIETVTELLIPYNSEFSL 540
 QY 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTIRGSGLTRKIBELISVKKYCAEF 600
 DB 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTIRGSGLTRKIBELISVKKYCAEF 600
 QY 601 RHDSCYEVHHOKLVFFAEDVGSNKGALIGVMGCVTATVITVLWMKKQYTSIHGV 660
 DB 601 RHDSCYEVHHOKLVFFAEDVGSNKGALIGVMGCVTATVITVLWMKKQYTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 697
 DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 697

RESULT 9
 AAEL0637 standard; protein: 597 AA.

AC AAEL0637;
 DT 10-DEC-2001 (first entry)
 DE Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.

KW Human: aspartyl protease 1; Aspl: amyloid precursor protein;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; mucotropic; neuroprotective;
 KW APP695-VF-KK; mutant; mutein.

OS Homo sapiens.
 OS Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 642 /note= "Wild-type Val substituted with Phe"

FN GB2357767-A.
 PD 04-JUL-2001.
 PF 22-SEP-2000; 2000GB-0023315.

PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.

PA (PRAA) PHARMACIA & UPJOHN CO.
 PI Bionkowsk; MJ, Gurney M;
 DR WPI: 2001-444209/48.
 DR N-PSDB: RAD17873.

XX Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease.

PS Example 8; Page 120-122; 187fp; English.

XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
 CC Aspl proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Aspl alpha-secretase

CC activity, which in turn is useful for identifying modulators of
 CC hu-Aspl alpha-secretase activity, where modulators that increase
 CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
 CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Aspl proteolytic activity. The present sequence is human amyloid
 CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence
 CC is obtained by the addition of two lysine residues (KK motif) at
 CC the C-terminus of APP695-VF isoform which is generated by the London
 CC mutation in APP695, where Val at position 642 is replaced with Phe.
 CC APP695-VF-KK isoform is useful for assaying the beta-secretase
 CC activity of human aspartyl protease 2a (hu-Asp2a) protein.

XX Sequence 597 AA:

Query Match 99.9%; Score 3546; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAMFCGRUNHMHNVQKWDSPSGTK 60
 DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAMFCGRUNHMHNVQKWDSPSGTK 60
 QY 61 TCIDTKESILQYQCEVYPELQITNVVEANQPVITQNMCKRGRKQCKTHPIHFV-PYRCLVG 120
 DB 61 TCIDTKESILQYQCEVYPELQITNVVEANQPVITQNMCKRGRKQCKTHPIHFV-PYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGDKDKR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGDKDKR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
 QY 241 EADDEDDEDEVEEAEPEYEATETTSIATTTTTESEVEEVVVPVTTAASIPDAV 300
 DB 241 EADDEDDEDEVEEAEPEYEATETTSIATTTTTESEVEEVVVPVTTAASIPDAV 300
 QY 301 DKYLETGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERCAKLPKADKKAVIQHF 360
 DB 301 DKYLETGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERCAKLPKADKKAVIQHF 360
 QY 361 QEKVESLQEAANERQQLVETIHNAKVEAMLNDRKRLALENYITLQAVPPRPRVFNMLK 420
 DB 361 QEKVESLQEAANERQQLVETIHNAKVEAMLNDRKRLALENYITLQAVPPRPRVFNMLK 420
 QY 421 KYVRAEOKDROHTLKHFHEHVMVDPKAAQIRSOVTHLRVYVERNMQSLSLYNPFAVA 480
 DB 421 KYVRAEOKDROHTLKHFHEHVMVDPKAAQIRSOVTHLRVYVERNMQSLSLYNPFAVA 480
 QY 481 FEIODEVDDELQKBNYSDDVLANMISEPRISYGNALMPSLTIETVTELLIPVNGEFSL 540
 DB 481 FEIODEVDDELQKBNYSDDVLANMISEPRISYGNALMPSLTIETVTELLIPVNGEFSL 540
 QY 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTIRGSGLTRKIBELISVKKYCAEF 600
 DB 541 DDLQPMHSFGADSVDPANTENEVEPVDPARPAADRGLTIRGSGLTRKIBELISVKKYCAEF 600
 QY 601 RHDSCYEVHHOKLVFFAEDVGSNKGALIGVMGCVTATVITVLWMKKQYTSIHGV 660
 DB 601 RHDSCYEVHHOKLVFFAEDVGSNKGALIGVMGCVTATVITVLWMKKQYTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 697
 DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMNKK 697

RESULT 10
 AAEL06867

AAE06867 standard; Protein; 697 AA.
AAE06867;
23-OCT-2001 (first entry)
Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.
Human: aspartyl protease; Asp: beta-amyloid precursor protein 695-VF-KK;
beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
neurofibrillary tangle; neuronal loss; amyloid-beta peptide; notropic;
neuroprotective; antisense therapy; gene therapy; APP695-VF-KK: mutant;
mutin.
Homo sapiens.
Synthetic.
Key location/Qualifiers
Misc-difference 642 /note= "Wild type Val substituted with Phe"
W0200150829-A2.
19-JUL-2001.
39-MAY-2001: 2001WO-1B00799.
09-MAY-2001: 2001WO-1B00799.
(BIEN/) BIENKOWSKI M J.
(GURN/) GURNEY M E.
(HEIN/) HEINRIKSON R L.
(PARO/) PARODI L A.
(FANR/) YAN R.
Hienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
WPI: 2001-483072/52.
N-PSDS: AAD13029.
Novel purified polypeptide comprising fragment of mammalian aspartyl
protease 2, lacking Asp2 transmembrane domain and retaining beta
secretase activity of Asp2 useful for identifying inhibitors of Asp2
activity -
Example 8: Page 150-152; 185pp: English.
The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
precursor protein (APP) isoforms and their corresponding DNA molecules.
Human aspartyl proteases can act as beta-secretase proteases useful for
treating Alzheimer's disease. APP isoforms are useful for identifying
modulators of amyloid-beta peptide production, for use in designing
therapeutics for the treatment and prevention of Alzheimer's disease,
dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
and neuronal loss. APP isoforms are also used in methods for identifying
inhibitors and modulators of human Asp2 activity. The invention relates
to a method for identifying agents that modulate the activity of human
aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
as a means to screen in cellular assays for the inhibitors of beta- and
gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
polymerase chain reactions (PCR). The probes are useful for detecting
Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
blots. The present sequence is modified human amyloid precursor
protein 695-VF-KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is
obtained by addition of two lys residues (XX motif) at the C-terminal
end of APP695-VF isoform. APP695-VF isoform is obtained by London V-F
mutation in APP695 isoform, where Val at position 642 is replaced with
Phe. APP695-VF-KK isoform is useful for assaying the beta-secretase
activity of human aspartyl protease 2a (Hu-Asp2a) protein.

Sequence 697 AA:

Query Match: 99.9%; Score 3646; DB 22; Length 697;

Best Local Similarity 99.9%; Pred. No. 4e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEQIAMFCGRLNMHMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEQIAMFCGRLNMHMVQNGKWDSPSGTK 60
QY 61 TCIDTKREGIILOXCOEYVPELQITNVVEANOPVTIONMKCRGRKQCKTHPHEVLPYRCLVG 120
DB 61 TCIDTKREGIILOXCOEYVPELQITNVVEANOPVTIONMKCRGRKQCKTHPHEVLPYRCLVG 120
QY 121 EFVSQALLVPDKCKFLHQRMDVDCETHLHWHTVAKETSEKSTNLHDYGMJLPCGIDKFR 180
DB 121 EFVSQALLVPDKCKFLHQRMDVDCETHLHWHTVAKETSEKSTNLHDYGMJLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATITTTTTSVEEVVRYPTTAASPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATITTTTTSVEEVVRYPTTAASPDVAV 300
QY 301 DKYLETPTGDFNEHAHFQKAKERLEAKHRMRMSQVMREWEAEAEQAKNLPKAKKAVIQHF 360
DB 301 DKYLETPTGDFNEHAHFQKAKERLEAKHRMRMSQVMREWEAEAEQAKNLPKAKKAVIQHF 360
QY 361 QEKVESLEQSAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQSAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAFQKDRQHTLKHFHVRVMDPKAAQIRSOVMTSLRVYIYERMNQSLSLYNNPVA 480
DB 421 KYVRAFQKDRQHTLKHFHVRVMDPKAAQIRSOVMTSLRVYIYERMNQSLSLYNNPVA 480
QY 481 EIQDQVDELLQKEQNYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
DB 481 EIQDQVDELLQKEQNYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DLQPMHSGFADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVKKDAEF 600
DB 541 DLQPMHSGFADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVKKDAEF 600
QY 601 RHDGSGYEVHQQKLVFPFAEDVGSNGKGAIGLMGVVVIATVIVILYMLKKKQVTSIHGV 660
DB 601 RHDGSGYEVHQQKLVFPFAEDVGSNGKGAIGLMGVVVIATVIVILYMLKKKQVTSIHGV 660
QY 661 VEYDAAVTPERHLSKMQQNGYENPTYKFEQUMONKK 697
DB 661 VEYDAAVTPERHLSKMQQNGYENPTYKFEQUMONKK 697
RESULT 11
AAU06611
ID AAU06611 standard; Protein: 697 AA.
XX AAU06611;
AC AAU06611;
XX 24-OCT-2001 (first entry)
DB 24-OCT-2001 (first entry)
DE Human: Amyloid precursor protein mutant, APP695-VF-KK.
KW Human: Aspartyl protease; Asp2b; beta-secretase; notropic;
KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; APP695-VF-KK; London mutant; mutant; mutin.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Key Misc-difference 642 /note= "Wild-type Val substituted by Phe"
FT Misc-difference 696..697
FT Misc-difference 696..697
FT /note= "2 Extra Lys residues added compared to

XX WPI: 2901-502548/55.
 DR N-PSDB: AAS11710.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX Example 8; Page 150-152; 185pp; English.
 XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, AP:695-VF-KK,
 CC used in the method of the invention.
 XX Sequence 697 AA:
 SQ

Query Match 99.9%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAMFCGRNLNMMHYQNGKWDSPSGTK 60
 Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAMFCGRNLNMMHYQNGKWDSPSGTK 60

Qy 61 TCIDTKGILQYCOEVPPELQITNWNANQDVTQNMCKGRKCKTHPIFVPIYRCLVG 120
 Db 61 TCIDTKGILQYCOEVPPELQITNWNANQDVTQNMCKGRKCKTHPIFVPIYRCLVG 120

Qy 121 EFVSDALLVPDKCFELHQRNDVCETHLHHTVAKETCSKSTNLDYGMLEPGIDKFR 180
 Db 121 EFVSDALLVPDKCFELHQRNDVCETHLHHTVAKETCSKSTNLDYGMLEPGIDKFR 180

Qy 181 GVERVCCPLAESONVSDAEDDDSDVWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
 Db 181 GVERVCCPLAESONVSDAEDDDSDVWGGADTDYADGSEDKVVEAEVEEVAEVEE 240

Qy 241 EADDDDEDDGDEVEEAEVEEATERTISIAITTTTTSVEFVVRVPTTASTDPAV 300
 Db 241 EADDDDEDDGDEVEEAEVEEATERTISIAITTTTTSVEFVVRVPTTASTDPAV 300

Qy 301 DKYLETPGDENEHAFKAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVTORF 360
 Db 301 DKYLETPGDENEHAFKAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVTORF 360

Qy 361 QEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPREFVNMK 420
 Db 361 QEKVESLEQEANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPREFVNMK 420

Qy 421 KYVRAEQDRGHTLKHFEHVRWDPKKAQIRSQVMTHLRIYIERMNSQLLYNVPAVA 480
 Db 421 KYVRAEQDRGHTLKHFEHVRWDPKKAQIRSQVMTHLRIYIERMNSQLLYNVPAVA 480

Qy 481 EEIQDEVELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540

Db 481 EEIQDEVELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
 Qy 541 DDLOPWHSTGADSVPAANTENEPVDARPAADAGLTTRPGSGLTNKTKTEISVKWDAEF 600
 Db 541 DDLOPWHSTGADSVPAANTENEPVDARPAADAGLTTRPGSGLTNKTKTEISVKWDAEF 600

Qy 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAIVITLVLMLKKKQYTSIHGV 660
 Db 601 RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIAIVITLVLMLKKKQYTSIHGV 660

Qy 661 VEYDAAVTPFERHLSKMQQNGYENPTYKPFQEQMNKK 697
 Db 661 VEYDAAVTPFERHLSKMQQNGYENPTYKPFQEQMNKK 697

RESULT 13
 AAE02589
 ID AAE02589 standard; Protein; 697 AA.
 XX AAE02589;
 AC AAE02589;
 XX 10-AUG-2001 (first entry)
 XX Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
 XX Human; alpha-secretase; therapy; amyloid precursor protein 695-VF-KK;
 KW APP695-VF-KK; Alzheimer's disease; antialzheimer's.
 XX Homo sapiens.
 OS Synthetic.
 XX WC200123533-A2.
 XX 05-APR-2001.
 XX 22-SEP-2000; 2000MO-US26080.
 XX 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WC-0520881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX (PRAA) PHARMACIA & UPJOHN CO.
 XX Gurney M, Bienkowski MC;
 PI WPI: 2001-290516/30.
 DR N-PSDB: AAD06747.
 XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease -
 XX Example 8; Page 149-151; 189pp; English.
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-VF-KK. This
 CC sequence is characterised by a v to f alteration at position 642
 CC and contains two carboxy-terminal lysine residues.
 XX Sequence 697 AA:
 SQ

Query Match 99.9%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 4e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0:

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPPQIAMFCGRNLNMMHYQNGKWDSPSGTK 60
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QY 61 TCIDTREGILOVCOEYVPELQITNVVEANQPTIQNMCKRGKQCKTHPHFVPIYRCIVG 120
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 QY 121 EFVSDALLVPDKCKFLHQRMDVCEIHLHWHIVAKETCSKSTNLHDYGMLLPGDIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCEIHLHWHIVAKETCSKSTNLHDYGMLLPGDIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPYEEATERTTSIATTTTTTTSVEEVVVPVTTAASTPDV 300
 DB 241 EADDDDEDDGDEVEEAEPYEEATERTTSIATTTTTTTSVEEVVVPVTTAASTPDV 300
 QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 QY 361 QEKVESLEOEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 DB 361 QEKVESLEOEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 QY 421 KYVRAECKDRQHTLKHFERHVMYDPKKAQIRSCVMIHLRVYIERNQSLSLYNVPAVA 480
 DB 421 KYVRAECKDRQHTLKHFERHVMYDPKKAQIRSCVMIHLRVYIERNQSLSLYNVPAVA 480
 QY 481 EETQDEVELLQEQNVSDIVLANMSEPRISYGNDAIMPSTLETITVELLPVNGEFSL 540
 DB 481 EETQDEVELLQEQNVSDIVLANMSEPRISYGNDAIMPSTLETITVELLPVNGEFSL 540
 QY 541 DDLQPHSFGADSVPAANTEVEPVDAARPAADRGLTTPGSGSLTNIKTEISEVKNDAFF 600
 DB 541 DDLQPHSFGADSVPAANTEVEPVDAARPAADRGLTTPGSGSLTNIKTEISEVKNDAFF 600
 QY 601 RHDSGVEVHQKLVFAEDVGSNGKALIGLWGVGVVIAIVITLVNKKKQVTSIHGV 660
 DB 601 RHDSGVEVHQKLVFAEDVGSNGKALIGLWGVGVVIAIVITLVNKKKQVTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
 DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 14
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 AC ABB78598 standard: Protein: 697 AA.
 AC ABB78598
 UI 16-JUL-2002 (first entry)
 DE Human APP695-VF-KK protein sequence SEQ ID NO:20.
 KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 KW proteolytic; amyloid precursor protein; App.
 OS Homo sapiens.
 PN GB2367060-A.
 PD 27-MAR-2002.
 XX 29-OCT-2001: 2001GR-0025934.
 PR 23-SEP-1999: 99JUS-155493P.
 PR 23-SEP-1999: 99WO-0404133.
 PR 13-OCT-1999: 99US-04:6901.
 PR 06-DEC-1999: 99US-162322P.
 PR 22-SEP-2000: 2000GB-0023315.

XX (PHAA) PHARMACIA & UPHOHN CO.
 PA Blenkowski MJ, Gurney M.
 XX WPI: 2002-396337/43.
 DR N-PSDB: ABL52465.
 XX Human aspartyl protease 1 substrates useful in assays to detect
 PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
 PT disease -
 XX Example 8: Page 120-122: 182pp; English.
 PS The present invention describes a human aspartyl protease 1 (hu-Asp1)
 CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-
 CC Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (1) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (III') comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)
 CC comprising (III) or (III') and (5) a host cell (V) transformed or
 CC transfected with (III), (III') and/or (IV). The hu-Asp1 protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents human amyloid precursor protein APP695-VF-KK, which
 CC is given in an example from the present invention.
 XX SQ Sequence 697 AA;
 QY Query Match 99.9%; Score 3646; DB 23; Length 697;
 DB Best Local Similarity 99.9%; Pred. No. 4e-255;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGIALLLAANTARALEVPTDGNAGLLAEPLQAMFCGRINMHNMVQNGKWDSPSGTK 60
 DB 1 MLPGIALLLAANTARALEVPTDGNAGLLAEPLQAMFCGRINMHNMVQNGKWDSPSGTK 60
 QY 61 TCIDTREGILOVCOEYVPELQITNVVEANQPTIQNMCKRGKQCKTHPHFVPIYRCIVG 120
 DB 61 TCIDTREGILOVCOEYVPELQITNVVEANQPTIQNMCKRGKQCKTHPHFVPIYRCIVG 120
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 DB 121 EFVSDALLVPDKCKFLHQRMDVCEIHLHWHIVAKETCSKSTNLHDYGMLLPGDIDKFR 180
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 DB 241 EADDDDEDDGDEVEEAEPYEEATERTTSIATTTTTTTSVEEVVVPVTTAASTPDV 300
 QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
 QY 361 QEKVESLEOEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
 DB 361 QEKVESLEOEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420

Qy 421 KYVRAEQKDRQHTLKHFEHVMVDPKAAQIRSOVMTHLRVYERMNQSLILNYPAVA 460
 Db 421 KYVRAEQKDRQHTLKHFEHVMVDPKAAQIRSOVMTHLRVYERMNQSLILNYPAVA 460
 Qy 481 EETDEYDELLQKQNYSCDVLANMISEPRISYGNALMPSLTSTKTVELLPVNGEFSL 540
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 Qy 541 DDLQPHSFSGADSVDPANTENEPVDPARPAADRLGTLTPRSGSLTNKTEISEVKMDAEF 600
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 Qy 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNK 697
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RESULT 15
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 ID AAY88429 standard; Protein: 697 AA.
 XX
 AC AAY88429;
 DT C3-AUG-2000 (first entry)
 XX
 DE Human APPSW-KK amino acid sequence.
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 KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
 KW Alzheimer's disease; beta secretase site; APPSW-KK.
 XX
 OS Homo sapiens.
 XX
 PN WO200017369-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 23-SEP-1999; 95WO-US20881.
 XX
 PR 24-SEP-1998; 98US-0101594.
 XX
 PA (PhAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney ME, Bienkowski NJ, Heinrichson RL, Parodi LA, Yan F;
 XX
 DR WPI: 2000-303209/26.
 DR N-PSDB: AAA15666.
 XX
 P: New enzyme designated human aspartase useful in research into
 P: Alzheimer's Disease is capable of cleaving amyloid protein precursor at
 P: the beta secretase site to produce amyloid beta peptide .
 XX
 PS Claim 133; Page 143-147; 183pp; English.
 XX

This sequence represents a modified version of the human amyloid precursor protein (APP) amino acid sequence. The sequence is used in an example of the method of the invention, to show that modification of APP increases beta amyloid protein processing. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DSG or DTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. CC proteolytic processing of APP produces the amyloid beta protein, which is CC possibly very important in Alzheimer's disease. The invention includes a CC nucleotide sequence encoding the protease, a vector containing the CC nucleotide sequence, and a cell line comprising the vector. Methods for CC screening for inhibitors of beta secretase activity are also given in the CC invention. The human aspartase protein and nucleotide sequences and the

CC methods for identifying inhibitors of the protease, are useful in the
 CC treatment of and research in to Alzheimer's disease.
 XX
 SQ Sequence 697 AA;
 Query Match 99.8%; Score 3643; DB 21; Length 697;
 Best Local Similarity 99.7%; Pred. No. 6.6e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 14:00:39 : Search time 39 Seconds
(without alignments)
2827.550 Million cell updates/sec

Title: US-09-806-194-16

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Scoring table: BLOSUM62
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Searched: 587654 seqs, 15812981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA:*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3651	100.0	697	9	US-09-795-847-16 Sequence 16, Appl
3	3651	100.0	697	9	US-09-794-743-16 Sequence 16, Appl
4	3651	100.0	697	9	US-09-794-748-16 Sequence 16, Appl
5	3651	100.0	697	9	US-09-794-925-16 Sequence 16, Appl
6	3651	100.0	697	9	US-09-681-442-16 Sequence 16, Appl
7	3651	100.0	697	11	US-09-869-414-16 Sequence 16, Appl
8	3651	100.0	697	11	US-09-548-366-16 Sequence 16, Appl
9	3646	99.9	697	9	US-09-794-927-20 Sequence 20, Appl
10	3646	99.9	697	9	US-09-795-847-20 Sequence 20, Appl
11	3646	99.9	697	9	US-09-794-743-20 Sequence 20, Appl
12	3646	99.9	697	9	US-09-794-748-20 Sequence 20, Appl
13	3646	99.9	697	9	US-09-794-925-20 Sequence 20, Appl
14	3646	99.9	697	9	US-09-681-442-20 Sequence 20, Appl
15	3646	99.9	697	11	US-09-869-414-20 Sequence 20, Appl

16	3646	99.9	697	11	US-09-548-366-20	Sequence 20, Appl
17	3643	99.8	697	9	US-09-794-927-18	Sequence 18, Appl
18	3643	99.8	697	9	US-09-795-847-18	Sequence 18, Appl
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20	3643	99.8	697	9	US-09-794-748-18	Sequence 18, Appl
21	3643	99.8	697	9	US-09-794-925-18	Sequence 18, Appl
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23	3643	99.8	697	11	US-09-869-414-18	Sequence 18, Appl
24	3643	99.8	697	11	US-09-548-366-18	Sequence 18, Appl
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26	3641	99.7	695	9	US-09-795-847-10	Sequence 10, Appl
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28	3641	99.7	695	9	US-09-794-748-10	Sequence 10, Appl
29	3641	99.7	695	9	US-09-794-925-10	Sequence 10, Appl
30	3641	99.7	695	9	US-09-681-442-10	Sequence 10, Appl
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36	3636	99.6	695	15	US-10-169-580-3	Sequence 1, Appl
37	3636	99.6	695	9	US-09-794-927-14	Sequence 14, Appl
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ALIGNMENTS

RESULT :

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US-09-794-927-16
; Sequence 16, Application US/09794927
; Patent No. US20010018324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Blenkowski, Michael J.
; APPLICANT: Heinikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16

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Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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US-09-795-847-16
: Sequence 16, Application US/09755847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, ADP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: US95
: FILE REFERENCE: 29341/6280DE
: CURRENT APPLICATION NUMBER: US/09/795,847
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/-55,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23

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RESULT 3

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US-09-794-743-16
: Sequence 16, Application US/09794743
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang

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: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-795-847-16

Query Match      100.0%; Score 3651; DB %; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,1e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLALLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHMVQNGKNDSPSGTK 60
DB 1 MLPGALLALLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHMVQNGKNDSPSGTK 60
QY 61 TCIDITKEGILQYCOEYVPELOITNVVEANGPVTIONWCKKCKCKTHPHFVPIYRCJVG 120
DB 61 TCIDITKEGILQYCOEYVPELOITNVVEANGPVTIONWCKKCKCKTHPHFVPIYRCJVG 120
QY 121 EFVSDALLVPDKCKFLHGERMOCVCEHILHWHITVAKETCSEKSTNLHDYGMILLPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHGERMOCVCEHILHWHITVAKETCSEKSTNLHDYGMILLPGGIDKFR 180
QY 181 GVEFVCCPLAESDNVSADAEEDSDVVMWGGADTDYAGSDEKVVVEVAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVSADAEEDSDVVMWGGADTDYAGSDEKVVVEVAEVEAEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEEATERTTSIAITTTTTSVEEVEVVRVPTTAASTPDAV 300
DB 241 EADDEDEDEGDEVEEAEPEEATERTTSIAITTTTTSVEEVEVVRVPTTAASTPDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMRWEAEAEAKNLPRADKKAIVQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMRWEAEAEAKNLPRADKKAIVQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITLQAVPPRRHVFNNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITLQAVPPRRHVFNNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVMYDPKKAQIRSOVMTHLRVYVERMQSLSLYNNPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVMYDPKKAQIRSOVMTHLRVYVERMQSLSLYNNPVA 480
QY 481 EIQDEVEDELLOKEQNYSDVLANMISEPRISYGNALMPSLTIETKTVELLPVNGEFSL 540
DB 481 EIQDEVEDELLOKEQNYSDVLANMISEPRISYGNALMPSLTIETKTVELLPVNGEFSL 540
QY 541 DDLQPHWSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNKTEETSEVKMDAEF 600
DB 541 DDLQPHWSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNKTEETSEVKMDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNGKAGIIGLMVGGVVIATVITLVMLKKKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNGKAGIIGLMVGGVVIATVITLVMLKKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFEQMONKK 697
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFEQMONKK 697

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; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND

; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMEFCGRLNHMNVQNGKWDSPGSK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMEFCGRLNHMNVQNGKWDSPGSK 60
QY 61 TCIDTKESILQYCOEVPYPELQITNVVEANQPVTIQNNCKRGRKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKESILQYCOEVPYPELQITNVVEANQPVTIQNNCKRGRKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEAEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTSTESVEEVVPTTAASTPDV 300
DB 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTSTESVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNLK 420
DB 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNLK 420
QY 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480
DB 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480
QY 661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMNKK 697

661 VEVDAAVTPERHLSKMQNGYENPTYKFFEQMNKK 697

RESULT 4

US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMEFCGRLNHMNVQNGKWDSPGSK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMEFCGRLNHMNVQNGKWDSPGSK 60
QY 61 TCIDTKESILQYCOEVPYPELQITNVVEANQPVTIQNNCKRGRKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKESILQYCOEVPYPELQITNVVEANQPVTIQNNCKRGRKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGGAOTDYADGSEDKVVEAEVEEAEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTSTESVEEVVPTTAASTPDV 300
DB 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTTSTESVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNLK 420
DB 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNNLK 420
QY 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSOVMTHLVRVIERMQSLSLLYNPAVA 480
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DB 481 EEIQDEVDLQEQNYSDVLANNKISEPRISYGNDA:MPSLTETKTIIVELLVNGEFSL 540
QY 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSG:LNKIKTEISEVKKMAEF 600
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DB 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSG:LNKIKTEISEVKKMAEF 600
QY 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVYATIV:VTLVNLKKKQYTSIHGGV 560
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DB 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVYATIV:VTLVNLKKKQYTSIHGGV 560
QY 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQCNKK 597
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DB 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQCNKK 597

RESULT 5
US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280H:
; CURRENT APPLICATION NUMBER: US/09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPQ:AMFCGRLNMHMNVQNGKNSDPSGK 60
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DB 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPQ:AMFCGRLNMHMNVQNGKNSDPSGK 60
QY 61 TCIDTKEGILQYQCVYPELQITNVVEANQPVTIQNMCKRGRKCKTHPHFVYRCLVG 120
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DB 61 TCIDTKEGILQYQCVYPELQITNVVEANQPVTIQNMCKRGRKCKTHPHFVYRCLVG 120
QY 121 EFVSDALLVPCKKFLHQBMDVCETHLHWHTVAKETQSKSTNLHDYGMLLPCGDKXER 180
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DB 121 EFVSDALLVPCKKFLHQBMDVCETHLHWHTVAKETQSKSTNLHDYGMLLPCGDKXER 180
QY 181 GVEFVCCPLAESDNVDSADAEDDDSVMMGGADTDYADSSDKVVEAEAEAEVVEFE 240
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DB 181 GVEFVCCPLAESDNVDSADAEDDDSVMMGGADTDYADSSDKVVEAEAEAEVVEFE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTT:SIATTTTTFESVEEVVVPPTTAA:SPDAV 400
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DB 241 EADDEDEDDGDEVEEAEPEEATERTT:SIATTTTTFESVEEVVVPPTTAA:SPDAV 300
QY 301 DKYLETPGDENEHAFPOKAKERLEAKHRERMSOVNREWEAEARQAKNLPRADKKAV:QHF 360
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DB 301 DKYLETPGDENEHAFPOKAKERLEAKHRERMSOVNREWEAEARQAKNLPRADKKAV:QHF 360
QY 301 QKVESLEQEAEANPRQQLVETHMARVEAMLNDRRLALENYITALQAVPRPHVFNKIK 420
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DB 301 QKVESLEQEAEANPRQQLVETHMARVEAMLNDRRLALENYITALQAVPRPHVFNKIK 420
QY 421 KYVRAEQKDRQHTLKHFEBHVRMDPKKAAQ:RSOVMTHLRLVIYERMNOS:SLLYNPAVA 480
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DB 421 KYVRAEQKDRQHTLKHFEBHVRMDPKKAAQ:RSOVMTHLRLVIYERMNOS:SLLYNPAVA 480
QY 481 EEIQDEVDLQEQNYSDVLANNKISEPRISYGNDA:MPSLTETKTIIVELLVNGEFSL 540
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 481 EEIQDEVDLQEQNYSDVLANNKISEPRISYGNDA:MPSLTETKTIIVELLVNGEFSL 540
QY 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSG:LNKIKTEISEVKKMAEF 600
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DB 541 DDLQPHSFGADSVDPANTENEVEPVDARPAADRG:LTTRPGSG:LNKIKTEISEVKKMAEF 600
QY 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVYATIV:VTLVNLKKKQYTSIHGGV 660
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DB 601 KHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVYATIV:VTLVNLKKKQYTSIHGGV 660
QY 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQCNKK 697
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DB 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQCNKK 697

RESULT 6
US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.le-225;
Matches 597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPQ:AMFCGRLNMHMNVQNGKNSDPSGK 60
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
DB 1 MLPGALLLLAAWTARALEVPTDGNAGLLAEPQ:AMFCGRLNMHMNVQNGKNSDPSGK 60
QY 61 TCIDTKEGILQYQCVYPELQITNVVEANQPVTIQNMCKRGRKCKTHPHFVYRCLVG 120
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Db 122 EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCSKSTNLDYGNLPLPGIDKFR 180
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QY 361 QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
Db 361 QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
Db 421 KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
QY 481 EIQDEVDLLOKQONYSDDVLANMISEPRISYGNDAIMPSTTKTIVELLPVNGEESL 540
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Db 541 DLQPHWSFGADSVPAANTEVEPVDPADPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIATVITVLMLKKKQYTSIHGV 660
Db 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIATVITVLMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 7
US-09-869-414-16
: Sequence 16, Application US/09369414
: Publication No. US2003007226A1
: GENERAL INFORMATION:
: APPLICANT: Beinowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: FILE REFERENCE: 28342/6280M
: CURRENT APPLICATION NUMBER: US/09/869,414
: PRIOR FILING DATE: 2001-06-27
: PRIOR FILING DATE: 09/416,901
: PRIOR FILING DATE: 1998-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-869-414-16
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Query Match 100.0%; Score 3651; DB 11; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,1c-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPLGLALLLAATARALEVPTDGNAGLLAEPQIAFMFCGRLLNMHMNTYONGKWDSDPSGK 60
Db 1 MLPLGLALLLAATARALEVPTDGNAGLLAEPQIAFMFCGRLLNMHMNTYONGKWDSDPSGK 60
QY 61 TCIDTKEGILQYCCQVEVPELQITNNVEANQPTVQNMCKRGKQCKTHPHFVPIYRCLVG 120
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QY 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCSKSTNLDYGNLPLPGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTVAKETCSKSTNLDYGNLPLPGIDKFR 180
QY 181 GVEFVCCPLAESUNVDSADAEEDSDVWVGADTDYADGSDKVVVEVAEEVEE 240
Db 181 GVEFVCCPLAESUNVDSADAEEDSDVWVGADTDYADGSDKVVVEVAEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIAITTTTITTESVEEVVRVPTAASTPDV 300
Db 241 EADDDDEDDGDEVEEAEPEYEATERTTSIAITTTTITTESVEEVVRVPTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVWREWEAEARQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVWREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
Db 361 QKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
Db 421 KYVRAEQKDROHTLKHFEHVRVMDPKKAAQIRSOVWTHLRVIYERMNOSLSLLYNPVA 480
QY 481 EIQDEVDLLOKQONYSDDVLANMISEPRISYGNDAIMPSTTKTIVELLPVNGEESL 540
Db 481 EIQDEVDLLOKQONYSDDVLANMISEPRISYGNDAIMPSTTKTIVELLPVNGEESL 540
QY 541 DLQPHWSFGADSVPAANTEVEPVDPADPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
Db 541 DLQPHWSFGADSVPAANTEVEPVDPADPAADRGLTTRPGSLTNIKTFEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIATVITVLMLKKKQYTSIHGV 660
Db 601 RHDGSEYVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIATVITVLMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 8
US-09-548-366-16
: Sequence 16, Application US/09548366
: Publication No. US20030104365A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
: FILE REFERENCE: 28341/6280A
: CURRENT APPLICATION NUMBER: US/09/548,366
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
```

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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-366-16

Query Match
  100.0%; Score 3651; DB 11; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.2e-225;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MLPLGALLLLAANTARALEVPTDGNAGLLAEPAQIAMFCGRLLNMHNMVQNGKWDSPSGTK 60
DB 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPAQIAMFCGRLLNMHNMVQNGKWDSPSGTK 60
QY 61 ICIDTREGILQYCOEYVPELOITNVVEANQPTIQWCKRGKCKCTHPIHFVYPCVLG 120
DB 61 ICIDTREGILQYCOEYVPELOITNVVEANQPTIQWCKRGKCKCTHPIHFVYPCVLG 120
QY 121 EFVSDALLVPDKCKFCHQERMDVCETHLHWHYVAKETSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFCHQERMDVCETHLHWHYVAKETSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEVEE 240
QY 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
DB 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEAEAEQAENLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEAEAEQAENLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLNLNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLNLNYPAVA 480
QY 481 EPIQDEVDELLOKEQYSDSVLANMISEPRISYGNDAIMPSTLTKITVELLPVNGEFS 540
DB 481 EPIQDEVDELLOKEQYSDSVLANMISEPRISYGNDAIMPSTLTKITVELLPVNGEFS 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
QY 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEYDAAVTPERHLSKMQQNGYENPTYKPFQEQMNKK 697
DB 661 VEYDAAVTPERHLSKMQQNGYENPTYKPFQEQMNKK 697
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RESULT 9

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US-09-794-927-20
; Sequence 20. Application: US/09794927
; Patent No. US20010016324a1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michae. J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
```

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; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: CSES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/415,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-20
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Query Match 99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPAQIAMFCGRLLNMHNMVQNGKWDSPSGTK 60
DB 1 MLPLGALLLLAANTARALEVPTDGNAGLLAEPAQIAMFCGRLLNMHNMVQNGKWDSPSGTK 60
QY 61 TCIDTREGILQYCOEYVPELOITNVVEANQPTIQWCKRGKCKCTHPIHFVYPCVLG 120
DB 61 TCIDTREGILQYCOEYVPELOITNVVEANQPTIQWCKRGKCKCTHPIHFVYPCVLG 120
QY 121 EFVSDALLVPDKCKFCHQERMDVCETHLHWHYVAKETSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFCHQERMDVCETHLHWHYVAKETSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEVEE 240
QY 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
DB 241 EADDEDEDEDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVVVPITAASTPDV 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEAEAEQAENLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEAEAEQAENLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLNLNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFHVRMVDPKKAAQIRSQVMTHLRVYIERMNSLNLNYPAVA 480
QY 481 EPIQDEVDELLOKEQYSDSVLANMISEPRISYGNDAIMPSTLTKITVELLPVNGEFS 540
DB 481 EPIQDEVDELLOKEQYSDSVLANMISEPRISYGNDAIMPSTLTKITVELLPVNGEFS 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEISEVKMDAEF 600
QY 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSCYEVHHQKLVFAEDVGSNKGAIIGLMWGGVVIATVITLVMLKKKQYTSIHGV 660
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QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMKNK 697
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMKNK 697

RESULT 10

US-09-795-847-20
: Sequence 20, Application US/09795847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S D-SEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280DE
: CURRENT APPLICATION NUMBER: US/09/795.847
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-795-847-20

Query Match 99.9% Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMYVNGKWDSPSGIK 60
DB 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMYVNGKWDSPSGIK 60
QY 61 TCIDTKESILQYCOEVYPELOITNVVEANQPVTIQNCKRGRKCKKTHPHFVPIYRCVLG 120
DB 61 TCIDTKESILQYCOEVYPELOITNVVEANQPVTIQNCKRGRKCKKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240
QY 241 FADDDDEDDGDEVEEAEPEYEATERITTSIAITTTTTTSTVEEVRVPTTAATPDV 300
DB 241 FADDDDEDDGDEVEEAEPEYEATERITTSIAITTTTTTSTVEEVRVPTTAATPDV 300
QY 301 DYLETPTGDEHAHFQAKERLEAKHREMSQVNVREWEAEERQAKNLPKADKKAVIQIF 360
DB 301 DYLETPTGDEHAHFQAKERLEAKHREMSQVNVREWEAEERQAKNLPKADKKAVIQIF 360
QY 361 QEKVLEQEAANEERQQLVETHMARVEAMLDNRRLALENITALQAVPPRRHVFNMK 420
DB 361 QEKVLEQEAANEERQQLVETHMARVEAMLDNRRLALENITALQAVPPRRHVFNMK 420
QY 421 KYVRAEQDKROHTLKHFEHVRVMDPKKAAQIRSQVTHLRLVIERMNOSLSLLYNPAPA 480
DB 421 KYVRAEQDKROHTLKHFEHVRVMDPKKAAQIRSQVTHLRLVIERMNOSLSLLYNPAPA 480

DB 421 KYVRAEQDKROHTLKHFEHVRVMDPKKAAQIRSQVTHLRLVIERMNOSLSLLYNPAPA 480
QY 481 EIQDEYDELLQKEQNSDYLANMISEPRISYNDALMPSLJETKTTVELLPVNGEFSL 540
DB 481 EIQDEYDELLQKEQNSDYLANMISEPRISYNDALMPSLJETKTTVELLPVNGEFSL 540
QY 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTEELSEVKMDAEF 600
DB 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTEELSEVKMDAEF 600
QY 601 RHDGSGYEVHHOKLVFFAEDVGSNGKGAIIGLMWGOWIATVITVLVMLKKQYISIHGV 660
DB 601 RHDGSGYEVHHOKLVFFAEDVGSNGKGAIIGLMWGOWIATVITVLVMLKKQYISIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMKNK 697
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMKNK 697

RESULT 11

US-09-794-743-20
: Sequence 20, Application US/09794743
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280BC
: CURRENT APPLICATION NUMBER: US/09/794.743
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-743-20

Query Match 99.9% Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMYVNGKWDSPSGIK 60
DB 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMYVNGKWDSPSGIK 60
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DB 61 TCIDTKESILQYCOEVYPELOITNVVEANQPVTIQNCKRGRKCKKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCFLHQRMDVCETHLHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWGWGADTDYADGSEDKVVEAEVEAEVEE 240


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-20

Query Match      99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNYONGKWDSDPSGK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNYONGKWDSDPSGK 60
QY 61 TCIDTKEGILQYCOEVPYPELOITNVVEANQPVTIONMCKRGKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEVPYPELOITNVVEANQPVTIONMCKRGKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAEESNVDSDAEDDDSDVMWGGADTDYADGSEDKVVEABEEVAEVEE 240
DB 181 GVEFVCCPLAEESNVDSDAEDDDSDVMWGGADTDYADGSEDKVVEABEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTTSTESVEEVVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTTSTESVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERCAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERCAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNKLK 420
DB 361 QEKVESLEQEAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNKLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMKNOSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMKNOSLSLLYNVPAVA 480
QY 481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
DB 481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGTLTTRPGSLTNIKTEEISEVKMDAEF 600
DB 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGTLTTRPGSLTNIKTEEISEVKMDAEF 600
QY 601 RHDSSGEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSSGEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 14
US-09-681-442-20
; Sequence 20, Application US/09581442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/6280fg
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; CURRENT APPLICATION NUMBER: US/09/681.442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 05/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 05/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-20
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Query Match      99.9%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 2.2e-225;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNYONGKWDSDPSGK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNYONGKWDSDPSGK 60
QY 61 TCIDTKEGILQYCOEVPYPELOITNVVEANQPVTIONMCKRGKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEVPYPELOITNVVEANQPVTIONMCKRGKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAEESNVDSDAEDDDSDVMWGGADTDYADGSEDKVVEABEEVAEVEE 240
DB 181 GVEFVCCPLAEESNVDSDAEDDDSDVMWGGADTDYADGSEDKVVEABEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTTSTESVEEVVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERITTSIATTTTTTSTESVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERCAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAEERCAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNKLK 420
DB 361 QEKVESLEQEAANEKQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNNKLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMKNOSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMKNOSLSLLYNVPAVA 480
QY 481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
DB 481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGTLTTRPGSLTNIKTEEISEVKMDAEF 600
DB 541 DDLOPWHSGADSVDPANTENEVEPVDARPAADRGTLTTRPGSLTNIKTEEISEVKMDAEF 600
QY 601 RHDSSGEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSSGEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 15

US-09-869-414-20
: Sequence 20, Application US/09869414
: Publication No. US2003007226A1
: GENERAL INFORMATION:
: APPLICANT: Bejakowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280M
: CURRENT APPLICATION NUMBER: US/09/869,414
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 66/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2. C
: SEQ ID NO 20
: LENGTH: 697
: TYPE: CPT
: ORGANISM: Homo sapiens
US-09-869-414-20

Query Match: 99.9%, Score 3646, DB 11, Length 697;
Best Local Similarity 99.9%, pred. No. 2,2e-225;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MLPGIALLLAATARALEVPTDGNAGLLAEPQIAMECGRLNMHNQVONCKWSDPSGTK	60
DB	1	MLPGIALLLAATARALEVPTDGNAGLLAEPQIAMECGRLNMHNQVONCKWSDPSGTK	60
QY	61	TC:DTKEGILQYCOEVPPELQITNVVEANQVPTIONCKKGRKCKTHPHFVPIYRCLVG	120
DB	61	TC:DTKEGILQYCOEVPPELQITNVVEANQVPTIONCKKGRKCKTHPHFVPIYRCLVG	120
QY	121	EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKECTCEKSTNLHDYGMLLPCGIDKFR	180
DB	121	EFVSDALLVPDKCKFLHQERMDVCETHLHMTVAKECTCEKSTNLHDYGMLLPCGIDKFR	180
QY	181	GVEFVCCPLAESDNVDSADAEEDSDSVMMGGADTDYADGSEDKVEVEAEVEEVEE	240
DB	181	GVEFVCCPLAESDNVDSADAEEDSDSVMMGGADTDYADGSEDKVEVEAEVEEVEE	240
QY	241	EADDDDEDDGDEVEEEAEPEEATERTTSTATTITTTTSTESVEEVVPTTAASTPDV	300
DB	241	EADDDDEDDGDEVEEEAEPEEATERTTSTATTITTTTSTESVEEVVPTTAASTPDV	300
QY	301	DKYLETPGDENEHAFQKAKERLEAKHREKNSQVMKWEAEARQAKNLPKADKAVTORF	360
DB	301	DKYLETPGDENEHAFQKAKERLEAKHREKNSQVMKWEAEARQAKNLPKADKAVTORF	360
QY	361	QEKVESLQEAANEQQQLVETMARVEAMLNDRRLALENVITAIQAVPPRPHVFNKCK	420
DB	361	QEKVESLQEAANEQQQLVETMARVEAMLNDRRLALENVITAIQAVPPRPHVFNKCK	420
QY	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQ:RSQVMTHLRVYIERMNOSLSLLYNPVA	480
DB	421	KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQ:RSQVMTHLRVYIERMNOSLSLLYNPVA	480
QY	481	BEIQDEVDHLLQKQENYSDVLANMISEPRIYNDALMPSLTETKTVELLPYNGEFSI	540
DB	481	BEIQDEVDHLLQKQENYSDVLANMISEPRIYNDALMPSLTETKTVELLPYNGEFSI	540
QY	541	DDLQPHSFSGADSVFANTENEVEPVDPADRDGLTTRPGSGLNTKTEISEVKMDAEF	600
DB	541	DDLQPHSFSGADSVFANTENEVEPVDPADRDGLTTRPGSGLNTKTEISEVKMDAEF	600

QY	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAIVITLVMLKKKQYTSIHGV	660
DB	601	RHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVIAIVITLVMLKKKQYTSIHGV	660
QY	661	VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK	697
DB	661	VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK	697

Search completed: October 2, 2003, 14:18:35
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 : Search time 16.6667 seconds
(without alignments)
4021.774 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651

Sequence: 1 MLPGLALLLAATARALEV.....QQNGYENPYKFFEQMUNKK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3641	99.7	695	1 A49795	Alzheimer's disease
2	3590.5	98.3	770	1 QRHUA4	Alzheimer's disease
3	3344	97.1	695	2 S00550	Alzheimer's disease
4	3519	96.4	695	2 A27485	Alzheimer's disease
5	3103	85.0	747	2 JH0773	Alzheimer's disease
6	2105	57.7	484	4 A32761	hypothetical Alzhe
7	1728	47.3	763	2 A49321	amyloid beta (A β)
8	1716	47.0	765	2 S42880	amyloid precursor-
9	1704	46.7	751	2 A49974	beta-amyloid precu
10	1185	32.5	653	2 A46362	amyloid precursor-
11	1143	31.3	511	2 JG1404	CDEI-box DNA-bind
12	817.5	22.4	686	2 T15795	hypothetical prote
13	747	20.5	886	2 A32758	beta-amyloid-like
14	706	19.3	246	2 S38344	CDEI-binding prote
15	411	11.3	82	2 PQ0438	Alzheimer's disease
16	296.5	9.1	191	2 A35981	sperm membrane pro
17	283	7.8	57	2 E60045	Alzheimer's disease
18	283	7.8	57	2 F60045	Alzheimer's disease
19	283	7.8	57	2 G60045	Alzheimer's disease
20	283	7.8	57	2 D60045	Alzheimer's disease
21	283	7.8	57	2 B60045	Alzheimer's disease
22	283	7.8	57	2 A60045	Alzheimer's disease
23	217	5.9	42	2 PN0512	beta-amyloid prote
24	192.5	5.3	1110	2 I51116	NF-180 - sea lamp
25	186	5.1	5170	2 T15348	hypothetical prote
26	185.5	5.1	407	1 EBBEQ3	immediate-early pr
27	185.5	5.1	993	2 S49461	synaptonemal compl
28	182	5.0	522	2 I32444	hypothetical prote
29	175.5	4.8	802	1 S48529	NAB3 protein - yea

zinc finger protei
microtubule bindin
hypothetical prote
150K golgi antigen
geldolin-related p
caldesmon - humar
h-caldesmon - chis
neurofilament trip
myelin transcript1
glutamate rich pro
gene 11-1 protein
tropoin I, cardia
hypothetical prote
ATP-dept. acyl-CoA
transcription fact
myod protein inhib

175.5 4.8 1188 2 146608
174.5 4.8 464 2 H90279
174.5 4.8 884 2 J20405
174 4.8 579 2 JH0823
174 4.8 1087 2 J30330
173.5 4.8 793 1 JH0628
172 4.7 771 1 A33430
172 4.7 784 2 FN0009
172 4.7 1182 2 T30189
171 4.7 1271 2 A45555
170 4.7 1948 2 S00485
169.5 4.6 298 1 TP0UTC
169.5 4.6 721 2 S29795
169 4.6 885 2 G71608
169 4.6 1187 2 T46637
168.5 4.6 675 2 T03744

ALIGNMENTS

RESULT 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Seikoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human suppo
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote
C:Keywords: alternative splicing

Query Match 99.7%; Score 3641; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 1 MLPGLALLLAATARALEVPTDGNAGLLAEPOIAMEFCGRLLMHNVQNGKWDSDPSGSK 60
Db 1 MLPGLALLLAATARALEVPTDGNAGLLAEPOIAMEFCGRLLMHNVQNGKWDSDPSGSK 60
Q7 TCIDTKEGILCYCOEYVPELOITNVVEANOPVTIONCKRGRKOCKTTPHFVTPYRCLVG 120
Db TCIDTKEGILCYCOEYVPELOITNVVEANOPVTIONCKRGRKOCKTTPHFVTPYRCLVG 120
Q7 EFVSDALLVPKCKFLHQRMDVCETHLHWHIVAKELCSEKSTNLHYGMLLPGGIDKFR 160
Db EFVSDALLVPKCKFLHQRMDVCETHLHWHIVAKELCSEKSTNLHYGMLLPGGIDKFR 160
Q7 GVEFVCCPLAESPNVDSADAEDDDSDVMWGGADTDYADGSEDKVFAVEEEVAEVEE 240
Db GVEFVCCPLAESPNVDSADAEDDDSDVMWGGADTDYADGSEDKVFAVEEEVAEVEE 240
Q7 EADDDEDEGDEVEEFAEPEYEATERITSIATTTTTSVEEVEVVRVPTTAASTPDV 300
Db EADDDEDEGDEVEEFAEPEYEATERITSIATTTTTSVEEVEVVRVPTTAASTPDV 300
Q7 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMREWEAEERQAKNLPRADKAVIQHF 360
Db DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMREWEAEERQAKNLPRADKAVIQHF 360
Q7 QEKVESLEQEAANERQQLVETHMARVEMLNDRLALENYITALQAVPPRPHVFNMLK 420
Db QEKVESLEQEAANERQQLVETHMARVEMLNDRLALENYITALQAVPPRPHVFNMLK 420
Q7 KYVRAEQKROHTLKHFHVRMVDPKAAQIRSOVMTHLRVIERMNSLILLYNPVAVA 480
Db KYVRAEQKROHTLKHFHVRMVDPKAAQIRSOVMTHLRVIERMNSLILLYNPVAVA 480

Db 421 KYVRAEQKORHTLKFEHVRWDPKKAQIRSQVTHLRVIERMNOQSLSLIYNVPAVA 480
 QY 481 EEIQDEVDELLOKEQNYSDVLANMISEPRI SYGNDALMPSITEIKTTVELLPVNGEFSL 540
 Db 481 EEIQDEVDELLOKEQNYSDVLANMISEPRI SYGNDALMPSLTEIKTTVELLPVNGEFSL 540
 QY 541 DLOPHNSGCAUSVPANTENEPVDARPAARGLITRPGSGSLTNIKTEISEVKNDAEP 600
 Db 541 DDQPHNSGCAUSVPANTENEPVDARPAARGLITRPGSGSLTNIKTEISEVKNDAEP 600
 QY 601 RHDSGVEVHHQKLVFAEDYGSNKGAIIGLMVGGVVIATVIVITLMLKKKYTSIHHCY 660
 Db 601 RHDSGVEVHHQKLVFAEDYGSNKGAIIGLMVGGVVIATVIVITLMLKKKYTSIHHCY 660
 QY 661 RHVDAATVTEERHLSKMQONGYENPTYKFFEQMKN 695
 Db 661 VEYDAATVTEERHLSKMQONGYENPTYKFFEQMKN 695
 RESULT 2
 ORCUA4
 Alzheimer's disease amyloid beta protein precursor (validated) - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xia inhibitor
 N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence revision 28-Jul-1995 #text change 15-Sep-2000
 C:Accession: S05194; A32277; A33260; A35426; 73452; I30451; I36453; I59562; A44
 468; A28583; A29302; A60805; J00038; S06121; A60355; A59011; A38384; S25076; S98322; S3
 K:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayre, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PrA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded i
 A:Reference number: S02260; MUID:89128427; PMID:2783775
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13456
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL data Library, November 1983
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:q35598; PIDN:CAA31830.1; PID:q871360
 A:Note: alternative splice form APP(695)
 R:LaFauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870; PMID:2538123
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GR:M24546; GB:M24547; NID:q341203; PIDN:AAQ13654.1; PID:q5-6074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030; PMID:2675937
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 655-737 <JOH>
 A:Cross-references: GR:M29270; NID:q178863; PIDN:AAA51768.1; PID:q178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244; PMID:2196678
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikawa, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318; PMID:2110105
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:q178613; PIDN:AA859502.1; PID:q178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from
 A:Molecule type: DNA
 A:Residues: 1-530, 'QMLNPVPAFWAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:q178608; PIDN:AA859501.1; PID:q178615
 R:Yoshikawa, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168; PMID:1908403
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, F.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral h
 A:Reference number: I39453; MUID:90260663; PMID:2111584
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:q178618; PIDN:AAA51727.1; PID:q178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Al
 A:Reference number: I59562; MUID:90222553; PMID:1925564
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'P', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:q236720; PIDN:AA19991.1; PID:q236721
 R:Kakino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; And
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; M
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds fo
 A:Reference number: A44017; MUID:93035397; PMID:1415269
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:q257377; PIDN:AA823645.1; PID:q257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:q257379; PIDN:AA823646.1; PID:q257380
 A:Experimental source: familial Alzheimer disease family LT
 A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik,
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-
 A:Reference number: A03134; MUID:87144572; PMID:2881207
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:q28525; PIDN:CAA68374.1; PID:q28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovasc
 A:Reference number: A29030; MUID:87231971; PMID:3035574
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:q178539; PIDN:AAA51722.1; PID:q178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:38312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, I.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:38264430; PMID:2968552
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1573681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase inhibitor
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane *status predicted <TM>

Query Match 97.1%; Score 3544; DB 2: Length 695;
Best Local Similarity 97.3%; Pred. No. 5e-179;
Matches 676; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MLPGALLLAATWATALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60
DB 1 MLPSALLLAATWATALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTIQNCKGRKQCKTHPEHFVPIYRCLVG 120
DB 61 TCIGTKEGILQYCOEYVPELQITNVVEANQPTIQNCKGRKQCKTHPEHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180

QY 181 GVEFVCCPLAESDSNVDSDAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDSNVDSDAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTIESVEEYVRYPTTAASTPDVAV 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTIESVEEYVRYPTTAASTPDVAV 300

QY 301 DKYLETPGNEHAHQKAKERLEAKHREMSQVREWEAEARQAKNLKADKAVIQHF 360
DB 301 DKYLETPGNEHAHQKAKERLEAKHREMSQVREWEAEARQAKNLKADKAVIQHF 360

QY 361 OEKVESLEQEAANERQOLVETIHARVEAMLNDRRLALENYITALQAVPRPRHVNMLK 420
DB 361 OEKVESLEQEAANERQOLVETIHARVEAMLNDRRLALENYITALQAVPRPRHVNMLK 420

QY 421 KYVRAEQRQHTLKHFEHVRMYDPKAAQIKRSQVTHLRYVERNMQSLSLCYRYPVAV 480
DB 421 KYVRAEQRQHTLKHFEHVRMYDPKAAQIKRSQVTHLRYVERNMQSLSLCYRYPVAV 480

QY 481 EETQDEVDLLOKEQNSDVLNMISEPRISYGNALMPSYETKTTVELLPVNGHPSL 540
DB 481 EETQDEVDLLOKEQNSDVLNMISEPRISYGNALMPSYETKTTVELLPVNGHPSL 540

QY 541 DDLPWHSFGADSVPAANTENVEVPDARPAADRLTTRPGSGLTNIKTEITSEVKMDAEF 600
DB 541 DDLPWHSFGADSVPAANTENVEVPDARPAADRLTTRPGSGLTNIKTEITSEVKMDAEF 600

QY 601 RHDSCYEVHHOKLAVFFAEDVGSNKGAIIGLMVGVIATVITLVMKKKQYTSIHGV 660
DB 601 RHDSCYEVHHOKLAVFFAEDVGSNKGAIIGLMVGVIATVITLVMKKKQYTSIHGV 660

QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMQN 695
DB 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMQN 695

RESULT 4
A27485
A:Title: Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
A:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 *sequence_revision 31-Mar-1989 *text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein.
A:Reference number: A27485; MUID:86106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M.8373; NID:g191568; PIDN:AAA37139.1; PID:g309085
A:Experimental source: brain
R:De Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1229, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210 'G', 212-220, 'S', 222-396, 'A', 398-402, 'I', 404-448, 'A', 450-695 <STR
A:Cross-references: EMBL:X59379
R:Zimml, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzhe
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Status: translated from GB/ENBL/2DRJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type protei
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 96.4%; Score 3519; DB 2: Length 695;
Best Local Similarity 96.8%; Pred. No. 1e-177;
Matches 673; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 MLPGALLLAATWATALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60
DB 1 MLPSALLLAATWATALEVPDGNAGLLAEPOIAFMCGRLNHHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTIQNCKGRKQCKTHPEHFVPIYRCLVG 120
DB 61 TCIGTKEGILQYCOEYVPELQITNVVEANQPTIQNCKGRKQCKTHPEHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180

QY 181 GVEFVCCPLAESDSNVDSDAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDSNVDSDAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTIESVEEYVRYPTTAASTPDVAV 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTIESVEEYVRYPTTAASTPDVAV 300

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Db 241 EADDDDEVDGDEVEEAESEPYEAEATERTTSIATTTTTTIESVEEVVRVPTTAASITDAV 400
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEFAERQAKNLPKADKKAVIOHF 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEFAERQAKNLPKADKKAVIOHF 360
QY 361 QKVESLEQZAAENERQOLVETIHARVEMALNDRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQZAAENERQOLVETIHARVEMALNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFHEHVMYDPPKAAQIRSOVMTHLRVIVYERANQOSLSLLYNYPAVA 480
Db 421 KYVRAEQKDRQHTLKHFHEHVMYDPPKAAQIRSOVMTHLRVIVYERANQOSLSLLYNYPAVA 480
QY 481 EETQDEVDLLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
Db 481 EETQDEVDLLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSL 540
QY 541 DDLQPHSHFGADSVPAANTEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKKHDAEP 600
Db 541 DDLQPHSHFGADSVPAANTEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKKHDAEP 600
QY 601 RHDSGYEVHROKLVFFAEDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
Db 601 RHDSGYEVHROKLVFFAEDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMON 695
Db 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1993
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MGID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:52417; NID:g263150; PID:AAE24853.1; PID:g26315;
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein: animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 85.08; Score 3103; DB 2; Length 747;
Best Local Similarity 81.08; Pred. No. 8.3e-156;
Matches 598; Conservative 35; Mismatches 41; Indels 64; Gaps 5;

QY 17 ALEVPTDGNAGLLAEPOIAMP-CRLNMNMVQNGKWDSPSGFKTIDTKESGLQVQGE 75
Db 15 ALEVLDVNGGLAEPOIAMPFSAVLNMNMVQNGKWDSPSG---CIGTKESGLQVQGE 71
QY 76 VYPELQITNVVYEAQNPVTIONMCKRGKQCKTHPHFVIPYRCILVGFVSVDALLVPDKCKF 135
Db 72 VYPELQITNVVYEAQNPVTIONMCKRGKQCKTHPHFVIPYRCILVGFVSVDALLVPDKCKF 131
QY 136 LQERMOVCFTHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDND 195
Db 132 LQERMDICTEHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDND 191
QY 196 VDSADAEEDSDVMWGADTDYADGSEDKVVEVAEVEEVEEAEADDEDDEDEGE 253
Db 192 FDSADAEEDSDVMWGADTDYADGSEDKVVEVAEVEEVEEAEADDEDDEDEGE 249
QY 254 VEEAEPEYEATERTTSIATTTTTTIESVEEVVR----- 288
Db 254 VEEAEPEYEATERTTSIATTTTTTIESVEEVVR----- 288

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Db 250 ABEEDPEPEYEATERTTSIATTTTTTIESVEEVVRVSEQAETGPCRAMISRWYDYDTE 309
QY 289 -----VPTTAASTPDADVDKYLETPGDENEHAHFQ 317
Db 310 SKCAQFIVGGCGGNRNKFNESDDYCMVAGCSVTPATAASTPDADVDKYLENPNNDENEDRFL 369
QY 318 KAKERLEAKHRERMSQVMREWEAEFAERQAKNLPKADKKAVIOHFQKVESLEQZAAENERQO 377
Db 370 KAKERLEAKHRERMSQVMREWEAEFAERQAKNLPKADKKAVIOHFQKVESLEQZAAENERQO 429
QY 378 LVEITHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKYYVRAEQKDRQHTLKHF 437
Db 430 LVEITHMARVEAMLNDRRLALENYITALQADPPRPHVFNMLKYYVRAEQKDRQHTLKHF 489
QY 438 EHVHVMYDPPKAAQIRSOVMTHLRVIVYERANQOSLSLLYNYPAVAEBEIQDEVDLLOKEQNY 497
Db 490 EHVHVMYDPPKAAQIRSOVMTHLRVIVYERANQOSLSLLYNYPAVAEBEIQDEVDLLOKEQNY 549
QY 498 SDDVLANMISEPRISYGNDAIMPSTETKTIVELLPVNGEFSLDDLOQFHWHSFGADSVPA 557
Db 550 SDDVMNMVSDHRVSYGNDAIMPSTETKTIVELLPVNGEFSLDDLOQFHWHSFGADSVPA 609
QY 558 TENVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEFRHDSGYEVHROKLVFFA 617
Db 610 TENVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDSEYRHDIAVEVHROKLVFFA 669
QY 618 EDVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGVVVEVDAAVTPPEERHLSKM 677
Db 670 EEVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTIHHGVVVEVDAAVTPPEERHLSKM 729
QY 678 QQNGYENPTYKFEQMON 695
Db 730 QQNGYENPTYKFEQMON 747

RESULT 6
A32761
Hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:De Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain
C:Keywords: cloning artifact

Query Match 57.7%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 1.4e-103;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;

QY 80 LQIINVYEAQNPVTIONMCKRGKQCKTHPHFVIPYRCILVGFVSVDALLVPDKCKFLHCE 139
Db 1 LQIINVYEAQNPVTIONMCKRGKQCKTHPHFVIPYRCILVGFVSVDALLVPDKCKFLHCE 60
QY 140 RMDVCETHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDNDVSA 199
Db 61 RMDVCETHLHWHTVAKETCSKSTNLHDYGNLLPCGIDKFRGVFCVCCPLAESDNDVSA 120
QY 200 DAEEDSDVMWGADTDYADGSEDKVVEVAEVEEVEEAEADDEDDEDEGEDEVEEAE 259
Db 121 DAEEDSDVMWGADTDYADGSEDKVVEVAEVEEVEEAEADDEDDEDEGEDEVEEAE 180
QY 260 EPEYEATERTTSIATTTTTTIESVEEVVR----- 288
Db 181 EPEYEATERTTSIATTTTTTIESVEEVVR----- 240

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QY 289 -----VPTTAISIPDAVKYLETGSDNEHAHFQAKAKR 323
Db 241 FYGGGGRNNFTREYCMVCGSAIPTTAASIPDAVKYLETGSDNEHAHFQAKAKR 300
QY 324 EAKHRRMSQVREWEAEQAKNLPKADKAVIQHFQKVESLQEAANERQQLVETIM 383
Db 301 EAKHRRMSQVREWEAEQAKNLPKADKAVIQHFQKVESLQEAANERQQLVETIM 360
QY 384 ARVEAMLNDRRLALENYITAIQAVPPRRPHVFNMLKKYVAFQKQKHFKHFRMV 443
Db 361 ARVEAMLNDRRLALENYITAIQAVPPRRPHVFNMLKKYVAFQKQKHFKHFRMV 420
QY 444 DPKKAQIRSQVNTHLRVYERMNQSLSLYNYPAVAEEIQEV 487
Db 421 DPKKAQIRSQVNTHLRVYERMNQSLSLYNYPAVAEEIQEV 464

RESULT 7
A49321
amyloid beta (A4) homolog 2 precursor - human
K:Alternate names: CDE1-binding protein
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-A-g-1993
C:Accession: A49321; S34644; S40519
R:Spracher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ex
A:Reference number: A49321; MUID:93250009; PMID:8485127
A:Accession: A49321
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: GB:S60099; NID:9300168; PIDN:AAAC60589.1; PID:9300169
A:Experimental source: placenta
A>Note: Sequence extracted from NCHI backbone (NCHIN:131198, NCBI:P:131198)
A>Note: Expression was shown in placenta, brain, heart, lung, liver, and kidney
R:Von der Kammer, H.; Klaunder, J.; Hanes, J.; Scheit, K.H.
submitted to The EMBL Data Library, April 1993
A:Description: The human homologue of the murine CDE1-binding protein is an amyloid pre
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <ON>
A:Cross-references: EMBL:222572; NID:9394763; PIDN:CAA80295.1; PID:9394764
R:Waco, W.; Gurubagavatula, S.; Paradis, M.; Romano, D.M.; Siodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94035131; PMID:8220435
A:Accession: S40519
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:9450391; PIDN:AAAC41701.1; PID:9450392
C:Genetics: GB:APLP2; APLP2
A:Gene: GB:APLP2; APLP2
A:Cross-references: GB:139159; ONIM:104776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.3%; Score 1728; DB 2; Length 763;
Best Local Similarity 47.1%; Pred. No. 1.7e-83;
Matches 372; Conservative 112; Mismatches 165; Indels 140; Gaps 20;

QY 5 LALLILAAWTARALEV-----PTDGAG---LAEQIAKFCGRLLNMHWNGKWDSP 56
Db 15 LLLLLVGLTAPALAGVIEALAAAGTGFAVEQIAKFCGRLLNMHWNIQTGWEP 74
QY 57 SGTKTCIDTIGLQYCOEYPELQITNVVNEQPTVQWCKGRKCKGKIHPEFV 116
Db 75 TGTKSCFEKEEVLOQCQENYPELQITNVVNEQPTVQWCKGRKCKGK---RFTVP 132

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QY 117 CLVGEFYSDALLVPDKCKFHQERQVQVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGI 176
Db 133 CLVGEFYSDVLLVPEKQCFHKEKMEVCENHQHWHVTYVKEACITQGMILYSYGMLLPCGV 192
QY 177 DKRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSDKVVVEAEVEEVAE 236
Db 193 DQFHTGEVCCPQTKIGTSVSKKEEEDDEE-----EEDEDEEDDYDYKSEFFTEAD 245
QY 237 VFE--EEA--DQDDDDDDGDEVEEAEPEY-----EEATERTTISATTTTTES 282
Db 246 LEDFTEAAVCEDDDEDEEGEVEEDRDYVYDTFKGDDYNEENPTPEGSDGTMSDKETHD 305
QY 283 VEEV-----VVP 290
Db 306 VKAVCSQEAITGPCRAVMPRWYFDLSKKGCVRFYTGCGGGRNNFESDEYCMVCKRAMIP 365
QY 291 TTAASIPDAVKYLETGSDNEHAHFQAKAKERLEAKHRRMSQVREWEAEQAKNLPK 350
Db 366 PTPLEPND--VDVYFETSDADNEHAFQAKAKQLIRHNRMDRVYKEMBEAELOAKNLPK 424
QY 351 ADKXAV-QHFOEKVESLEQEAANERQQLVETIMHARVEAMLNDRRLALENYITAIQAVPP 410
Db 425 AERQTEIQHFQAVKALEKEAAASEKQQLVETHLARVEAMLNDRRLALENYITAIQAVPP 484
QY 411 RPRHVFNMKKYVRAEQKDRQHLKHFHEHVRVMDPKAAQIRSOVMTHLRYVIERMNSL 470
Db 485 RPRILQALRYVRAENKDRHLIRHQHVLAVDPEKAAQKSOVMTHLRYVIERMNSL 544
QY 471 SLLYNPVAEAEIQDEVDDELQKQENYSDVVIANLSEPRISYGNDAIMPGLTETKTIVE 530
Db 545 SLLKVPYVAQEIQEEIDELIQEQF-----ADM-----DQFTASISPEVDVR 587
QY 531 LLPVNGEFS--DDLQPMHSGADSVNPANTEVEPVDPARPADROLITTPGSCILN----- 585
Db 586 ---VSSES-EEIPFPFPP--HPFPAJFENE-----DTQPELYHPM--KKGSGVGEQDGL 635
QY 586 IKTEE--ISFVKMDAEFRHDSGVVHROKLVFAEDVGS-----NKG 625
Db 636 IGAEKVINSKNKYDENMVIDETLDV--KEMTFNARVGVGLEEERESVGPLRDFSLSS 692
QY 626 AITGLMGVGVVIATVIVITVNLKKQYTSIIHGVVEVDAAVTPPEERHLSKMOONGYENP 685
Db 694 ALIGLLVIAVAIATVIVISVNLKRGYQTISHGIVEVDPMITPEERHLNKNMHNQYENP 753
QY 686 TYKFEQMQ 694
Db 754 TYKLEQMQ 762

RESULT 8
S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid p
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type protein

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C:Keywords: alternative splicing

F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.0%; Score 1716; DB 2; Length 765;
Best Local Similarity 46.2%; Pred. No. 7.2e-83;
Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;

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QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPQIAMFCGRNHHMNVQNGKWDSDP 56
DB 15 LVLLLLGLGTAPAAALAGYIEALANAGTGFAVAEPQIAFMFCGLNNHVNIOCTGKWEPPD 74
QY 57 SGTKICIDITKEGILQYCOEYVPELQITNVZANGPVTIONNCKRGKCKOCTHPHFVPIYR 116
DB 75 TGTKSLCTGKEVLGYCOEYVPELQITNVMEANQPNVDSNCRDRKQCKRS--HIVIPFK 132
QY 117 CLVGFFVSADLLVPDKCKFLHQERMDVCETHLHHHTVAKETCSEKSTNHHYGNMLPCGI 176
DB 133 CLVGFEVDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSGMLPCGV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYA--DGSEDKVYVVAEEER 233
DB 193 DQFHGTGYVCCPQTKVYDSSTMSKEEBEE---DEEEDYALCKSEFTPEADJEDFT 248
QY 234 VAEVEEBEADDEDEDDEVEEAEPEYEE-----ATERTISTATTTTITTESVEEV 287
DB 249 EAAADEDEEBEVEEVEEDRDYYDSFKGDDYNEENPTPESSDGLISDREIAHDV 308
QY 288 R-----VPT 291
DB 309 KAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNRNNFESEDCYMAVKTMIIPR 368
QY 292 TAASPTDAVDKYLETPGDENEHAHFQAKERLEAKHRRMSQVMPWEAEASQAKNLPKA 351
DB 369 TPLPTND--VDYFETSADNEHARFQAKERLEIHRHRMDRVKKEEAEELQAKNLPKA 427
QY 352 DKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRJALENYITALQAVPR 411
DB 428 ERQTLIQHFOAMVKALEKAASEKQOLVETHLARVEAMLNDRRRJALENYLAALQSDPR 487
QY 412 PRHVFNMKKYVRAEQKQROHTLKHFEHVRMVDPKKAAQIRSQVTHLKVYERKNQSL 471
DB 488 PHRIQLARRYVRAENKDRLHTIRHYOVLAVDPEKAAQMSQVTHLHVIERKNQSL 547
QY 472 LLYNPVAAEEIQDEVDLQEKQNSDDVLANNMISEPRISYGNDAIMPSTICTIVEL 531
DB 548 LLYKPYVAQELQESIDELQEQR-----ADM-----DQTSISSSENTPVDVR- 589
QY 532 LPVNGEFLDCLQPHSFQADSPANTENEVEPVDAHFAADRGLTTPGSGLTN----- 586
DB 590 --VSSEES--EIPFPHPF--HPFPPLSENE---DTPQLVYHPM--KXSGMAEEDGLI 638
QY 587 KTEE---ISEVKMAEAFRHDSGYEVHHQKLVFFAEVGS-----NKGA 626
DB 639 GAFEVKNSKNKMDENMVIDETLDV--KEMIFNAERVGGCLKEEPDSVGPQREDFSSSA 696
QY 627 IIGLVGVGVVIAIVITVLMLKKQYTSIHGVEVDAAVTPEERHLSKMGQCYENPT 686
DB 697 IIGLVVIAVIAIVITVISLMLKKQYGTISHGIVEVHPMLTPEERHLNKKGNHYENPT 756
QY 687 YKFFEQMQ 694
DB 757 YKYLEQMQ 764
```

RESULT 9

A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999

C:Accession: A49974

R:Slunt, H.H.; Thirakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.

J. Biol. Chem. 269, 2637-2644, 1994

A:Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid

A:Reference number: A49974; MUID:94132029; PMID:8306594

A:Accession: A49974

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-751 <SU3>

A:Cross-references: GB:C15571; NID:g558467; PIDN:AAA0603.1; PID:g558468

A:Note: sequence extracted from NCBI backbone (NCBIP:144636)

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote

F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.7%; Score 1704; DB 2; Length 751;
Best Local Similarity 45.9%; Pred. No. 3e-82;
Matches 363; Conservative 113; Mismatches 159; Indels 156; Gaps 20;

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QY 5 LALLLLAANTARALEV-----PTDGNAG---LIAEPQIAMFCGRNHHMNVQNGKWDSDP 56
DB 15 LVLLLLGLGTAPAAALAGYIEALANAGTGFAVAEPQIAFMFCGLNNHVNIOCTGKWEPPD 74
QY 57 SGTKICIDITKEGILQYCOEYVPELQITNVZANGPVTIONNCKRGKCKOCTHPHFVPIYR 116
DB 75 TGTKSLCTGKEVLGYCOEYVPELQITNVMEANQPNVDSNCRDRKQCKRS--HIVIPFK 132
QY 117 CLVGFFVSADLLVPDKCKFLHQERMDVCETHLHHHTVAKETCSEKSTNHHYGNMLPCGI 176
DB 133 CLVGFEVDVLLVPDNCQFFHQERMEVCEKHQRWHTLVKEACLTEGLTLYSGMLPCGV 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVWVGADTDYADGSEDKVYVVAE---E 231
DB 193 DQFHGTGYVCCPQTKVYDSSTMSKEEBEE---DEEEDYDLDKSEFPTE 243
QY 232 BEVAVEEBEAD--DEDEDGDEVEEE-----AEPYEEATERTISTATTI 276
DB 244 ADLEDFTAAADEEBEVEEVEDRDYYDFFKDDYNEENPTPESEGTIS----- 298
QY 277 TTTTSEVEV----- 286
DB 299 --DKIEVHDVKAVCSQEAMTGPCRAVMPRWYFDLSKGKCVRFYGGCGGNRNNFESEDCY 356
QY 287 -----VRVPTTAASPTDAVDKYLETPGDENEHAHFQAKERLEAKHRRMSQVMPWEAEA 341
DB 357 MAVCKAMIPPTPIPTND--VDYFETSADNEHARFQAKERLEIHRHRMDRVKKEWEEA 415
QY 342 ERQAKNLPKADKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRJALENY 401
DB 416 ELQAKNLPKTPERQTLIQHFOAMVKALEKAASEKQOLVETHLARVEAMLNDRRRJALENY 475
QY 402 ITALQAVPPRRHVFNMKKYVRAEQKQROHTLKHFEHVRMVDPKKAAQIRSQVTHLVR 461
DB 476 LAALQSDPPRPHRIQLARRYVRAENKDRLHTIRHYOVLAVDPEKAAQMSQVTHLHV 535
QY 462 IYHRMNSLSLLYNPVAAEEIQDEVDLQEKQNSDDVLANNMISEPRISYGNDAIMP 521
DB 536 IERNSNLSLLYKVPYVAQELQESIDELQEQR-----ADM-----DQTS 578
QY 522 LTERKTIVELLPVNGEFLDCLQPHSFQADSPANTENEVEPVDAHFAADRGLTTPGSG 591
DB 579 ISENPVSVRSSESE--EIPFPHPF--HPFPPLSENE-----PSLSENE-----GSGMAEQD 621
QY 582 GLTNKTRTET--SEVKMAEAFRHDSGYEVHHQKLVFFAEVGS-----N 623
DB 622 GLIGAEKVKNSKNKMDENMVIDETLDV--KEMIFNAERVGGLEEEEPESVGPQREDFSL 679
QY 624 KGALIGLVGVGVVIAIVITVLMLKKQYTSIHGVEVDAAVTPEERHLSKMGQCYE 683
DB 680 SNALIGLVVIAVIAIVITVISLMLKKQYGTISHGIVEVDPMLTPEERHLNKKGNHYE 739
QY 684 NPTKYFEQMQ 694
DB 740 NPTKYLEQMQ 750
```

RESULT 10

A46362

amyloid precursor-like protein; - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Wasco, W.; Bupp, K.; Magendanz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer's disease amyloid beta protein; animal Kuritz-type protease
 A:Reference number: A46362; MUID:93066322; PMID:1279693
 A:Accession: A46362
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence inconsistent with NCBI backbone (NCBI:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kuritz-type protease
 C:Keywords: transmembrane protein

Query Match 32.5%; Score 1185; DB 2; Length 653;
 Best Local Similarity 38.6%; Pred. No. 4, 9e-55;
 Matches 270; Conservative 121; Mismatches 231; Indels 78; Gaps 17;

QY 1 MEGALLALLAAMTARA-LEVPDGNAGLAEPIAMFCGRLLNMNVONGKQSDPSGT 59
 DB 22 LPL-LSLAIAOLAVGNLAVGSPSAAPGSAOVAGLCGRLLTHRLDNLGWRPFPQS 80
 QY 60 KTCIDTKEGILQYCOEYVPELQITNVYEAQPVITIGNWKGRKCKCKTHPFI-VIFYRCL 118
 DB 81 RRLDLPQVLYCYROMYFELHIAVEQAQAIPMEWCGGTSGRCALPHVEVYFHLCL 140
 QY 119 VGEFSDALLVPDKKFLHQRMDVCEHLHWHITVAKC:CEKSTNLHDYGLMPCGIDK 178
 DB 141 PGFVSEALLVPGCRFLHQRMDVCESTRHOENAGACSSGGLILHSGMALLPGSGSR 200
 QY 179 FRGVFVCCPLAESDNVSDADEEDUDVW-WGACIDYACSEPKVYVEAFEEVAEV 237
 DB 201 FRGVFVCCP-PPAIPNPSGMAAGDSTKSWPLGGR-AAAAAGGED-EEVES 248
 QY 238 EEEFAEDDEDEGDEVEEAEPYEAETERTISATITTTESVEVVRVPT-AASTP 297
 DB 249 PQVDQYFVEPPQAEDEEEERAPPSPHTPVKSVRTPTPR-PT-PT-PT-PT-PT-PT-PT 294
 QY 298 DAVDKYLETPGDENEHAFQKAKERLEAKHRRMSQVHWEFAERQAKNIPKADKAVI 357
 DB 295 DGVGVYFGMPGETGEHEGF-KAKMDLEERKMRQINEMKRENAMDSQSKLEKADQALN 354
 QY 358 QHFQEKVESLEQANERQOLVETHMARVEAM-NDRRRLALENYITALQAVPRPKHVEN 417
 DB 355 EHFQSTIQTLDEQVSGERQKLVETHATRVITAI:INDQRRALFGFTAAALQDPPQAE:RVLM 414
 QY 418 MLKKYVRAEQQRHTLKHFHVRVMDPKKAAQIRSQVMTHLRVYERNQSLSLYVNP 477
 DB 415 ALRRYLRAEQKEQRHTLRH:QHVAAVDPEKAQMRFOVTHLOVIERKNGSLGLLDQNP 474
 QY 478 AVAEELODEVDELQKQNYSDVLANLMISEPRI:SYGNDAIMP-SUTETKTCTVGL:PVNG 536
 DB 475 HLAQELRPQTELL-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA-AAAAA 510
 QY 537 EFS:DDLOPHSFGADSVPAANTENEVPVDARAAORGLTTRGSGLLINIKTEISEVVK 596
 DB 511 -----GSLQP-----PSKDDPPVTLF-PSKDDQSSSSGREGKITPLEQYEQ 551
 QY 597 DAEFRHDSGYEVHH-OK-VFFAEVDGSKNGA:IGLMVGGVVIAIVITVLM-LKKQ 652
 DB 552 KVNASAPRGFPFHSSDIQRLDELAPSGTGVSRREALSGLLINGAGGSLIV:SLLLLRKKRP 611
 QY 653 YTSIHGQVEVDAVTPPEERHLSKMQONGYENTYKFFEQ 692
 DB 612 YGT:SHGWEVDPMLTLEEQQLRELQGHGYNPTYFLEE 651

RESULT 11
 JCI1404

CDEI-box DNA-binding protein; - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
 C:Accession: JCI1404
 R:Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
 Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
 A:Title: A murine sequence-specific DNA binding protein shows extensive local similarity
 A:Reference number: JCI1404; MUID:93129193; PMID:1482349
 A:Accession: JCI1404
 A:Molecule type: mRNA
 A:Residues: 1-511 <VID>
 C:Comment: This protein plays an important role in the early development of the mouse
 C:Keywords: DNA binding; transmembrane protein

Query Match 31.3%; Score 1143; DB 2; Length 511;
 Best Local Similarity 45.8%; Pred. No. 5, 8e-53;
 Matches 253; Conservative 92; Mismatches 128; Indels 80; Gaps 16;

QY 174 CGIDKFRGVFVCCPLAE--ESUNVDSADAEEDSDVMGADTDYAPGSEDKYVEVAE- 230
 DB 6 CGVDFHGTETVCCPQ:KTVDSDTSMKEEEEE-----DEDEEEDYDLKSEF 56
 QY 231 --EEVAVEVEEAD-DEDEDEKIDEVEEAE-----EPYEAETERTISATITTTI 279
 DB 57 PTEAEEDFTFAAADDEEED:EEEGEEVEVEDRDYVDFPKGDYNE--ENPTSPSSEGTIS 314
 QY 280 TESVEEVVRVPTTAAS:PDADVKYLETPGDENEHAFQKAKERLEAKHRRMSQVHWE 339
 DB 115 KKEIVHDVKKVPTPLPTND-VDVIFETSADNNEHAFQKAKERLEIRNRMRVKKEWE 173
 QY 340 EAERQAKNIPKADKAVI:QHFQEKVESLEQEPAAERQOLVETHMARVEAM:LNDRRLALE 399
 DB 174 EAE-QAKNLPKTERITLL:QHFQAMVKALEKASEKQOLVETHLARVEAM:LNDRRLALE 233
 QY 400 NYITALQAVPRPKHVRVMDPKKAAQIRSQVMTHL 459
 DB 234 NYLAALSDPPRPHRIQALRRYRAENKORLHTIRHQVLAVDPEKAAQKQSVMTHL 293
 QY 460 RVIVERMNQS:SLIYNVFAVAEEIQDEVDELQKQNYSDVLANLMISEPRI:SYGNDAIMP 519
 DB 294 HVIERRNQS:SLIKVVPVYVQETQEEIDELQQR-----ADM-----DOFT 336
 QY 520 PSLITKTKTITVLLPVNGEFLSDUQPHSFGADSVPAANTENEVPVDARPAACHGLTTRP 579
 DB 337 SSISENPVDVRVSSSESE-EIPPPHPLHPF-----PSLSENE-----GSGMAEQD 380
 QY 580 GSGLTNIKTEEL-SEVKMDAERHDSGYEVHHQKLVFEAEVGS----- 622
 DB 381 G-GLIGAEKVINSKNMKNMNVITDELTDV--KEMIFNAERVGGLEEEPEPSVGPLREDPS 437
 QY 623 -NKGAIIGLMVGGVVIAIVITVLMKKKQYTSIHGQVEVDAVTPPEERHLSKMQONG 681
 DB 438 LSSNALIGLLVIAVIAIVITVLSVLMKRYGIISHGIVEVDPMLTTEERHLNKMONG 497
 QY 682 YENPTYKFFEQM 694
 DB 498 YENPTYKYLRQMQ 510

RESULT 12
 T15795
 hypothetical protein C42D8.8 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
 C:Accession: T15795; A49414
 R:Hallsworth, K.
 submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid C42D8.
 A:Reference number: Z18405
 A:Accession: T15795
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-686 <HAL>


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QY 7 LLLLAWTARALEVPTIUGNAGLIA-----EPQIAMEFC--GRLNHHMV-ONGKWDSPSG 58
DB 9 LLLLSLWVVLAI-----GTAQVAAASPRWPOIATVCEAGOIYOPQYLSBGRWVTLDSK 63
QY 59 T---KTCIDTKEGILQXCQEVPELOITINVEANOPVITQNMCKRG---RKQCKTHPHFV 112
DB 64 KTTGPTCLROKMDLLDYCKKAYPNRDITNIVESSHYOKIGWCPOGALNAACKCKGSHRWI 123
QY 113 IPRKLVGEFVSODALLVPDKCKFLHQBRMDVCETHLHWHTYAKETCSEKSTINLHDYGMLL 172
DB 124 KPFRCL-GPFGSDALLVPEGLCDPHIHNASRCWPFRWNO-GAAACQERGQMGRIFAMLL 182
QY 173 PCGIDKFRGVEYCCP-----LAEESDNYD---SA 191
DB 183 PCGISVFGVEFVCCPKEFKTEIHKVKITLPLVM:AAQINSANDEIMNDEDSNYSK 242
QY 200 DAEFDSGVWVGADTYADGSEDKVVEVAEEFV-----AEV 237
DB 243 DANEDLLD-----DEDLMGDDDEDMVADAEATAGSPNTGSGDSNSGLDDINAEY 296
QY 238 EE-DEADDDDEDDGDRVESEAEFVY-----BEAFERT 269
DB 297 DSGECCNYEEDGAGSEAEVEASWDSGGAKVSLKSDSSPSSAPVAPAEKAPVKS 356
QY 270 TSIATTTITTESVEEV-----RVPTTAATPDPAVKYLETFGDENCHAHFQK 318
DB 357 ESVTSTPOLSASAAFAAANSNGNSGTGAGAPPSTAQPTIS---DPYTHFDPHYERQSYKV 413
QY 319 AKERLEAKHRPMSONKRENEAEERQAKNLPKADKA-----VICHFEKVESLSQEA 371
DB 414 SQRLESERREKVTYRVNKMDSLDEEKYQDMRLADPKAAQSFQKWTARFQTSVQALBEEG 473
QY 372 ANERQQLVETHMARVEAMI,NDRRLALENYITALQAVPPRRHVFNMLKYYVRAEQKDRQ 431
DB 474 NAEKHOLAAHQORVLAHINORKREAMTCYTOALTEQPPNAHHVEKCLOKLLRALHAKDRA 533
QY 432 HTLKHPFH-VRWVDP---KKAQIIRSQVYTHLRVIYERMNOSLILYNVPAVAEEI-----483
DB 534 HALAHYRHLLNSGGPGGLEAAASERPRTLERLIDIRAVNQSMTMIKRYPELSAKIAQLM 593
QY 484 -----QDEV-----487
DB 594 NDYITALRSKDDIPGSS:GNSEEAEGILDOKRYRVEIERKVAEKERLRLAEKQKORAAE 653
QY 488 -----DELLOKEQNYSDDVLANMTSE-----PRISYGNDAIM 519
DB 654 REKLREKRLRAKKVDDMLKSOVAEBOSSQTSSTOSQAOQOQOQKSLPGKELGPDAAI 713

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QY 520 -----PSLTETKTYVELLPYNGEFLSDLOPWHSGFADSVFPAFTIENEVEPVDAKPRADRG 574
Db 714 VTAANPLETTKS-----EKDLSDE-----YGEATVSTTKVQTIVLFTVJDDAVQRA 760
QY 575 LTRPGSLINIKTEEISEVKMDAEFRHDSGYEVHHQKLVF-----FALDVGSKN---GA 626
Db 761 VEDVAAA-----VAHGEAPQVQHFMTHDLGHRESSFSLRREFAQHAAKGRNV 811
QY 627 IGLMVGGVVIAIVITLMLKKQYTSIH-HGVVEVDAAVTF-----EERHLSKMQQ 679
Db 812 YFTLSFAGIALMAAVFVGVAKWRISRSRPHAGQFTEVDQNVITHHPVIVREKIVPMQI 871
QY 580 NGYENPTYKFE 691
Db 372 NGYENPTYKFE 883

RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May 1996
C:Accession: S38344
R:Hanes, J.; Von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A:Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A:Reference number: S38344; MUID:94032480; PMID:8218408
A:Accession: S38344
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-246 <HAN>
A:Cross-references: EMBL:222592
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 19.3%; Score 706; DB 2; Length 246;
Best local Similarity 51.5%; Pred. No. 2.2e-30;
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;
QY 5 LALLLAANTARALEV-----PTDGNAG---LAEPTQIMFGGRLNHNKNVQCKKDSOP 54
Db 15 LIVLLGLTAPAAALAGYTEALAAAGTGAFAEPQAMLCCKLNHNVN:QTKRKEPOP 74
QY 57 SGTKICIDTREGILOVCEVVPQLQITNVVEANQPV:IGNMKRGRKCKTETHEFVTPYR 114
Db 75 TGTKSCLCITKEVLYQCEIYPELQITNVMEANQPVNIDSWCRDRKROCKS--HIVIPK 122
QY 117 CLVGFVSDALLVPHDKCKFLHQRMDVCEVTHLHWHTVAKETCKSTNLDYQMLPCGI 176
Db 133 CLVGEFVSDVLLVPDNCQFFQERMEVCEKHQRWHLTVKEACLTESGLTLYSGMLPCGV 192
QY 177 DKPRGVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEFEVAE 236
Db 193 DQFHGTIVCCP---QTKTVDS-----DSTMSKEEEEEE--- 222
QY 237 VESEADDDDEDSDGSEVEFEAE 259
Db 223 -EEDDEDEEDYDLKSEFFTEAD 245

RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maron, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: PQ0438; MUID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide 1
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome
Query Match 11.3%; Score 411; DB 2; Length 82;
Best local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 581 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATV 640
Db 1 SGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATV 60
QY 641 IVITLVMKKKKQYTSIHHCVVVE 662
Db 61 IVITLVMKKKKQYTSIHHCVVVE 82

Search completed: October 2, 2003, 14:00:31
Job time : 20.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 : Search time 16 Seconds

(without alignments)

3277.761 Million cell updates/sec

Title: US-09-806-194-16

Perfect score: 3651

Sequence: 1 MLFGLALLLAANTARALEV.....QQNGYENPTYKFEQMKNK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3590.5	98.3	770	1 A4_HUMAN	P05067 h amyloid b
2	3590.5	98.3	770	1 A4_MACFA	P53601 m amyloid b
3	3584	98.2	751	1 A4_SAISC	O93243 s amyloid b
4	3535.5	96.8	770	1 A4_PTG	P73307 s amyloid b
5	3522.5	96.5	770	1 A4_CAVPO	Q60495 c amyloid b
6	3493.5	95.7	770	1 A4_MOUSE	P12023 m amyloid b
7	3493.5	95.7	770	1 A4_RAT	P08592 r amyloid b
8	1735	47.5	695	1 APP2_MOUSE	Q05335 mus musculu
9	1728	47.3	763	1 APP2_HUMAN	Q05481 homc sapien
10	1716	47.0	765	1 APP2_RAT	P15843 rattus norv
11	1190	32.6	650	1 APPL_HUMAN	P51693 homo sapien
12	1185	32.5	653	1 APPL_MOUSE	Q03157 mus musculu
13	817.5	22.4	686	1 A4_CAEEL	Q10551 caenorhabdi
14	748.5	20.5	887	1 A4_DROME	P14599 drosophila
15	292	8.0	59	1 A4_BOVIN	Q28053 bos taurus
16	288	7.9	58	1 A4_RABIT	Q28748 cryptotagus
17	288	7.9	58	1 A4_SHEEP	Q28757 ovis aries
18	287	7.9	58	1 A4_CANFA	Q28290 canis fami
19	283	7.8	57	1 A4_URSCA	Q29149 ursus marit
20	185.5	5.1	407	1 IE68_HSVSA	Q01042 herpesvirs
21	185.5	5.1	993	1 SGP1_MOUSE	Q62205 mus musculu
22	176	4.8	2034	1 M22_HUMAN	Q92734 homo sapien
23	175.5	4.8	802	1 NAB3_YEAST	P38996 saccharomyc
24	174	4.8	579	1 G150_HUMAN	Q08378 homo sapien
25	173.5	4.8	793	1 CALD_HUMAN	Q05682 homo sapien
26	172	4.7	771	1 CALD_CHICK	P12957 gallus gall
27	169.5	4.6	297	1 TRP2_HUMAN	P45379 homo sapien
28	169.5	4.6	721	1 YCF2_OENPI	P31568 oenothera p
29	168.5	4.6	1875	1 MLP1_YEAST	Q02455 saccharomyc
30	168	4.6	1240	1 YNUL_YEAST	P35935 saccharomyc
31	167.5	4.6	1976	1 MYHA_HUMAN	P35580 homo sapien
32	166.5	4.6	816	1 YG3A_YEAST	P53276 saccharomyc
33	166.5	4.6	1976	1 MYHA_RAT	Q93110 rattus norv

34	164.5	4.5	1325	1 G160_MOUSE	P55937 mus musculu
35	163.5	4.5	681	1 MP10_HUMAN	O00566 homo sapien
36	163	4.5	2017	1 MYSN_DROME	Q99323 drosophila
37	162.5	4.5	712	1 NUCL_RAT	P13383 rattus norv
38	160.5	4.4	1976	1 MYHA_BOVIN	Q27991 bos taurus
39	160	4.4	694	1 NUCL_CHICK	P15771 gallus gall
40	159.5	4.4	1955	1 PJMA_PARUN	O61308 parascaris
41	158	4.3	301	1 TRT2_CHICK	P02642 gallus gall
42	157.5	4.3	706	1 NUCL_HUMAN	P19338 homo sapien
43	156.5	4.3	1332	1 SPT7_YEAST	P35177 saccharomyc
44	156.5	4.3	5596	1 MDN1_HUMAN	Q9nu22 homo sapien
45	155	4.3	1433	1 REST_CHICK	O42184 gallus gall

ALIGNMENTS

RESULT 1
A4_HUMAN
ID A4_HUMAN STANDARD; PRT: 770 AA.
AC P05067; P09000; P78438; Q13778; Q13793; Q16011; Q9BF38;
AC Q9UCB6; Q9U058;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE nexin-II) (PN-II) (APPI) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE (Amyloid intracellular domain 50) (AID(50)); C31].
GN APP OR A4 OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GX NCBI_TaxID=9606;
[.]
RN SEQUENCE FROM N.A. (ISOFORM APP695).
RP TISSUE=Brain;
PC MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
cell-surface receptor.";
RL Nature 325:733-736(1987).
[2]
RN SEQUENCE FROM N.A. (ISOFORM APP751).
RP TISSUE=Brain;
RC MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
protease inhibitors.";
RL Nature 331:525-527(1988).
[3]
RN SEQUENCE FROM N.A. (ISOFORM APP695).
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
[4]
RN SEQUENCE FROM N.A. (ISOFORM APP770).
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
gene.";

RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RX Yoshikaki S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.:
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RX TISSUE=Leukocyte; PubMed=1587857;
 RX MEDLINE=92286136;
 RA Koenig G., Moening U., Czern C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.:
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells."
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RX MEDLINE=97263807; PubMed=9103164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.:
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus."
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RX TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausch R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshuler S.F., Zengler B., Auetow K.H., Schafer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Esieh F.,
 RA Diatchenko L., Marusina K., Parker A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavali T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Cartierci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson P.D., McElhinny S.C.,
 RA Bosak S.A., McSwan K.J., McKorman K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hite S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Vallalona D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltor E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.S.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.:
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.:
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN [10]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.:
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [11]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165870; PubMed=2538123;
 RA La Fauce G., Lahiri D.K., Satton S.R., Robakis N.K.:
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene."
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [12]
 RP SEQUENCE OF 18-50.
 RX TISSUE=Fibroblast;
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.:
 RT "Purification of protease nexin II from human fibroblasts."
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RX TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.:
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein."
 RL Science 245:651-653(1989).
 RN [14]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RX TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ranakrishna N., Wolfe G., Wisniewski H.M.:
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [15]
 RP SEQUENCE OF 286-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Nere R.L.:
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease."
 RL Nature 331:528-530(1988).
 RN [16]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.:
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity."
 RL Nature 331:530-532(1988).
 RN [17]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Choo W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.:
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [18]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.:
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I."
 RL J. Biol. Chem. 271:1614-1620(1996).
 RN [19]
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.:
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor."
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [20]
 RP SEQUENCE OF 672-681.
 RX TISSUE=Brain cortex;
 RX MEDLINE=88035004; PubMed=3312495;
 RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.:
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels."
 RL J. Neurochem. 49:1394-1401(1987).
 RN [21]
 RP SEQUENCE OF 674-770 FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.:
 RT "Characterization and chromosomal localization of a cDNA encoding
 RT brain amyloid of Alzheimer's disease."

```

Query Match      98.3%   Score 3590.5;   DS 1;   Length 770;
Best Local Similarity 90.1%;   Pred. No. 3,2e-17.;
Matches 694;   Conservative 1;   Mismatches 0;   Indels 75;   Gaps 1;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEFGIAMFGRLNMHNVNQNKWSDPFSUTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEFGIAMFGRLNMHNVNQNKWSDPFSUTK 60
QY 61 TCIDITKEGILQYCGVEYPELQITNNVFANQPVTCNNCKRGKCKOCHPHEVPIYRGLVG 120
DB 61 TCIDITKEGILQYCGVEYPELQITNNVFANQPVTCNNCKRGKCKOCHPHEVPIYRGLVG 120
QY 122 EFVSDALLVPCKCFHQRWDVCEITHLHWIHVAKETCSEKSTNLHDGMGLFGGLDKFR 180
DB 122 EFVSDALLVPCKCFHQRWDVCEITHLHWIHVAKETCSEKSTNLHDGMGLFGGLDKFR 180
QY 181 GVEFVCCPLAESNVDSADAEEDSDVWVGAGTDVADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESNVDSADAEEDSDVWVGAGTDVADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEYERATERITTSIAITTTTTSVEEVEEVR----- 288
DB 241 EADDDEDDGDEVEEAEPEYERATERITTSIAITTTTTSVEEVEEVR----- 288
QY 289 ----- 288
DB 289 ----- 288
QY 301 RAMISRWFVDTGKCAFFYGGGGGNNRNFDTPEYCMVCGSAMSGELLITDPEIARD 360
DB 301 RAMISRWFVDTGKCAFFYGGGGGNNRNFDTPEYCMVCGSAMSGELLITDPEIARD 360
QY 289 ---VPTTAASPDVADKYLETGPDENEHAFQKAKERLEAKHREKMSQVMREWEAEARQA 345
DB 361 PVKLPTTAASPDVADKYLETGPDENEHAFQKAKERLEAKHREKMSQVMREWEAEARQA 420
QY 346 KNLPRADKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 405
DB 421 KNLPRADKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITAL 480
QY 406 QAVPPRPRHVNMLKKYRAEKQKDRHTLKHFHVRVMDPKKAAQIRSOVATHLRVIVYER 465
DB 481 QAVPPRPRHVNMLKKYRAEKQKDRHTLKHFHVRVMDPKKAAQIRSOVATHLRVIVYER 540
QY 466 MNQSLSLLYNPVAAEETODEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSTET 525
DB 541 MNQSLSLLYNPVAAEETODEVELLOKEQNSDDVLANMISEPRISYGNDAIMPSTET 600
QY 526 KTIVELLPVNGEESLDQLPHRSFGADSPVANTENEVFVAPARPAADRGILTTPGSGGJTN 585
DB 601 KTIVELLPVNGEESLDQLPHRSFGADSPVANTENEVFVAPARPAADRGILTTPGSGGJTN 660
QY 586 IKTEIISFVKMDAEPRHDSGYEVHHQKLVFFAELVGSNKGAIIGLMVGGVVIATVIVITL 645
DB 661 IKTEIISFVKMDAEPRHDSGYEVHHQKLVFFAELVGSNKGAIIGLMVGGVVIATVIVITL 720
QY 646 VMLKKKQYTSIHGGVVEVDAAVTPERHLSKMQQNGYENPTYKFEQMQN 695
DB 721 VMLKKKQYTSIHGGVVEVDAAVTPERHLSKMQQNGYENPTYKFEQMQN 770

RESULT 2
A4_MACFA
AC P53601; Q95KN7;
DI 01-OCT-1996 (Rel. 34, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(42);
DE Gamma-Ctf(59) (Gamma-secretase C-terminal fragment 59); Gamma-Ctf(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-Ctf(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.

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US Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecinae; Macaca.
CC NCBI_TaxID=9541;
CC [1];
CC SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
CC RN TISSUE=Cerebellum;
CC RC TISSUE=Cerebellum;
CC RA MEDLINE=91273117; PubMed=1905108;
CC RA Podlisky M.B., Tolan D.R., Selkoe D.J.;
CC "Homology of the amyloid beta protein precursor in monkey and human
CC RT supports a primate model for beta amyloidosis in Alzheimer's
CC RT disease";
CC RL Am. J. Pathol. 138:1423-1435(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-Ctf peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APPA
CC family, MAPK8IP1, and SHC1, Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein Bpp, FPR1, APPB1, IBL, KNS2
CC (via its IPR domains) (By similarity), APPB2 (via BASS) and DBP1.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCtf(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoId=P53601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=P53601-2; Sequence=VSP_000010, VSP_000011;
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PTB domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete

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interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42), major components of amyloid plaques, and the cytotoxic C-terminal fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and O-linked glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity).

-!- Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: BELONGS TO THE APP FAMILY.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL: M58727; AAA36829.1; -
 EMBL: M58726; AAA36828.1; -
 HSP: P05067; IAAP.
 InterPro: IPR001868; A4_APP.
 InterPro: IPR002223; Kunitz_RPT1.
 Pfam: PF02177; A4_EXTRA; 1.
 Pfam: PF03494; Beta-APP; 1.
 Pfam: PF00014; Kunitz_BPT1; 1.
 PRINTS: PR00755; BASICPTASE.
 ProDom: PD000222; Kunitz_RPT1; 1.
 SMART: SM00006; A4_EXTRA; 1.
 SMART: SM00131; KU; 1.
 PROSITE: PS00319; A4_EXTRA; 1.
 PROSITE: PS00320; A4_INTRA; 1.
 PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 K W Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 K W Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 K W Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 K W Proteoglycan; Alternative splicing; Amyloid.
 SIGNAL 1 17
 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (POTENTIAL).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (POTENTIAL).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (POTENTIAL).
 FT CHAIN 688 770 C83 (POTENTIAL).
 FT CHAIN 688 713 P3(42) (POTENTIAL).
 FT CHAIN 688 711 P3(40) (POTENTIAL).
 FT CHAIN

FT CHAIN 712 770
 FT CHAIN 714 770
 FT CHAIN 721 770
 FT CHAIN 740 770
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 231 341
 FT DOMAIN 331 423
 FT DOMAIN 491 522
 FT DOMAIN 523 540
 FT DOMAIN 732 751
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 144
 FT FT
 FT ACT_SITE 301 302
 FT SITE 671 672
 FT SITE 672 673
 FT SITE 687 688
 FT SITE 704 704
 FT SITE 706 706
 FT SITE 711 712
 FT SITE 713 714
 FT SITE 720 721
 FT SITE 724 734
 FT SITE 739 740
 FT SITE 757 760
 FT SITE 759 762
 FT
 Query Match: 98.3%; Score 3590.5; DB 1; Length 770;
 Best local Similarity 90.1%; Pred. No. 3.2e-17;
 Matches 594; Conservative 1; Mismatches 0; Indels 75; Gaps 1;
 QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAPGIAFCGRNLNMHNVONGKWDSPGSK 60
 DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAPGIAFCGRNLNMHNVONGKWDSPGSK 60
 QY 61 TCIDTKEGILOVCQEVYPELOITINNVFEANQPVITONWCKRGKCKCTHPHEVIPYRCILVG 120
 DB 61 TCIDTKEGILOVCQEVYPELOITINNVFEANQPVITONWCKRGKCKCTHPHEVIPYRCILVG 120
 QY 121 EYVSDALLVPDKCFLEHQRMDVCTHLHWHITVAKETCEKSTKLNLDYGMLLPGIDKFR 180
 DB 121 EYVSDALLVPDKCFLEHQRMDVCTHLHWHITVAKETCEKSTKLNLDYGMLLPGIDKFR 180
 QY 181 GVEFYCCPLAESDNVDSADAFEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
 DB 181 GVEFYCCPLAESDNVDSADAFEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
 QY 241 EADDDEDDGDEVEEAEPEEYEEATERTTSIATTTTTTTSVEEVVR----- 288
 DB 241 EADDDEDDGDEVEEAEPEEYEEATERTTSIATTTTTTTSVEEVVR----- 288
 QY 289 ----- 288
 DB 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNFTDEEYCMVCGSVMSQSLRKTTRPLTRD 360
 QY 289 ---VPTTAASPTDAVDKYLETFGDENEHAHQKAKERLEAKHREHMSQVMREWEAEERQA 345
 DB 361 PVKLTPTAASPTDAVDKYLETFGDENEHAHQKAKERLEAKHREHMSQVMREWEAEERQA 420

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QY 346 KNLKPAQKAVIOHFOEKVESLEQEAANERQQLVETHWARYEAMLNDRARRALNNY:ITAL 405
DB 421 KNLKPAQKAVIOHFOEKVESLEQEAANERQQLVETHWARYEAMLNDRARRALNNY:ITAL 480
QY 406 QAVPRPRSHVNMUKKYVRAQKQROHFLKHFHVRVMVDPKKAQIRSQVM:HLRV:YER 465
DB 481 QAVPRPRSHVNMUKKYVRAQKQROHFLKHFHVRVMVDPKKAQIRSQVM:HLRV:YER 540
QY 466 MNQSLSLYNPVAVAEITQDEVELLOKEQNSDDVLAMN:SEPRISYGVNDALMPSUTET 525
DB 541 MNQSLSLYNPVAVAEITQDEVELLOKEQNSDDVLAMN:SEPRISYGVNDALMPSUTET 600
QY 526 KTVRL:PVNGFFSLDQLOPHSGAGSVNPANTEVEPVLARPAADHCLIRGSLTN 585
DB 601 KTVRL:PVNGFFSLDQLOPHSGAGSVNPANTEVEPVLARPAADHCLIRGSLTN 660
QY 586 IKTEISVKNMADFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGGVIA:VIVITL 645
DB 661 IKTEISVKNMADFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGGVIA:VIVITL 720
QY 646 VMLKKKQVTSIHGVEVDAVTPTEERHLSKMQNGYENPTYKFEQMN 695
DB 721 VMLKKKQVTSIHGVEVDAVTPTEERHLSKMQNGYENPTYKFEQMN 770

RESULT 3
A4_SAISC STANDARD: PRT: 751 AA.
AC Q95241:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
DE APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
OS Samiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craciata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Liver:
RX MEDJINF-96108492; PubMed=8532114;
RA Levy F., Ancrini A., Frangione B., Walker L.G.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with
RL cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB-1/p160 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(I) and JIP (By
CC similarity). Inhibits G(I) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC
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CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-C1F peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APP3 family members, the APBA
CC family, MAPK1P1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IBI, KNS2
CC (via its TPR domains) (By similarity), APPBP2 (via RaSS) and DORI.
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Comment-Additional isoforms seem to exist;
CC Name-APP770;
CC IsoId=Q95241-1; Sequence=Displayed;
CC Name-APP695;
CC IsoId=Q95241-2; Sequence=Not described;
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPLY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).
CC -!- PM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC similarity).
CC -!- PM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).
CC -!- PM: N- and O-linked glycosylated (By similarity).
CC -!- PM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
```

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: S81024; RAD14347.1; --
 DR HSSP: P05067; JAAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; A0YLOIDA4.
 DR PRINTS: PR00759; BASICTPASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00278; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neutrophil; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 751
 FT CHAIN 18 668
 FT CHAIN 18 652
 FT CHAIN 653 751
 FT CHAIN 653 694
 FT CHAIN 653 692
 FT CHAIN 669 751
 FT CHAIN 669 694
 FT CHAIN 669 692
 FT CHAIN 693 751
 FT CHAIN 695 751
 FT CHAIN 702 751
 FT CHAIN 721 751
 FT DOMAIN 18 680
 FT TRANSMEM 681 704
 FT DOMAIN 705 751
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 291 341
 FT DOMAIN 316 344
 FT DOMAIN 363 428
 FT DOMAIN 504 521
 FT DOMAIN 713 732
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 144
 FT ACT_SITE 301 302
 FT SITE 652 653
 FT SITE 653 654
 FT SITE 668 669
 FT SITE 685 685
 FT SITE 687 687
 FT SITE 692 693
 FT SITE 694 695
 FT SITE 695 695

FT SITE 701 702 CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
 FT SITE 705 715 (BY SIMILARITY).
 FT SITE 720 721 BASOLATERAL SORTING SIGNAL
 FT SITE 721 741 (BY SIMILARITY).
 FT SITE 741 741 CLEAVAGE (BY CASPASE-3, -6, -8 OR -9)
 FT SITE 743 743 (BY SIMILARITY).
 FT METAL 137 137 ENDOCYTOSIS SIGNAL.
 NPKY MOTIF.
 COPPER (BY SIMILARITY).
 Query Match 98.2%; Score 3584; DB 1; Length 751;
 Best Local Similarity 92.0%; Pred. No. 6.6e-171;
 Matches 691; Conservative 2; Mismatches 2; Indels 56; Gaps 1;
 QY 1 MLPGLALLLAATWARTALEVPTDGNAGLLAEPAQIAMFCGRLLMMHNNVONGKWDSPSGTK 60
 DB 1 MLPGLALLLAATWARTALEVPTDGNAGLLAEPAQIAMFCGRLLMMHNNVONGKWDSPSGTK 60
 QY 61 TCIDITKEGILQYCOEYVPELOQITNVVEANOPTVIONMCKRGRKCKTHPHFVLPYRCLVG 120
 DB 61 TCIDITKEGILQYCOEYVPELOQITNVVEANOPTVIONMCKRGRKCKTHPHFVLPYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHHTVAKETGSEKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCEVTHLHHTVAKETGSEKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GYFVCCPLAEESDNDVSDADEEDSDVWGGADTDYADGSEDKVVEVAEEVAEEVEE 240
 DB 181 GYFVCCPLAEESDNDVSDADEEDSDVWGGADTDYADGSEDKVVEVAEEVAEEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEEYEAETKTSIAITTTTTTTSVEVVR----- 288
 DB 241 EADDDDEDDGDEVEEAEPEEYEAETKTSIAITTTTTTTSVEVVR----- 288
 QY 289 -----VPTTAASTPDVADKYL 304
 DB 301 RAMISRWYFDVTGKCAPFFYGGCGGNRNFDTEECYMAVCGSVIPTTTAASTPDVADKYL 360
 QY 305 ETPGDENEHAFQKAKERLEAKRERMMSOVMEWEAEAEQAQNLKADKKAIVIOHFQEKV 364
 DB 361 ETPGDENEHAFQKAKERLEAKRERMMSOVMEWEAEAEQAQNLKADKKAIVIOHFQEKV 420
 QY 365 ESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLKKYVR 424
 DB 421 ESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFENMLKKYVR 480
 QY 425 AQOKURQHTLKHFEHVRMYDPKKAQIRSOVTHLKVYIERMNSLSLLYNYPVAEEIQ 484
 DB 481 AQOKURQHTLKHFEHVRMYDPKKAQIRSOVTHLKVYIERMNSLSLLYNYPVAEEIQ 540
 QY 485 DEVDLLOKEQYSDDLVLANMISEPRISYGNALMPSLTETKTIVELLPVNGEFLDLDLQ 544
 DB 541 DEVDLLOKEQYSDDLVLANMISEPRISYGNALMPSLTETKTIVELLPVNGEFLDLDLQ 600
 QY 545 PWHFSGADSVPAANTEVEFVDARPAACRGLTRPGSGLTNKTETSEISKVMDAEFRHDS 604
 DB 601 PWHFSGADSVPAANTEVEFVDARPAACRGLTRPGSGLTNKTETSEISKVMDAEFRHDS 660
 QY 605 GYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGVEVD 664
 DB 661 GYEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGVEVD 720
 QY 665 AAVTPEERHLSKMOONGYENPTYKFFEQMON 695
 DB 721 AAVTPEERHLSKMOONGYENPTYKFFEQMON 751
 RESULT 4
 A4_PIG
 ID A4_PIG STANDARD: PRT: 770 AA.
 AC P75307: Q29023; Q9TU10;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
DE secretase C-terminal fragment 50); C31].

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Kimura A., Takahashi T.;

RT "Amyloid precursor protein 70.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-136 FROM N.A.

RC TISSUE=Small intestine;

RA Winteroe A.K., Fredholm M.;

RT "Evaluation and characterization of a porcine small intestine cDNA
RT library.";

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 667-723 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB/rip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity).

CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).

CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C3-, are potent enhancers of neuronal
CC apoptosis (By similarity).

CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APBA
CC family, MAPK6IP1, and SACL. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, EPRL1, APPBP1, IBI, KKS2
CC (via its TPR domains) (By similarity). APPBP2 (via Bass) and APP1
CC In vitro, it binds MAPT via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of ATP
CC and in a kinesin-dependent manner (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and

CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).

CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).

CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue. The NPXY site is also involved in clathrin-mediated
CC endocytosis (By similarity).

CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC C83 and C99. Subsequent processing of C83 by gamma-secretase
CC yields P3 peptides. This is the major secretory pathway and is
CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
CC gamma-secretase processing of C99 releases the amyloid beta
CC peptide, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
CC major components of amyloid plaques, and the cytotoxic C-terminal
CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
CC results in the production of the neurotoxic C31 peptide and the
CC increased production of beta-amyloid peptides (By similarity).

CC -!- PTM: N- and O-linked glycosylated (By similarity).

CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific. Phosphorylation can affect APP
CC processing, neuronal differentiation and interaction with other
CC proteins (By similarity).

CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).

CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates (By similarity).
CC Extracellular zinc-binding increases binding of heparin to APP and
CC inhibits collagen-binding (By similarity).

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -----

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CC -----

DR EMBL: AB032550; BAB4580.1; -
DR EMBL: Z84022; CAB06313.1; -
DR EMBL: X56127; CAA39592.1; -
DR HSSP: P05067; IAAP.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR008154; A4-extra.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE; PS00260; BPTI_KUNII12.1;
 DR PROSITE; PS00279; BPTI_KUNII12.2; 1;
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN;
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 18 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 C83 (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59).
 FT CHAIN 714 770 GAMMA-CTF(57).
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 135 155 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNII2 INHIBITOR.
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SHCR-ASE; SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
 Query Match 96.8%; Score 3535.5; DR 1; Length 770;
 Best Local Similarity 88.4%; Pred. No. 1.7e-168;
 Matches 681; Conservative 8; Mismatches 5; Indels 75; Gaps 1;
 QY 1 MLPGLALLLAATARALETVDGNAGLAPQAFMFCGRLLNMHMYQNGKWSQSGTK 60
 Db 1 MLPGLALVLAATARALETVDGNAGLAPQAVAMFCGKLLNMHMYQNGKWSQSGTK 60
 QY 61 TCIDTKGILQYCEVYPELOITNVVEANQPVTTQNMCKRKGRKCKTHPHFVYRCGLV 120
 Db 61 TCIDTKGILQYCEVYPELOITNVVEANQPVTTQNMCKRSRCKCKTHPHFVYRCGLV 120
 QY 121 EFVSDALLVPKCKFLHQRMDVCETHLHWTAVAKETCSKSTNLHDYGMILPGIDKFR 180
 Db 121 EFVSDALLVPKCKFLHQRMDVCETHLHWTAVAKETCSKSTNLHDYGMILPGIDKFR 180
 QY 181 GVEFVCCPLAESNDVSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 Db 181 GVEFVCCPLAESNDVSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
 QY 241 EADDEDEDEGDEVEEAEPEYERATRTTSIATTTTTTIESVEEVEVVCSEQAEGHC 300
 Db 241 EADDEDEDEGDEVEEAEPEYERATRTTSIATTTTTTIESVEEVEVVCSEQAEGHC 300

Db 241 EADDEDEDEGDEVEEAEPEYERATRTTSIATTTTTTIESVEEVEVVCSEQAEGHC 300
 QY 289 -----
 Db 301 RAMISRWYFLVTEGKCAPFEYGGCGGNRNFPDTEECMAVCGSVMSQSLKTTQEHLPQ 360
 QY 289 ---VPIAASTPDVDKY-ETVGDENEHAHFQKAKERLEAKHRRMSQVMREKEAEQA 345
 Db 361 PVKLPITAASTPDVDKYLETFGDENEHAHFQKAKERLEAKHRRMSQVMREKEAEQA 420
 QY 346 KNLPRADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAT 405
 Db 421 KNLPRADKKAVIQHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAT 480
 QY 406 QAVPPRRHVFNMLKYYVRAEOKDRQHTLKHFHVHVMYDPKAAQTRSOVMTHLRVYER 465
 Db 481 QAVPPRRHVFNMLKYYVRAEOKDRQHTLKHFHVHVMYDPKAAQTRSOVMTHLRVYER 540
 QY 466 MNGSLLNVPAAVEEIODEVDELLOKEQNTSDVLANMISEPRISYNDALMPSLTET 525
 Db 541 MNGSLLNVPAAVEEIODEVDELLOKEQNTSDVLANMISEPRISYNDALMPSLTET 600
 QY 526 KTTVELLPVNGEFSDDLQPHSHFGADSVDPANTENEVEPVDARPAADRGILTTPSGSLTN 585
 Db 601 KTTVELLPVNGEFSDDLQPHSHFGADSVDPANTENEVEPVDARPAADRGILTTPSGSLTN 660
 QY 586 IKTEELSEYKMDAEFRHDSGYEVHOKLVFPADVCSNGKAIIGLMVGGVVATVITL 645
 Db 661 IKTEELSEYKMDAEFRHDSGYEVHOKLVFPADVCSNGKAIIGLMVGGVVATVITL 720
 QY 646 VMLKKQYTSIIHGVVVEVDAAVTPEERHLSKMQNGYENPTYKFFEQMON 695
 Db 721 VMLKKQYTSIIHGVVVEVDAAVTPEERHLSKMQNGYENPTYKFFEQMON 770
 RESULT 5
 A4_CAVPO STANDARD; PRI: 770 AA.
 AC Q5C495; Q60496;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC "SSUE-Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Muelier D., Bigi V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing.";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Meckie J.B., Matsubara E., Governale S., Miquel C.,
 RA Miao W., Mccomb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;

RA Beck M., Brückner M.K., Holzer M., Kaep S., Kanneke J., Arendt I.,
RA Bigl V.;
RI *Guinea-pig primary cell cultures provide a model to study expression
RI and amyloidogenic processing of endogenous amyloid precursor
RI protein.*;
RI Neurosci 95:243-254(2000).
RN [4].
RX GAMMA-SECRETASE PROCESSING.
RX MEDLINE-20576391; PubMed-11035007;
RA Pinnix I., Mushnuru U., Fun H., Sridharan A., Goide T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RI "A novel gamma-secretase assay based on detection of the putative
RI C-terminal fragment-gamma of amyloid beta protein precursor";
RI J. Biol. Chem. 276:481-487(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G0 and JIP (By
CC similarity). Inhibits G0 alpha Arpase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen 2 and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC -!- FUNCTION: Apicicans elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC -!- FUNCTION: The gamma-CRF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APB8 family members, the ABEA
CC family, MAP6BPI, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APPBP1, IB1, KNS2
CC (via its IPR domains), APPBP2 (via BASS) and DBL1 (By similarity).
CC Associates with microtubules in the presence of ATP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC ApoE3 appears to be the preferred amyloid binding isoform, while
CC the ApoE4 isoform-beta-Apo40 complex is capable of being
CC transported across the blood-brain barrier.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N-
CC glycosylated in the endoplasmic reticulum) moves to the Golgi
CC complex where complete maturation occurs (O-glycosylated and
CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms, missing exons 7,6 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC apicicans;
CC Name=APP770;

CC IsoId=060495-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=060495-2; Sequence=VSP_007221, VSP_007222;
CC TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the BPTI domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC -!- INDUCTION: Increased levels during neuronal differentiation.
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPXY site is also involved in
CC clathrin-mediated endocytosis.
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC gamma-secretase yields p3 peptides. This is the major secretory
CC pathway and is nonamyloidogenic. Alternatively,
CC presenilin/alpha-secretase-mediated gamma-secretase processing of CTF-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC sulfate to the L-APP isoforms produces the APP proteoglycan core
CC proteins, the apicicans (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X97631; CAA66230.1; -;
CC EMBL: X99198; CAA67589.1; -;
CC HSSP: P05067; 1BA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC PRODom: PD000222; Kunitz_BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; K0; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., McIlahy S.J.,
 RA Hosak S.A., McEwan P.J., McKernan K.J., Malok J.A., Gnatatno P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Li X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
 RA Blakesley K.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.L., Skalska G., Smalius D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marisa M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 281-330 FROM N.A., AND ALTERNATIVE SPLICING.
 RC --SGSE-Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=24933250;
 RA Yamada T., Sasaki H., Dohura K., Goto T., Sakaki Y.;
 RA "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor";
 RT Biochem. Biophys. Res. Commun. 158:906-912(1989).
 RN [8]
 RP SEQUENCE OF 285-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2559710;
 RA Fukuchi K., Martin G.M., Deab S.S.;
 RA "Sequence of the protease inhibitor domain of the A1 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [9]
 RP SEQUENCE OF 656-737 FROM N.A.
 RC STRAIN=129/Sv;
 RA Wragg M.A., Busfield F., Duff K., Korenblat K., Capecechi M.,
 RA Loring J.F., Goate A.M.;
 RT "Introduction of six mutations into the mouse genome using 'Hit and
 RT Run' gene-targeting: introduction of familial Alzheimer's disease
 RT mutations into the mouse amyloid precursor protein gene and
 RT humanization of the A-beta fragment";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS.
 RX PubMed=8510506;
 RA Sola C., Mengo G., Ghetti B., Palacios J.M., Triarhou L.C.;
 RT "Regional distribution of the alternatively spliced isoforms of beta
 RT APP RNA transcript in the brain of normal, heterozygous and
 RT homozygous weaver mutant mice as revealed by in situ hybridization
 RT histochemistry.";
 RL Brain Res. Mol. Brain Res. 17:340-346(1993).
 RN [11]
 RP INTERACTION WITH KNS2.
 RX PubMed=11144355;
 RA Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.;
 RT "Axonal transport of amyloid precursor protein is mediated by direct
 RT binding to the kinesin light chain subunit of kinesin-1";
 RL Neuron 28:449-459(2000).
 RN [12]
 RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-725;
 RP THR-743; TYR-757; ASN-759 AND TYR-762.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Honma Y., Ito Y., Niihara T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.;
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [13]
 RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION.
 RX MEDLINE=22628091; PubMed=11312189;
 RA Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki I.;
 RT "Interaction of Alzheimer's beta-amyloid precursor family proteins
 RT with scaffold proteins of the JNK signaling cascade.";
 RL J. Biol. Chem. 277:20070-20078(2002).

RN [14]
 RP INTERACTION OF CTF PEPTIDES WITH NUMB.
 RX PubMed=12011466;
 RA Roncarati R., Sestau N., Scheinfeld M.H., Berechid B.E., Lopez P.A.,
 RA Meucci O., McGlade J.C., Rakic P., D'Adamo L.;
 RT "The gamma-secretase generated intracellular domain of beta-amyloid
 RT precursor protein binds Numb and inhibits Notch signaling.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).
 RN [15]
 RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APPB1.
 RX PubMed=11553691;
 RA Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.;
 RT "The amyloid precursor protein (APP)-cytoplasmic fragment generated by
 RT gamma-secretase is rapidly degraded but distributes partially in a
 RL nuclear fraction of neurons in culture.";
 RL J. Neurochem. 78:1168-1178(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions. Can promote transcription activation through binding
 CC to APPB1/Tip60 and inhibit Notch signaling through interaction
 CC with Numb. Couples to apoptosis-inducing pathways such as those
 CC mediated by G(O) and JIP. Inhibits G(O) alpha Arpase activity (By
 CC similarity). Acts as a kinesin I membrane receptor, mediating the
 CC axonal transport of beta-secretase and presenilin 1. May be
 CC involved in copper homeostasis/oxidative stress through copper ion
 CC reduction. Can regulate neurite outgrowth through binding to
 CC components of the extracellular matrix such as heparin and
 CC collagen I and IV (By similarity). The splice isoforms that
 CC contain the BPT1 domain possess protease inhibitor activity (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis.
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APBA
 CC family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits
 CC its serine phosphorylation. Also interacts with GPCR-like protein
 CC BPT, FPR1, APPBP1, IBI, KNS2 (via its IPR domains), APPBP2 (via
 CC Bass) and DDB1 (By similarity). In vitro, it binds MAPT via the
 CC MT-binding domains (By similarity). Associates with microtubules
 CC in the presence of ATP and in a kinesin-dependent manner (By
 CC similarity). Interacts, through a C-terminal domain, with GNAO1.
 CC (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal
 CC neurons (By similarity). Beta-amyloid associates with HADH2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs.
 CC Query Match 95.7%; Score 3493.5; DB 1; Length 770;
 CC Best Local Similarity 87.8%; Pred. No. 2.1e-166;
 CC Matches 676; Conservative 6; Mismatches 13; Indels 75; Gaps 1;
 QY 1 MIPGJALLLAATARALEVPTDGNAGLAEQIAEFCGRLLNHHMNVONGKWDSPSGTK 60
 DB 1 MLPSLAULLLAATVRALEVPTDGNAGLAEQIAEFCGRLLNHHMNVONGKWDSPSGTK 60
 QY 61 TCIDTKEGILQYCOEVYPELOITVWVEANQPVTTONMKCKRGKCKOCTHPHPIVYRCLVG 120
 DB 61 TCIGTKEGILQYCOEVYPELOITVWVEANQPVTTONMKCKRGKCKOCTHTHIVIPYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180

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Db 121 EFVSDALLVPOKFLHQRMDVGCETHLHHTVAKETCSSEKSNLHDYGMLLPGGIDKFR 130
QY 181 GVEFFCCPLATESONVYGSADAEEDSDVWVGADTDVAGSDKVAEVEEESVAEVEE 240
Db 181 GVEFFCCPLATESONVYGSADAEEDSDVWVGADTDVAGSDKVAEVEEESVAEVEE 240
QY 241 EADDDEDDDDGDEVEEFAFEYEATERITSIATTTTTTTSVEVEYK----- 288
Db 241 EADDDEDDDDGDEVEEFAFEYEATERITSIATTTTTTTSVEVEYK----- 288
QY 289 ----- 289
Db 301 RANISRWYFDVTEKCVFFYFGGCGNRRNFDTEYCGMANGSVSTQSLIKITSEPLPQC 340
QY 289 ---VPTTAASPDVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREAEARQA 345
Db 361 PDKLPTTAASPDVDKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREAEARQA 420
QY 346 KNLPRADKAVIQHFORKVESLEGEAANEROLVETIMARVENMNDRRRLALENYITAL 405
Db 421 KNLPRADKAVIQHFORKVESLEGEAANEROLVETIMARVENMNDRRRLALENYITAL 480
QY 406 QAVPPRPVRHVNMLKKYVRAEQKDRQHTLKHFEHVRWVDPKKAQIRSOVMTHLRVIYER 455
Db 481 QAVPPRPVRHVNMLKKYVRAEQKDRQHTLKHFEHVRWVDPKKAQIRSOVMTHLRVIYER 540
QY 466 MNQSLSLYNYPVAAEELQDEVELLOKEQNSDDVLANNISEPRI SYGNDA LPSITET 525
Db 541 MNQSLSLYNYPVAAEELQDEVELLOKEQNSDDVLANNISEPRI SYGNDA LPSITET 600
QY 526 KTTVELLPVNGEFSDDLQPMHSGADSVPAANTENEVPVDPARPAADRGTLRPGSLTN 585
Db 601 KTTVELLPVNGEFSDDLQPMHSGADSVPAANTENEVPVDPARPAADRGTLRPGSLTN 640
QY 586 IKTEPISVKMDAEPHDSQVEYVHRQKLVFAEDVGSNKGAILGLMVGGVVIAVIVITL 645
Db 661 IKTEPISVKMDAEPHDSQVEYVHRQKLVFAEDVGSNKGAILGLMVGGVVIAVIVITL 720
QY 646 VMLKKKQYTSIHGVEVVECAVTPERHLSKMOONGYENPTYKFFQOMON 695
Db 721 VMLKKKQYTSIHGVEVVECAVTPERHLSKMOONGYENPTYKFFQOMON 770
RESULI 7
A4_RAT STANDARD PRI: 770 AA.
AC P06592:
DI 01-AUG-1988 (Rel. 08. Created)
DI 01-DEC-1992 (Rel. 24. Last sequence update)
DI 15-SEP-2003 (Rel. 42. Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) (Amyloidogenic glycoprotein) (AG) [Contains: Soluble
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-Ctf(59); (Gamma-secretase C-terminal
DE fragment 59); Gamma-Ctf(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-Ctf(50); (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
CS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=68312583; PubMed=2903758;
RA Shivers B.D., Hilbich C., Multhaup G., Saibum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RL in rat brain suggests a role in cell contact.";
RN [2]
EMBO J. 7:1365-1370(1988).
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RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Møller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RC Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopoulou D.,
RA Wyllieou C., Margolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX PubMed=9930726;
RA Watanabe T., Sukegawa J., Tomita S., Iijima K.-i., Oguchi S.;
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND H7S-733.
RX PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouliot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Gq heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthimiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cuajungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
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RA Liu S.T., Howlett G., Barrow C.J.,
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 of the A beta peptide of Alzheimer's disease.";
 RL Biochem. Biophys. Acta 1586:190-198(2001).
 RN [121]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 GLY-704.
 RX PubMed-11959460;
 RA Kanski J., Varadarajan S., Aksanova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX PubMed-9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Iim G.S., Isohara T., Candy S.E.,
 RA Greengard P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX PubMed-10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno T.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 THR-743.
 RX MEDLINE-99274744; PubMed-10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX PubMed-10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX PubMed-11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 contains chondroitin sulfate E in the repeating disaccharide region
 and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell motility and transcription regulation through protein-protein
 interactions (By similarity). Can promote transcription activation
 through binding to APBB1/Tip60 and inhibit Notch signaling through
 interaction with Numb (By similarity). Couples to apoptosis-
 inducing pathways such as those mediated by G(O) and JIP. Inhibits
 G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 mediating the axonal transport of beta-secretase and presenilin 1
 (By similarity). May be involved in copper homeostasis/oxidative
 stress through copper ion reduction. Can regulate neurite
 outgrowth through binding to components of the extracellular
 matrix such as heparin and collagen I and IV (By similarity). The
 splice isoforms that contain the APTI domain possess protease
 inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPK II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAP4B1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FRL1, APPB1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC pits. Query Match 95.7%; Score 3493.5; DB 1; Length 770;
 Best Local Similarity 87.7%; Pred. No. 2.le:166;
 Matches 675; Conservative 8; Mismatches 12; Indels 75; Gaps 1;
 QY 1 MRLGLALLLLAANTARALEVPTDGNAGLAEPOIAMFCGRLLNMHNVONGKWDSPGSK 60
 DB 1 MRLGLALLLLAANTARALEVPTDGNAGLAEPOIAMFCGRLLNMHNVONGKWDSPGSK 60
 QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVTONMCKRGKCKKTHPHFVPIYRCLVG 120
 DB 61 TCIGTKEGILQYCOEYVPELQITNVVEANQPVTONMCKRGKCKKTHPHFVPIYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHORMDVCETHLHWHVAKETCSKSTNLHVDYGMLLPGCIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHORMDVCETHLHWHVAKETCSKSTNLHVDYGMLLPGCIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVAEEVEE 240
 DB 181 GVEFVCCPLAESDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVAEEVAEEVEE 240
 QY 241 EADDEDEDGDEVEEEAEPEEATERTTSIATITTTTSTESVEEVR----- 288
 DB 241 EADEDEVEDGDEVEEEAEPEEATERTTSIATITTTTSTESVEEVR----- 300
 QY 289 ----- 289
 DB 301 RAMISRWFVDTEGKCAPFFYGGCGGNRNFTDEEYCMVCGSVSSQSLLKTTSEPLPD 360
 QY 289 ---VPTTAASPDAVDKYLETPGDENEHAHFKAKERLEAKHREMSVMVWEAEAEQA 345
 DB 361 PVKLPITTAAS:PDVDKYLETPGDENEHAHFKAKERLEAKHREMSVMVWEAEAEQA 420
 QY 346 KNLPRADKAVIQIFQEKVESLEGEAANERQOLVETHMARVEAMLNRRRLALENYITAL 405
 DB 421 KNLPRADKAVIQIFQEKVESLEGEAANERQOLVETHMARVEAMLNRRRLALENYITAL 480
 QY 406 QAVPPRPHVFMUKKYYRAKOKRQHTLKHFEHVVMVDPKKAAQIRSQVTHLRVIYER 465
 DB 481 QAVPPRPHVFMUKKYYRAKOKRQHTLKHFEHVVMVDPKKAAQIRSQVTHLRVIYER 540
 QY 466 MNQSLSLYNYPAAVEETQDEVDLLOKEQYSDVLANMISEPRISYCNALPSTLET 525
 DB 541 MNQSLSLYNYPAAVEETQDEVDLLOKEQYSDVLANMISEPRISYCNALPSTLET 600
 QY 526 KTTVELLPVNGEFSLDDLPNRSFCADSVPAANTEVEPEVDARPAADRGLTTRPGSLTN 585

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Db 601 KITVELLVNGEESDDQPMHPEGVDSVPANTENEVEPVDARPAADKGLTREGSLIN 660
QY 586 IKTEISEVKMDAERHDSGVEVHHOKLVFFARVDSNKGAIIGLMVGGVYATVIVITL 645
Db 661 IKTEISEVKMDAERHDSGVEVHHOKLVFFARVDSNKGAIIGLMVGGVYATVIVITL 720
QY 646 VMLKKKQYTSIHGGVVEVJAAVTPERHLSKMQNGYENPYKXFEQMON 695
Db 721 VMLKKKQYTSIHGGVVEVJAAVTPERHLSKMQNGYENPYKXFEQMON 770

RESULT 8
APP2_MOUSE STANDARD: PRT: 695 AA.
AC Q06335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CJSEBF).
GN APLP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SKQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RA von der Kammer H.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-246 FROM N.A.
RX MEDLINE=94032480; PubMed=8218408;
RA Hanes J., von der Kammer H., Kristjansson G.L., Scheit K. et al.
RT "The complete cDNA coding sequence for the mouse CDEI box-binding
RT protein."
RL Biochim. Biophys. Acta 1216:154-156(1993).
RN [3]
RP SEQUENCE OF 185-695 FROM N.A.
RX SURATN=PALB/C; TISSUE=Heart;
RL MEDLINE=93129193; PubMed=1482349;
RA Vidal F., Blangy A., Rassoulzadegan M., Cuzin F.;
RT "A murine sequence-specific DNA binding protein shows extensive local
RT similarities to the amyloid precursor protein."
RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN [4]
RP SEQUENCE OF 1-35 FROM N.A.
RX STRATN=129/Sv;
RL MEDLINE=96029629; PubMed=7592716;
RA von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT "The mouse APLP2 gene. Chromosomal localization and promoter
RT characterization."
RL J. Biol. Chem. 270:26475-26480(1995).
CC -1- FUNCTION: BINDS TO THE DNA 5'-GTGACATG-3' (CDEI BOX) WHICH PLAYS
CC AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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DR MGD: MGI:86047; APLP2.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR Transmembrane: DNA-binding; Signal: Nuclear protein.
KW SIGNAL 1 29
FT CHAIN 30 695
FT DOMAIN 30 624
FT TRANSMEM 625 648
FT TRANSMEM 649 695
FT DOMAIN 218 294
FT DOMAIN 218 231
FT DOMAIN 236 266
FT CARBOHYD 485 485
FT CONFLICT 185 185
SQ SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

Query Match 47.5%; Score 1735; DB 1; Length 595;
Best Local Similarity 49.3%; Pred. No. 3.3e-79;
Matches 360; Conservative 118; Mismatches 162; Indels 90; Gaps 19;

QY 5 LALLLLAANTARALEV-----PTDGNAG-----LLAEPQIAMFCGRLLNMHMVQNGKWDSDP 56
Db 15 LLLVLLGLTAPAAALAGVIEAALANAGTGFAVAEPQIAMLCGLNMHMVNIQTCKWEDP 74
QY 57 SGTKCIDTKEG:LYQCQEVYPELQITNVNANQVPTIQNMCKRGKCKTHPHFVPIYR 116
Db 75 TGTKSLGTKEEVLYQCQEIYPELQITNVNANQVPTIQNMCKRGKCKTHPHFVPIYR 132
QY 117 CLVGFVSALLVPCKFLHQRMDVCTHLHWHIVAKETCSEKSTNLHRYGMLPCGI 176
Db 133 CLVGFVSALLVPCKFLHQRMDVCTHLHWHIVAKETCSEKSTNLHRYGMLPCGI 192
QY 177 DKFRGVFVCCPLAE--ESDNYSDADAEEDSDVMWGGADTGYAGSEKVVVEVAE---E 231
Db 193 DQFHGT:EYVCCPQTKTVSDSTNSKEEFEEF-----DESEDEYDLDKSEFTE 243
QY 232 EYVAEVEEREAD--DDEDDGDEVEEEAE-----EPYEEATERT:SIATITTTTIES 282
Db 244 ADUEDTEAAADEEEDESEGEVEVEDRDYDDPKFGDDYNE--ENPTPESEGTISDKE 301
QY 283 VEVVVRVPTAASPTDAVDKYLETQDENEHAFQKAKERLEAKRKERMSQVMREWEFAE 342
Db 302 IVHDVKVPT:PLPTND--VDVYLETSAODNEHAFQKAKERLEAKRKERMSQVMREWEFAE 360
QY 343 RQAKNLPKADKKAVIQHOFQEKVESLEQEAERQQLVETHMARVEAM:NDRRRLALENYI 402
Db 361 LQAKNLPKTERQTI:QHFQAKYKALEKAASEKQQLVETHLARVEAM:NDRRRLALENYI 420
QY 403 TALQAVPRPRHVFNMKKYVRAFQKDRQRT:LKHEHVRKVPKKAQOTRSQVMTHLRVI 462
Db 421 AALQSDPPRPR:LOAI:RRYVRAENKDRLHTIRHYQVLYAVDEKAAQMKSQVMTHLVI 480
QY 463 YERNQSLSLN:VYFAVEIQDVEDEILQKEQVSDVVIANNISEPRISVYNDALMPSL 522
Db 481 EERRNGSLTLYKVPYVAQEIQDEIDELLQEQR-----ADM-----DOFISSI 523
QY 523 TERTKTVELLPVNGEESDLODPWHSFGADSPANTENEVEPVDARPAADKGLTTRPGSG 582
Db 524 SENPVDVRSSSEKSE:EIPFPFLHPF-----PSUSENE-----GSGMAEQD-G 566
QY 583 LTNIKITEEI:SEYKMDAEFRHDSGVEVHHQKLVFFAEVDGVS-----NK 624
Db 567 LIGAEKVKNSKNKMDENNVIDETLDV--KEMIFNARVGGLEEBEPESVGPLREDFSLSS 624
QY 625 GATIGLMVGQWVIATVIVITLVLMLKKQYTSIHGGVVEVJAAVTPERHLSKMQNGYEN 684
Db 625 NALIGLLVIAVAIATVIVISLMLRKQYGTISHGIVEVDPMLTPEERHLNKNQNGYEN 684
QY 685 PTYKFEQMQ 694
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DB      635 PYYKLEQW 694
||||| |||
APP2_HUMAN
ID      APP2_HUMAN      STANDARD:      PRT:      763 AA.
AC      Q06481.
DI      01-JUN-1994 (Rel. 29, Created)
DI      01-OCT-1996 (Rel. 34, Last sequence update)
DI      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE      (CDEI-box binding protein) (CNEBP).
GN      APLP2 OR APPL2
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RC      TISSUE=Placenta;
RX      MEDLINE=93250009; PubMed=8495127;
RA      Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA      Norris K., Foster D.C.;
RT      "Molecular cloning of the cDNA for a human amyloid precursor protein:
RT      homolog; evidence for a multigene family.";
RL      Biochemistry 32:4481-4486(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Ovary;
RX      MEDLINE=95217334; PubMed=7702756;
RA      von der Kammer H., Hanes J., Klaudiny J., Schreit K.H.;
RT      "A human amyloid precursor-like protein is highly homologous to a
RT      mouse sequence-specific DNA-binding protein.";
RL      DNA Cell Biol. 13:1137-1143(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=94035131; PubMed=8220435;
RA      Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA      Hyman B.T., Neve R.L., Tanzi R.E.;
RT      "Isolation and characterization of APLP2 encoding a homologue of the
RT      Alzheimer's associated amyloid beta protein precursor.";
RL      Nat. Genet. 5:95-99(1993).
RN      [4]
RP      SEQUENCE FROM N.A. (ISOFORM 3).
RC      TISSUE=Lung;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuier G.D.,
RA      Altschul S.F., Zeeberg B., Huotow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
RA      Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA      Brownstein M.J., Ussid T.B., Toshitoki S., Carninci P., Prange C.,
RA      Kaha S.S., Loughlan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Ketteran M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grumman J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 5,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC      SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC      FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC      MAY BIND TO THE DNA 5'-GTCACTG-3' (CDEI BOX).
CC      -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR

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Query Match      47.3%; Score 1728; DB 1; Length 763;
Best Local Similarity 47.1%; Pred. No. 8,1e-79;
Matches 372; Conservative 112; Mismatches 165; Idels 140; Gaps 20;

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QY 5 LALLLAANTARALEV-----PTDGNAG-----LLAEPCIAMFGRLNMKNVQKQWSDRP 56
DQ 11 LLLL LLLVGLAPALALAGY TEALANAGATGFAVAEPQIAEFCCKI NMHVNITQKWEPPF 74
QY 57 SGTCTGDTKFGILOQYCOEYVPELOIINVFANQPVITQSKCKRGKQCKIHPHFVPIYK 116
DQ 75 TGTASCFTKEEVLOYCOEYVPELOIINVFANQPVITQSKCKRGKQCKIHPHFVPIYK 132
QY 117 CLVGEFVSADLLVPDKCKFKHQEMQVCEPHJRHVTAKETCSEKSTNLDYQMLLPQGI 176
DQ 133 CLVGEFVSADLLVPDKCKFKHQEMQVCEPHJRHVTAKETCSEKSTNLDYQMLLPQGI 192
QY 177 DKFGVGFVCCPLAEESDNDSDADREDDSDVWNGCADIDYAGSDKDKVVEAESEKVAE 236
DQ 193 DQFGITVCCPQTKIGSVKSEEEDEE-----EEEEDEEDDYVYKSEFTPEAD 245
QY 237 VEE--SEA--DDEDEDDGDEVEEAEPEY-----FEATERITISATITTTTIS 282
DQ 246 LEDTEAAVDEDDDEGEVEVEDRDYYDTKGGDYNEENPTPGSDCTMSDKELIHD 305
QY 283 VEEV-----VAVP 290
DQ 306 VKAVCSQEAHTGPKAVYPRWYFDLSKGCVKVRFYGGCGNRRNPFSEDIYCMVCKAN:P 365
QY 291 TTAASTPDADVKKYLEITPCDENFHAHFQKAKERLEAKHREKMSOVNREWEFAEPOAKNLXP 350
DQ 366 PTLPLTND-VDVYFETSDADNEHAFQKAKEQLEIRHRNRMCRVKKEWEAELOAKNLXP 424
QY 351 ADKAAVTOHFOEKVESLEQPAANROOLVETHKARVEAMLNDRRRLALENYITALQAVPP 410
DQ 425 AEROTLTOHFOEAMKALEKAASEKQOLVETHLARVEAMLNDRRRLALENYITALQAVPP 464
QY 411 RPRHVENMLKKYRASOKDROHTLKHFEHVMVLPKKAQAIRSOVMTILRVIVERNQSL 470
DQ 485 RPRHVENMLKKYRASOKDROHTLKHFEHVMVLPKKAQAIRSOVMTILRVIVERNQSL 544
QY 471 SLNVPAVAPEIQDEYDELQKQEQNYSDVVIANMISEPRISYNDALMPSLFEKTIVE 530
DQ 545 SLNVKVPVAQEIQDEIDELIQEQ-----ADM-----DQFTASLSETPVDVR 587
QY 532 LLPVNGFSLDLOPHSFADSVPAENTENEVEFVDAKPAADHGLITRPSGLTN----- 585
DQ 588 ---VSSEES-EEIPPHPF--HPPFALPENE---DTQPELYHPM--KKGSGVGVGGGL 635
QY 586 IKTEE---ISVKMDAEFRDQSGVEVHHQKLVFAEDVGS-----NKG 625
DQ 636 IGAEKVINSKKNVDENVNIDELDV--KENIFNAERVGGIIEERKSVGLRDFSLSS 683
QY 626 AILGLMGVGVVIAVITVLVNLAKKQYTSIHGQVVEVQAAVTFEERHLSKMGQNGYHNP 695
DQ 694 AILGLLVIAVIAVITVLSVLMKRGQYTSIHGQVVEVQAAVTFEERHLSKMGQNGYHNP 753
QY 685 IYKFFEQMO 694
DQ 754 IYKYLEQMO 762

RESULT 10
APP2_RAT
ID APP2_RAT STANDARD; PKT: 765 AA.
AC P15943;
DI 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid-like protein 2 precursor (Sperm membrane protein Ywk-II).
GN APLP2
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-627 FROM N.A.
```

```
RC STRAIN=Swistar; LISSUB=Brain, and Heart;
RX MEDLINE=94368849; PubMed=8086458;
RA Sandrink R., Masters C.L., Beyreuther K.;
RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT difference to human and murine homologues.";
RL Biochim. Biophys. Acta 1219:167-170(1994).
RN [2]
RP SEQUENCE OF 575-765 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=90207205; PubMed=16590887;
RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT "Characterization of cDNA encoding a human sperm membrane protein
RT related to A4 amyloid protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
RC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC IsoId=P15943-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P15943-2; Sequence=VSP_000021;
CC Name=C;
CC IsoId=P15943-3; Sequence=VSP_000020;
CC Name=D;
CC IsoId=P15943-4; Sequence=VSP_000020, VSP_000021;
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X77934; CAA54906.1; .
CC EMBL: M31322; AAA42352.1; .
CC PIR: A35981; A35981.
CC PIR: S42880; S42880.
CC HSP: P05067; IIMP.
CC InterPro: IPR001868; A4_APP.
CC InterPro: IPR002223; Kunitz_BPTI.
CC Pfam: PF02177; A4_EXTRA; .
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC PRINTS: PR00759; BASICPTASE.
CC PRODOM: P000022; Kunitz_BPTI; 1.
CC SMART: SM00005; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE: PS00279; BPTI_KUNITZ_2; 1.
CC Transmembrane: Alternative splicing; Serine protease inhibitor;
CC Signal: Glycoprotein.
CC SIGNAL: 1 29
CC CHAIN: 30 765
CC DOMAIN: 30 595
CC TRANSMEM: 596 718
CC DOMAIN: 719 765
CC DOMAIN: 218 282
CC DOMAIN: 308 366
CC ACT_SITE: 322 323
CC DISULFID: 312 362
CC DISULFID: 321 345
CC DISULFID: 337 358
CC DOMAIN: 218 229
CC CARBOHYD: 628 628
CC VARSPIC: 311 365
CC VARSFLIC: 616 627
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FI  CONFLICT 575 577 /FTID-VSP_000021.
FT  DQF -> EFV (IN REF. 2).
SQ  SEQUENCE 765 AA: 86882 MW:  CFS1PCCE30SA0CF CRC64:

Query Match 47.0%: Score 1716; DB 1: Length 765;
Best Local Similarity 46.2%: Pred. No. 3,26-78;
Matches 364; Conservative 122; Mismatches 166; Indels 136; Gaps 20;

QY 5 LALLLLAAWTARALEV-----FTDGNAG---LLAEPOIAHKCGRLNHHMNVCKKSLSDP 56
DB 15 LVVLLGLTAPAAALAGYIEALANAGTGFAVAEPQIAFCGKLNMEVNTCTGRKWFDP 74
QY 57 SGTGICIDTKEGILQYCEVYPELQITNVZPANGPVTIQNMCKKGRKCKTHPFEVTPYK 116
DB 75 TGTSCSLGTKEVLQYCEVYPELQITNVZPANGPVTIQNMCKKGRKCKTHPFEVTPYK 116
QY 117 CLVGFVSDALLVPDKKFLHQERMDVCETHLHHHTYAKESCSSEKSNLHEDYGMLLPGY 176
DB 133 CLVGFVSDALLVPDKKFLHQERMDVCETHLHHHTYAKESCSSEKSNLHEDYGMLLPGY 176
QY 177 DKFKGVFVCCPLAE--ESDNVVSADAEEDSDVKNVGGADTDYA-DGSEKVVVEVAPEER 233
DB 193 DQFHGTVEVCCFOTKVVVDSSTKKEKEKEFESE-----DEEDYALDKSEPTHEADLFT 248
QY 234 VAEEVEEADDDDEDGVEVEEAEPEYEE-----ATERTISTATITTTTTSVEEVV 287
DB 249 EAAADEDEDEFEDEEVEVVEDDYVYUSFKGIDVNEENPTPESSDGTISDKFAHGV 308
QY 288 R-----VPT 292
DB 309 KAVCSQEAHTGPCRAVMPRWYEDLSKGVRYFGCGGGRNNEFESENYCMVAGTKTIPP 368
QY 292 TAASTPDADVKTLETPGDENEHAFOKAKEMIAKHHRMSQVMREFAEFAKQAKNLPKA 352
DB 369 TPLPND-VVYFEISADNEHAFQKAKQLEIHRSRMDRVKKEWEAEALQAKNLPKA 427
QY 352 DKKAVIQHFQKVESLEQEAANERQOLVETHHARVEAMLNDRRRLALENYITA-QAVPPR 411
DB 428 EROTLIQHFQAVKALEFAASEKQQLVETHLARVEAMLNDRRRLALENYLAALQSDPPR 487
QY 412 PRHVNMLKVVYRAOKDROHTLKHFEHVRVMDPKAAQIRSOVMTHLRVIYERNNOSLS 471
DB 488 PHRLQALRRVYRAENKDRHLHIIRYOHVLAVDEPKAAQMSQVMTHLRVIYERNNOSLS 547
QY 472 LYNVYPAVAEEIQDEVDLLOKEQNYSDVLANNMISEPRISYGNDA-MPSLITE-KTIVEL 531
DB 548 LLYKVPYVAQIEQIEIDELQEQR-----ADM-----DOFTSSISENPVDVR- 599
QY 532 LPVNGEFLDLOPHSHSGADSVANTENEVEPYDAPADRGLTTRPGSLTN-----I 596
DB 590 --VSSEES-EEIPFPHP--HPFFSLSENE---DTQPELYHPM--KKGSQMAEQDGGIT 638
QY 587 KTEE---ISEVKMAEPRHDSGYEVHHOKLVFFAEEDVGS-----NKGK 626
DB 639 GAEEKVINKKNKMDENWYDTELTV-KEMFNKERVGGILEEEDPSVGLPREDTSLSSA 696
QY 627 IGLMGVGVATVITVITLVMLKKQKQYTSIHGGVVEVJAAVYTPPEERHLKSKQONSYPNT 693
DB 697 LIGLIVIAVAIATVIVISVLMRLKQYGTLSHGIVEVHPMLTPEERHLKKNHONHYENPT 756
QY 687 YKFEQCMQ 694
DB 757 YKYLFOQM 764

RESULT 11
APPL_HUMAN
ID APPL_HUMAN STANDARD: PRI: 650 AA.
AC P51693; O00113; Q96A92;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP-1) [Contains: C30].
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GN APLP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98088960; PubMed=9428584;
RA Paliga K., Peraus G., Kreyer S., Duwrrwang U., Hesse L., Muthaup G.,
RA Masters C.L., Beyreuther K., Weidmann A.;
RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RT expression in COS-7 cells and identification of soluble forms in the
RT cerebrospinal fluid.";
RL Eur. J. Biochem. 250:354-363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98180887; PubMed=9521586;
RA Lenkner U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA Olsen A., Tryggvason K.;
RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT 19q13.1.";
RL Hum. Genet. 102:192-196(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE-Ovary;
RP MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dergo J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=96115107; PubMed=7494461;
RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA Black I.B.;
RT "Selective localization of amyloid precursor-like protein 1 in the
RT cerebral cortex postsynaptic density.";
RL Brain Res. Mol. Brain Res. 32:36-44(1995).
RN [5]
RP HEPARIN AND ZINC BINDING.
RX MEDLINE=95014513; PubMed=7929392;
RA Bush A.T., Pettingell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT "The amyloid beta-protein precursor and its mammalian homologues.
RT Evidence for a zinc-modulated heparin-binding superfamily.";
RL J. Biol. Chem. 269:26618-26621(1994).
RN [6]
RP INTERACTION WITH APOA2.
RX MEDLINE=99107877; PubMed=9890987;
RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA Sakiyama S., Kirino Y., Suzuki T.;
RT "Interaction of a neuron-specific protein containing PDZ domains with
RT Alzheimer's amyloid precursor protein.";
RL J. Biol. Chem. 274:2243-2254(1999).
RN [7]
RP EXTRACELLULAR COPPER-BINDING.
RX MEDLINE=22130992; PubMed=12135352;
RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Fipkorn R.,
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APPL_MOUSE
ID APPL_MOUSE STANDARD; PRG: 653 AA.
AC 003157; Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DI 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN APLP1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
ON [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC TISSUE=Brain;
RX MEDLINE=93065322; PubMed=1279693;
RA Wasco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E.,
[1]
RT "Identification of a mouse brain cDNA that encodes a protein related
to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10759-10762(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Schenken C.M., Schuler G.E.,
RA Atschul S.P., Zeeberg B., Huotow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McWen P.J., McKernan K.C., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muny D.M., Sodergren E.J., Li X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903(2002).
RN [3]
RP COLLAGEN-BINDING.
RX MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse I., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [4]
RP INTERACTION WITH DAB1.
RX MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
protein 1.";
RL J. Neurosci. 13:7507-7515(1999).
RN [5]
RP INTERACTION WITH MAPK8IP1.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Hemma Y., Ito Y., Niikura T., Hiseki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Chersi E., Laky K., Fowkes B.J., D'Adamo L.;

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RT Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
secretase regulates transcription.;
RL J. Biol. Chem. 277:44195-44201(2002).
CC !- FUNCTION: May play a role in postsynaptic function. The C-terminal
gamma-secretase processed fragment, ALD1, activates transcription
activation through APBB1 (Fe65) binding. Couples to JIP signal
transduction through C-terminal binding. May interact with
cellular G-protein signaling pathways. Can regulate neurite
outgrowth through binding to components of the extracellular
matrix such as heparin and collagen I.
CC !- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
neuronal apoptosis (By similarity).
CC !- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
cytoplasmic proteins, including APBB and APBA family members, its
MAPK8IP1 and Dab1 (by similarity). Binding to Dab1 inhibits its
serine phosphorylation.
CC !- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
processed in the Golgi complex.
CC !- DOMAIN: The NPXY sequence motif found in many tyrosine-
phosphorylated proteins is required for the specific binding of
the PID domain. However additional amino acids either N- or C-
terminal to the NPXY motif are often required for complete
interaction. The NPXY site is also involved in clathrin-mediated
endocytosis.
CC !- PTM: Proteolytically cleaved by caspases during neuronal
apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
similarity).
CC !- PTM: N-glycosylated.
CC !- PTM: O-glycosylated.
CC !- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
Zinc-binding increases heparin binding. No Cu(II) reducing
activity with copper-binding.
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@sib-sib.ch).
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DR EMBL: L04538; AAA37247.1;
DR EMBL: BC021877; AAA21877.1;
DR PIR: A46362; A46362.
DR HSP: P05067; LMWP.
DR MGD: MGI:88046; Aplpl.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
KW Glycoprotein.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 553 AMYLOID-LIKE PROTEIN 1.
FT DOMAIN 624 653 C30 (BY SIMILARITY).
FT TRANSMEM 38 583 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 594 606 POTENTIAL.
FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 157 177 COPPER-BINDING.
FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 263 271 POLY-GLU.
FT DOMAIN 535 538 POLY-SER.
FT DOMAIN 601 606 POLY-LEU.
FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
SIMILARITY).
FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY

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[illegible]

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DB 6 LMIGLLIPILVA-TVYAEAGSPAGSKRHEKFIPTVAFSGYRNQYM-TEEGSKTKDDEHYA 63
QY 61 TCIDIKEGILQYCEVPELOITVNVFANQPVTTQWCKRGRKCKCKTHPRVIVIPRLVG 120
DB 64 TCFSGKDLILKYCKAPVSMITIVIVESHVSISOMCREEGSPCK-WTHSVRYPHGIDG 122
QY 121 EFVSADLLVPCKKFLFOERMDVCETHLHWHITVAKETCSEKSTN-----LHCVGMGLLPC 174
DB 123 EFHSEALVPHDCQFHSVNSQCNDYOHWDKAGCKCKTKSKGNKDMIVKSFVAVLEPC 182
QY 175 GIDPRGVFEVCCPLAESDNVDSADAEEDSDVWVGADPYAGSGCKVVEAAEEHY 234
DB 183 ALDMFIFGVFEVCCP-----NDQTNKTDVQTK----- 209
QY 235 AEVDEEADDEDDGDEVEEAEPEPEPATERTISATTTITTESVEVVRVPTTAA 294
DB 210 ---EDDDGDDDDDAYEDSYSEEDKDEE----- 236
QY 295 STPDADVRLTPTGDENEHAHFQKAKERLEAKHRMSQVWKEFEA-----EPOAKNLP 349
DB 237 -EPSQDPFYKIANWNEHDDFKAEHMDKHKVKDKYKWKNGDLETRVNEOKAKD-P 294
QY 350 KADKKAVQ--HFQEKVESLEQEAANERQOLVETHMARVEMAMLRRCALFNVTAL- 405
DB 295 KGAEKFSQMARFQKTVSSLEEDHKRMRKEIEAVHEEVRQAMLNKKRSDATHDYKQALA 354
QY 406 -QAVPPEPRHVENMLKTVRAEQDROHTLKHFEHVRMVPDKKAAQ-RSQVWTHLAVIYE 464
DB 355 THVKNPKNHSVLQSKAVIRAEEDKDRMHTLNKYLKADSKAEAAKVPVTHHRTYIDL 414
QY 465 RHNOSLSLLYNP-----AVA--FFIQDEVZELIQFQNVSDVLANVISEPRTSY 513
DB 415 RINGTFLAMLRDEPDKLVKRVPIANTYKNKYDVSQISVSE----DSELTFLHDEDFSK 470
QY 514 GN--DALMPSLT-----EKTIVVELLPVNGFSLDQLQWHSFGADSVDPANT---ENEVEP 564
DB 471 NAKLDVKAPTITIAKPVKCTDNKAVLPTFASDSEEEADVEYDEDEQVKKTPDKKKVKV 530
QY 565 VDARP-----AADRLTTPGSGSLNITEE-----ISEVKMDA 596
DB 531 VDIPKELKVTIEBKAPKLVETSVQTDDEDDSSSTSSSESDDEDKNKELRVET 590
QY 599 E-----FRHDSGVEVHQKLVFAEDVGSNKGALIGVMGVVATVITLVMLK 649
DB 591 EPIIDEPASFYRD-----KLIQSPVEVSASSVPQPVLASAMFITAICIIAFAIT 642
QY 650 KKQVTSIHGVVEYDAAVTPERHLSKMQQNGYENPTYKFFE 691
DB 643 NARRRRAMRGFIEVD-VYTPERHVAGVQNGYENPTYSFED 683
RESULT 14
AA_DROME STANDARD: PRT; 897 AA.
AC P14599; Q91VW0; Q9U4H3; Q9W5F1;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-amyloid-like protein precursor.
GN APPL OR VND OR BCDNA:GH0413 OR EG:65F1.5 OR CG7727.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea; Drosophilidae; Diptera; Brachycera; Muscomorpha;
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69184650; PubMed=2434667;
RA Rosen D.R., Martin-Norris L., Luo L., White K.;
RI "A Drosophila gene encoding a protein resembling the human
RL beta-amyloid protein precursor.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berhan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtils K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pa.Cs B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fogle C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeigwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith I.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sw.Shas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhu G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP REVISIONS.
RC STRAIN=Berkeley;
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Borman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review.";
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Oregon-R;
RA MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrall B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Urquano S., Gloux S., Lelaure V., Mortier S., Galibert F., Rorkova D.,
RA Papaannakis G., Spanos L., Cox S., Siden-Kiamos I., Bolshakov S.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Vaienti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster.";
RN Science 287:2220-2222(2000).
RN [5]
```

SEQUENCE FROM N.A.
 STRAIN=Berkeley; TISSUE=Ovary;
 MEDLINE=20196012; PubMed=10731138;
 Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
 Stapleton M., Harvey D.A.,
 "A Drosophila complementary DNA resource";
 Science 287:2222-2224 (2000).
 [6]
 SEQUENCE OF 1-83 FROM N.A.
 MEDLINE=91184006; PubMed=2127912;
 Martin-Morris L.E., White K.;
 "The Drosophila transcript encoded by the beta-amyloid protein
 precursor-like gene is restricted to the nervous system";
 Development 110:185-193 (1995).
 CC -!- FUNCTION: Probably corresponds to the protein encoded by the
 essential locus vnd, a gene required for embryonic nervous system
 development.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
 central and peripheral nervous systems. Within the nervous system
 transcripts are not observed in neuroblasts, newly generated
 neurons and at least one class of presumed glia cells.
 CC -!- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
 CC -!- DOMAIN: The clathrin-binding site is essential for its association
 with alpha-, beta-, and gamma-. The sequence specific
 recognition extends to peptide residues that are C-terminal to the
 NPXY motif. This interaction appears to be independent of
 phosphorylation (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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 DR EMBL; J04516; AAA28874.1; .
 DR EMBL; AF003418; AAF45520.2; .
 DR EMBL; AL031883; CAA21409.1; .
 DR EMBL; AL022139; CAA21409.1; JOINED.
 DR EMBL; AL022139; CAA18093.1; .
 DR EMBL; AL031883; CAA18093.1; JOINED.
 DR EMBL; AF181628; AAC55414.1; .
 DR EMBL; X55774; CAA39294.1; .
 DR EMBL; X55775; CAA39294.1; JOINED.
 DR PIR; A32758; A32758.
 DR HSP; P05067; IIMP.
 DR FlyBase; FBgn000108; App.
 DR GO; GO:0005576; C:extracellular; IDA.
 DR GO; GO:0005886; C:plasma membrane; IDA.
 DR InterPro; IPR001968; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; .
 DR SMART; SM00006; A4_EXTRA; .
 DR PROSITE; PS00319; A4_EXTRA; .
 DR PROSITE; PS00320; A4_INTRA; .
 KW Signal; Transmembrane; Amyloid; Neurogenesis.
 FT SIGNAL 1 27
 FT CHAIN 28 887
 FT DOMAIN 28 813
 FT TRANSMEM 814 834
 FT DOMAIN 835 887
 FT DOMAIN 877 880
 FT CARBOHYD 150 150
 FT CARBOHYD 161 161
 FT CARBOHYD 237 237
 FT CARBOHYD 240 240
 FT CARBOHYD 574 574
 FT CONFLICT 177 177
 FT CONFLICT 229 229
 FT CONFLICT 332 332
 FT CONFLICT 743 743
 S -> T (IN REF. 1).
 MISSING (IN REF. 1).
 V -> M (IN REF. 4).
 S -> T (IN REF. 1).

RP	SEQUENCE	887 AA:	98332 MW:	P0F0855AD65A5275	CRCS4;
RC	Query Match		20.5%;	Score 748.5;	DB 1; Length 887;
RX	Best Local Similarity		25.5%;	Pred. No. 3.8e-30;	
RA	Matches	233;	Conservative 128;	Mismatches 287;	Indels 265; Gaps 25;
RY		7	ILLANNTARALEVPTQGNAGLLA----	EPQIATMFC--GRLNHNHY--QNGKRDSDPS;	58
RY		9	ILLRSAAVLA-----CTAGVAAAPRWEPOIAVLCEAGQIYQPYLSEPRGWV--DLK	63	
RY		59	2---KICDTEKGILOXCOEYVPELQITNVVEANOPVTLQNMCKRG---RKCKTHHFV	112	
RY		64	KTGPTCLDAKVELLDYCKKAYPNEDITNIVESHYKIGGWCAGCALNAACKGSIRMI	123	
RY		113	IPYCLGVFFVSDALLVPDKCKFLHQBEMDVCEPHLHHTVAKETCEKTNJHDYGMLL	172	
RY		124	KPFRCL--GPFOSDALLVPEGLFDHINASRCMPFVRWNTGAAACQERGMQRSEFAMLL	182	
RY		173	PCGTDKRGVEVCCP-----	LAESDNVD---S	198
RY		183	FCGLSVFSGVEFCPCPKFKTDEIHWKKIDLPMVPAQAQINSANDELVMNDEDDSNUSNY	242	
RY		199	ADAEEDSDVMWGADTSDYADSDCKVVEVAEEV-----AE	236	
RY		243	KDANEDDL-----DEDDLMGDEDDMDVADEAATAGGSPNTGSSGSDNSGLDDINAE	296	
RY		237	VEE--PEADDDDEDDGDEVEEAEPEY-----EATER	268	
RY		267	YDSGEYNGYEDGAGSEAEVBSNDQSGGAKVWSLKSDSSPSPAPVAPAEKAPVK	356	
RY		269	TTSATITTTTTTSEVEV-----RVPTTAASIPDAVDKYLETFGDENEAHFQ	317	
RY		357	SESVTSTPOLSASAAAFVAANSNGSGTGAGAPPSTAQPTS---DPVTFHDPVYEHQSYK	413	
RY		318	KAKELEKAKPERMSOVMREWEAEAKNLPKADKA-----VLOHFOEKVESLEQE	370	
RY		414	VSOKRESHREKTRVIRKOWMSDLBEKYQDMRLADPRAAQSFKORWTARFQTSVQALEEE	473	
RY		371	ANERQQLVETHMARVEAMLRRLALENYITLQAVPPRPRHVFNMLKYYVRAEKOR	430	
RY		474	GNAEKHQLAAMHQORVLAHINORKREAMTCYQALTEOPNNAHVEKCIQKLLRALHKDR	533	
RY		431	QHTLKHFEI--VRNVDP---KKAQIRSOVMTHLVIYERKNSLSLLYNNYPAVAEEI---	483	
RY		534	AHALAHYHLLNSGCGPGGLEAAASERPRHIERLIDIDRAVNSQSKTMRKRYFELSAQOL	593	
RY		484	-----QDEV-----	487	
RY		594	MNDYILALRSKDDINGSSLSGMSSEAEAGILDKYRVEIKRYAEKURKLAEKORKEQRAA	653	
RY		488	-----DELIOKEQNSDDVLNWISE-----PRISYGNIAL	518	
RY		654	EKEKLEEKLRLEAKKVDMLKSOVAFOOSOPTOSS--QSOAQOQOQPKSLPGKELGPAA	713	
RY		519	M-----PSLIEKTKTVELLPVNGEFSLDLPWHSFGADSVPAANTENEVEPVDARPAADR	573	
RY		714	LVIAANPNLE--TKS-----EKDLSDE-----YGEATVSSTKVOTVLTPTVDDDAVQR	760	
RY		574	SLTTPRSGSLNLIKTEISEVKMDAEFHDHSGYEVHOKLVF-----PAEDVSNK---G	625	
RY		761	AVEDVAAA-----VAHQEAEPQVQHFMTHDLGHRESSFSLRREFQAHAHAKEGRN	811	
RY		626	ATIGLVGVGVVATVIVITLVKLLKKOYTSIH-HGVVEVDAAVTP-----EERHLSKMQ	678	
RY		812	VYTFISFAGIALMAAFVGVAVAKWRTSRSPAOGFTEVDQNTVTHHPIVREKIPVNMQ	871	
RY		679	QNGYENPYKFFE	691	
RY		872	INGYENPYKFE	884	

RESULT 15
 A4_BOVIN

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;

RV SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.:
 RT "Amyloid Precursor Protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AB032550; BAA84580.1; -;
 DR HSSP: P05067; IAP.
 DR InterPro: IPR001866; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR InterPro: IPR002223; Kunitz_BPT1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_BPT1; 1.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Kunitz_BPT1; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPT1_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPT1_KUNITZ_2; 1.
 KW protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 770 AA; 86% MW; 5F7A1DCR2BC050AE CRC64;

Query Match 96.8%; Score 3535.5; FR 5; Length 770;
 Best Local Similarity 88.4%; Pred. No. 5.6e-205;
 Matches 561; Conservative 8; Mismatches 5; Indels 75; Gaps 1.

QY 1 MLPGLALLLLAAWTARALEVFDGNAGLLAEPOIAFMFCGRLLNMHMYQNGKWDSPSGTK 60
 DB 1 MLPGLALLLLAAWTARALEVFDGNAGLLAEPOIAFMFCGRLLNMHMYQNGKWDSPSGTK 60
 QY 61 TCIDTKESGILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYKCLVG 120
 DB 61 TCIDTKESGILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYKCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVPE--VAESEEVAEVE 238
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVPE--VAESEEVAEVE 238
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVPE--VAESEEVAEVE 240
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVPE--VAESEEVAEVE 240
 QY 239 EEEADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVPTTAASTPD 298
 DB 239 EEEADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVPTTAASTPD 298
 QY 241 DEDADDD--DDDDGDEI--EETEEVEEATERTTSIATTTTTSVEEVVPTTAASTPD 298
 DB 241 DEDADDD--DDDDGDEI--EETEEVEEATERTTSIATTTTTSVEEVVPTTAASTPD 298
 QY 299 AVDKYLETPGDNENHAHFQAKERLEAKHRERMSQVWREWEAEERAKNLPKADKKAVIO 358
 DB 299 AVDKYLETPGDNENHAHFQAKERLEAKHRERMSQVWREWEAEERAKNLPKADKKAVIO 358
 QY 359 HFQKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENTITALQAVPPRPVFNFM 418
 DB 359 HFQKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENTITALQAVPPRPVFNFM 418

DB 601 KTVLELLPVNGEFSDDLQPKWPFVDSVPANTENEVEPVDARPAADRGITTRPGSLJN 660
 QY 586 KTEIEISFVKMDAEFRHDSGYEVHOKLVFFAEDVGSNGKGAIGLVGGVVIATVIVITL 645
 DB 661 IKTEIEISFVKMDAEFRHDSGYEVHOKLVFFAEDVGSNGKGAIGLVGGVVIATVIVITL 720
 QY 646 VMLKKQVTSIHGQVVEVDAVTPERHLSKMQONGYENPTYKFFEQMQN 695
 DB 721 VMLKKQVTSIHGQVVEVDAVTPERHLSKMQONGYENPTYKFFEQMQN 770

RESULT 4
 Q9DQJ8 PRELIMINARY; PRI: 695 AA.
 AC Q9DQJ8;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodosse A., Sorribas V.:
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RI isoforms.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF269218; AAG00593.1; -;
 DR HSSP: P05067; IBA4.
 DR InterPro: IPR001866; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR PRINTS: PR00263; AMYLCIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC54;

Query Match 93.9%; Score 3428; DB 13; Length 695;
 Best Local Similarity 94.0%; Pred. No. 1.5e-198;
 Matches 655; Conservative 17; Mismatches 21; Indels 4; Gaps 3;

QY 1 MLPGLALLLLAAWTARALEVFDGNAGLLAEPOIAFMFCGRLLNMHMYQNGKWDSPSGTK 60
 DB 1 MLPGLALLLLAAWTARALEVFDGNAGLLAEPOIAFMFCGRLLNMHMYQNGKWDSPSGTK 60
 QY 61 TCIDTKESGILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYKCLVG 120
 DB 61 TCIDTKESGILQYCOEVYPELQITNVVEANOPVTIONCKRGRKCKTHPHFVTPYKCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSTNLDYGMLLPCGIDKPR 180
 QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVPE--VAESEEVAEVE 238
 DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVPE--VAESEEVAEVE 240
 QY 239 EEEADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVPTTAASTPD 298
 DB 241 DEDADDD--DDDDGDEI--EETEEVEEATERTTSIATTTTTSVEEVVPTTAASTPD 298
 QY 299 AVDKYLETPGDNENHAHFQAKERLEAKHRERMSQVWREWEAEERAKNLPKADKKAVIO 358
 DB 299 AVDKYLETPGDNENHAHFQAKERLEAKHRERMSQVWREWEAEERAKNLPKADKKAVIO 358
 QY 359 HFQKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENTITALQAVPPRPVFNFM 418
 DB 359 HFQKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENTITALQAVPPRPVFNFM 418

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Db 359 HFGEKVESLEQSAAREKQJLVETHMARVEAMLNDRKRIALENYITATQTVPPRPHVFN 478
QY 419 LAKYVRAEKQKQROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPA 478
Db 419 LAKYVRAEKQKQROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPA 478
QY 479 VAEETODEVDELLQKQNYSDVIANMISEPRISYGNDAIMPSTETKTIVVELLPVNGEF 538
Db 479 VAEETODEVDELLQKQNYSDVIANMISEPRISYGNDAIMPSTETKTIVVELLPVNGEF 538
QY 539 SLEDDQPHKSHFCADSVNPANTENEVEPVDARPAADRGHTIRPGSGLIN:KTFEISEVKKCA 598
Db 539 SLEDDQPHKSHFCADSVNPANTENEVEPVDARPAADRGHTIRPGSGLIN:KTFEISEVKKCA 598
QY 599 EFRHDSGVEVHHQKLVFFAEADVGSNGKALIGLWGGVVIATVITLVN:KKKQYTSLEH 659
Db 599 EFRHDSGVEVHHQKLVFFAEADVGSNGKALIGLWGGVVIATVITLVN:KKKQYTSLEH 659
QY 659 GYVEVDAVTPPERHLSKMQONGYENPTYKFFEQMGN 695
Db 659 GYVEVDAVTPPERHLSKMQONGYENPTYKFFEQMGN 695

RESULT 5
QSDGJ7
ID QSDGJ7 PRELIMINARY: PRT: 751 AA.
AC QSDGJ7;
DI 01-MAR-2001 (T-EMBLrel. 16, Created)
DI 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DI 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolase A., Sorribas V.;
RT *Cloning of full-length chicken beta-amyloid precursor protein:
RT isoforms.
RJ Submitted (JUL-2000) to the EMBL/GenBank/CCDB databases.
DR EMBL: AF289219; AAG00594.1;
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD00222; Kunitz_BPTI; 1.
DR SMART: SM00306; A4_EXTRA; 1.
DR SMART: SM00331; Kunitz; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_Kunitz_1; 1.
DR PROSITE: PS00279; BPTI_Kunitz_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA: 64705 MW: 87894.34863094 CMC64;

Query Match: 92.8%; Score 3387; DB 13; Length 751;
Best Local Similarity 96.9%; Pred. NO. 4.9e-196;
Matches 654; Conservative 18; Mismatches 21; Indels 60; Gaps 4;

QY 1 MLPGLALLLAANTARALVPTSGNAGLLAEPCAMFGRLNHNHNVNGSKWDSFGSTK 60
Db 1 MLPGLALLLAAGAAALEVPDAGNAGLLAEPCAMFGRLNHNHNVNGSKWDSFGSTK 60
QY 61 TCIDTREGILQYCOEYVPELQITNVYEAQPTIQNKKRGKQCKTHPHFV:PYRCLVG 120
Db 61 TCIDTREGILQYCOEYVPELQITNVYEAQPTIQNKKRGKQCKTHPHFV:PYRCLVG 120

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QY 121 EFVSALLVPDKCKFJHOERMDVCETHLHWHITVAKETSEKSTNLHDYGMILPGCIDKFR 180
Db 121 EFVSALLVPDKCKLHQBEMDVCETHLHWHITVAKESCSEKSMNLHDYGMILPGCIDKFR 180
QY 181 GYFVCCCLPAESDNVDSADAEDSDVWWSGADTDYAGSGEDKVVE--VAEEVEVAEVE 238
Db 181 GYFVCCCLPAESDNLDSDADAEDSDVWWSGADTDYAGSDKVVVEEPECEBELIYVE 240
QY 239 EBEAEDEDEDEDDGDFVEEAEPEYBEATERTSIAITTTTTTSEVEEVR----- 288
Db 241 DEADDD--DODDGDDEL--EETSEYEAEATERTSIAITTTTTTSEVEEVRSEQAEATG 298
QY 269 -----VPTTAASPTDAVDK 302
Db 299 PGRAMLSRMYFVFAEKGCAFFYGGCGGNRNFDSEYCMVCGSVLPTTAASPTDAVDK 358
QY 303 YLETPGDENEHAHFOKAKERLEAKHRMSQVMREWEAEAKKLPKADKKAIVIQHFE 362
Db 359 YLETPGDENEHAHFOKAKERLEAKHRMSQVMREWEAEAKKLPKADKKAIVIQHFE 418
QY 363 KYESLEQEAANERQQLVETHMARVEAMLNDRKRLAENYITATQVPPRPHVFNMLKKY 422
Db 419 KYESLEQEAANERQQLVETHMARVEAMLNDRRRIALENYITATQVPPRPHVFNMLKKY 478
QY 423 VRAEQKQKROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPAVEE 482
Db 479 VRAEQKQKROHTLKHFEHVRMYDPKKAQAKSQVNTHLRVYERMNQSLSLYNVPAVEE 538
QY 483 IQDEVDDELQKQNYSDVIANMISEPRISYGNDAIMPSTETKTIVVELLPVNGEFLDD 542
Db 539 IQDEVDDELQKQNYSDVIANMISEPRISYGNDAIMPSTETKTIVVELLPVNGEFLDD 598
QY 543 LQPHHSGFADSVNPANTENEVEPVDARPAADRGHTIRPGSGLIN:KTEISEVKKMDAEFRH 602
Db 599 LQPHHSGFADSVNPANTENEVEPVDARPAADRGHTIRPGSGLIN:KTEISEVKKMDAEFRH 658
QY 603 DSGYEVHHQKLVFFAEADVGSNGKALIGLWGGVVIATVITLVN:KKKQYTSIHGVE 662
Db 659 DSGYEVHHQKLVFFAEADVGSNGKALIGLWGGVVIATVITLVN:KKKQYTSIHGVE 718
QY 663 VDAANTPEERHLSKMQONGYENPTYKFFEQMGN 695
Db 719 VDAANTPEERHLSKMQONGYENPTYKFFEQMGN 751

RESULT 6
Q98SG0
ID Q98SG0 PRELIMINARY: PRT: 593 AA.
AC Q98SG0;
DI 01-JUN-2001 (T-EMBLrel. 17, Created)
DI 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DI 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein A.
OS APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hark W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1;
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00306; A4_EXTRA; 1.

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Q91963
ID O91963 PRELIMINARY: PRI: 747 AA.
AC Q91963;
DT 01-NOV-1996 (TREMblrel. 01, Created);
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update);
DE 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodidae.
OX NCBI_taxonomy=8353;
RN [1];
RS SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1232805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL: S52417; AAB24853.1;
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 85.0%; Score 3103; DB 13; Length 747;
Best Local Similarity 81.0%; Pred. No. 6.4e-179;
Matches 598; Conservative 35; Mismatches 41; Indels 54; Gaps 5;

Qy 17 ALEVPDGNAGLLAEPOIAMF-CGRLNHMHNVQNGKWDSPSGTKTCIDTREGILQYQCF 75
Db 15 ALEVLVDGNGLLAEPOIAMFVARLNHMHNVQNGKWDSPSGTKTCIDTREGILQYQCF 7;

Qy 76 VYPELOITNVVEANQPVTTQNNCKRGKCKTTHPHFVTPYRCLGVEFVSDALLVPDKCKP 235
Db 72 VYPELOITNVVEANQPVTTQNNCKRGKCKTTHPHFVTPYRCLGVEFVSDALLVPDKCKP 131

Qy 136 LHQERMDVCETHLHWHTVAKETCSKSTN:HDYGMCLPGCIDKFRGVFVCCPAAFEHSON 195
Db 132 LHQERMDVCETHLHWHTVAKETCSKSTN:HDYGMCLPGCIDKFRGVFVCCPAAFEHSON 191

Qy 196 VDSADAEEDSDVWNGCATDYADGSEKVFVA--EEVEAEVEEAEADDEDEKGE 253
Db 192 FDSADAEEDSDVWNGCATDYADGSEKVFVA--EEVEAEVEEAEADDEDEKGE 249

Qy 254 VEAEAEPEPEEATERTSTATTITTESVEEVVR----- 286
Db 250 AEPEPEPEEATERTSTATTITTESVEEVVR----- 286

Qy 289 -----VPTTAASTFDADVKTLETPENPHAPPO 317
Db 310 SKCAQFIYGGCGNRNFEEDDYCMVCGSV:PAATAASTFDADVKTLETPENPHAPPO 317

Qy 318 KAKERJAKERAKRMSQVNRWESEARQAKNPKADKKAVIQHFKVEKVESLEAEANERQ 377
Db 370 KAKERJAKERAKRMSQVNRWESEARQAKNPKADKKAVIQHFKVEKVESLEAEANERQ 377

Qy 378 LVETHMARVEAMINDRRRIALENYITAILOADPPRPHRVFNMLKKYVRAEQKDRQHTLKH 437
Db 378 LVETHMARVEAMINDRRRIALENYITAILOADPPRPHRVFNMLKKYVRAEQKDRQHTLKH 437
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DQ 125 VPRCLVGEFVSALLVPCKCKFLHREKMDCTCHSHLYWLVAKETGCKIMNLNDYGMILL 164
QY 173 PCGIDKFRGVFEVCCPIARESDNWDSDADAEEDSDSYWVGADTDYADGSEDKVVEVAERE 232
DB 185 PCGIDFRGVFEVCCPIPEENDKIDS-DMDEEDSDYWVGDDADYADGG-DKTV-----EW 238
QY 233 EVAVEVEEEDDEDEDEDEVEVEE-ABEPPYEATERIT-SIATITTTTTTIESVEEVVVP 291
DB 239 KPTEEEEEEDESIDDEDDDDLDDEVEEDYEDPTERTS---STTTTIEAEEVVVVP: 295
QY 292 TAASITDAVDKYLTPGDENEHAHFOKAKERLEAKHRERMSQVMEWEAEARQAKKLPKA 351
DB 296 TAASITDAVDKYLTPGDENEHAHFOKAKERLEAKHRERMSKIMREWEAEARQAKKLPKA 355
QY 352 DKXAVIOHFQKVESLEGEAANERQOLVETHMARVEAMLNDRRRALENY-TALQAVPPK 411
DB 356 DKXAVIOFQKVESLEGEAASRQOLVETHMARVEAMLNDRRRALENYLAALQADPPK 415
QY 412 PRHVFNMKKYVRAEQKDSCHTLKHFPHVRMVDPKKAACTRSQVMTHLVLYERMNOSLS 471
DB 416 PRHVLNALKKYSRAEQKDRHTLKHDFHVRVDPKXAACTRSQVMTHLVLYERMNOSLS 475
QY 472 LLYNVPAAVEFIQDEVDLQKQNYSDVLANMISEPRISYNDALMPSLTETKTVEEL 531
DB 476 LLYKVPAAVEEIQDEVDLQKQNSYNDOMMANSVSDTRISYNDALVPSLSEIKTYTIE 535
QY 532 LPVNGEFLSDDLQFPHSFGADSVPAANTENEVEVDARPAADRGITTPRSGSLTNKTES 591
DB 536 LPDNGEFLSDDLQFPHFVIESIPANTENEVEVDARPAADRGITTPRSGSLTNKTES 595
QY 592 SEVKMDAEFRHDSGYEYVHOKLVFFAEEDVGSNGKAGIIGLVGGVVIATVITVLVMIKK 651
DB 596 AELKMETEFQDSDGYEYVHOKLVFFAEEDVGSNGKAGIIGLVGGVVIATVITVLVMIKK 655
QY 652 QYTSIHGGVVEVDAATFEERHLSKMOONGYENPTYKFFEQMKN 695
DB 656 QYTSIHGGVVEVDAATFEERHLSKMOONGYENPTYKFFEQMKN 699

RESULT 10
Q9PVL1 PRELIMINARY: PRT: 569 AA.
AC Q9PVL1:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Palica K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor superegene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2003).
DR EMBL: AF030341; AAF12698.1; .
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA: 64753 MW: 9AB8B851863A19D CKC64;

Query Match 75.8%; Score 2767.5; DB 13; Length 569;
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Best Local Similarity 93.5%; Pred. No. 7.6e-159;
Matches 535; Conservative 14; Mismatches 18; Indels 5; Gaps 4;
QY 126 ALLVPDKCFURQERMDVCETELHWHRTYAKETSEKSTNLHDYGMLLPCGIDKFRGVFEV 185
DB 1 ALLVPDKCKLLHQBMDVCETELHWHRTYAKESCEKSNLHDYGMLLSCGIDKFRGVFEV 60
QY 186 CQPLAEESNDVSDADEEDSDVWVGADTDYADGSEDKVVE--VAEEVEVAEVEEEDAD 243
DB 61 CQPLAEESNDVSDADEEDSDVWVGADADYADGSDKVVEEQPEDEELTVVEDEAD 120
QY 244 DDEDDGDEVEVEEAEFEYEAETRTTSIATITTTTTIESVEEVVVPITAASTDVADKY 303
DB 121 DD-DDDDGDEL-EETEVEYEATERITTSIATITTTTTIESVEEVVVPITAASTDVADKY 178
QY 304 LETPGDENEHAHFOKAKERLEAKHRERMSQVMEWEAEARQAKNLPKADKKAVIQHFOEK 363
DB 179 LETPGDENEHAHFOKAKERLEAKHRERMSQVMEWEAEARQAKNLPKADKKAVIQHFOEK 238
QY 364 VESLEGEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRHRHVFNMKKYV 423
DB 239 VESLEGEAANERQOLVETHMARVEAMLNDRRRLALENYITALQVTPRPRHVFNMKKYV 298
QY 424 RAEQKDRQHTLKHFPVRMVDPKKAACTRSQVMTHLVLYERMNOSLSLLYNVPAAVEE 483
DB 299 RAEQKDRQHTLKHFPVRMVDPKKAACTRSQVMTHLVLYERMNOSLSFLYNVPAAVEE 358
QY 484 QDEVDRLAQKQNYSDVLANMISEPRISYNDALMPSLTETKTVEELPVNGEFLSDDL 543
DB 359 QDEVDRLAQKQNYSDVLANMISEPRISYNDALMPSLTETKTVEELPVNGEFLSDDL 418
QY 544 QPHSFGADSVPAANTENEVEVDARPAADRGITTPRSGSLTNKTESSEVKMDAEFRHD 603
DB 419 QPHSFGADSVPAANTENEVEVDARPAADRGITTPRSGSLTNKTESSEVKMDAEFRHD 478
QY 604 SGYEYVHOKLVFFAEEDVGSNGKAGIIGLVGGVVIATVITVLVMIKKQYTSIHGGVVEV 663
DB 479 SGYEYVHOKLVFFAEEDVGSNGKAGIIGLVGGVVIATVITVLVMIKKQYTSIHGGVVEV 538
QY 664 DAATVTEERHLSKMOONGYENPTYKFFEQMKN 695
DB 539 DAATVTEERHLSKMOONGYENPTYKFFEQMKN 569

RESULT 1:
Q99K32 PRELIMINARY: PRT: 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 58.4 kDa protein (fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005490; AAH05490.1; .
DR HSSP: P05067; IAAAP.
DR MGD: MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
```

```
DR SMART: SMO0311; KU: 1.
DR PROSITE: PS00319; A4_EXTRA: 1.
DR PROSITE: PS00320; A4_INTRA: 1.
DR PROSITE: PS00280; BPT_KIN172_1: 1.
DR PROSITE: PS00279; BPT_KIN172_2: 1.
KW Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA: 68391 MW: 68022.4C9A7D172 CRC64:
      72.2%; Score 2635.5; DB 11; Length 607;
Query Match
Best Local Similarity 85.7%; Pred. No. 7 5e-152;
Matches 520; Conservative 4; Mismatches 8; Indels 75; Gaps 1;
QY 164 NLHDYGMLLPCGIDKFRGVFVCCPLAEESDVSADAEEDSDVMWGADIDVAGSDE 223
DB 1 NLHDYGMLLPCGIDKFRGVFVCCPLAEESDVSADAEEDSDVMWGADIDVAGSDE 60
QY 224 KYVEVAEEVAEEVEEEDDDDDGDEVEEEAEPEYEATERTISTATITTTTIESV 283
DB 61 KYVEVAEEVAEEVEEEDDDDDGDEVEEEAEPEYEATERTISTATITTTTIESV 120
QY 284 EYVVR----- 288
DB 121 EYVREVCSQEAETGPRAMISRWYFDVTEGKCVDFYCGCGGNKNNEDTEYCVAGCS 190
QY 289 -----VPTAASTPDVDKYLETPGDENEHAHFQKAKERLEAKHR 328
DB 181 VSTGSLTKTTSPLPDQPKLPTTAASTPDVDKYLETPGDENEHAHFQKAKERLEAKHR 240
QY 329 ERMSQVREWEAEERQAKNLPRADKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEA 386
DB 241 ERMSQVREWEAEERQAKNLPRADKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEA 300
QY 389 MLNDRESALENVITALQAVPRPRHVFNNLKKYVRAEQKQKHILKHFPHVRYVDPKKA 449
DB 301 MLNDRRRLALENVITALQAVPRPRHVFNNLKKYVRAEQKQKHILKHFPHVRYVDPKKA 360
QY 449 AQRISQVMTLRLVYIERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISE 508
DB 361 AQRISQVMTLRLVYIERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISE 420
QY 509 PRISYGNDAIMPSTETKTTVELLPVNGEFLDDLPWHSGFADSVPAANTEVEFPVDAR 568
DB 421 PRISYGNDAIMPSTETKTTVELLPVNGEFLDDLPWHSGFADSVPAANTEVEFPVDAR 480
QY 569 PAADRGLTTPGSLNKTIERISEVKMDAEFRHDSGVEVHHQKLVFFAEVDGSKNGAI 628
DB 481 PAADRGLTTPGSLNKTIERISEVKMDAEFRHDSGVEVHHQKLVFFAEVDGSKNGAI 540
QY 629 GLMVGGVVIAIVITVLMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYK 688
DB 541 GLMVGGVVIAIVITVLMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYK 600
QY 689 FFEQMQN 695
DB 601 FFEQMQN 607
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RESULT 12

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O93296
ID O93296 PRELIMINARY; PRI: 534 AA.
AC O93296;
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
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RESULT 13

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O73683
ID O73683 PRELIMINARY; PRI: 780 AA.
AC O73683;
DI 01-AUG-1998 (TrEMBLrel. 07, Created)
DI 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor {Contains:
DE beta-amyloid protein (Beta-APP) (A-beta)}.
DN APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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RX MEDLINE:98337885; PubMed:9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
R "increased production of amyloid precursor protein provides a
R substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EXRL: AF042098; AAC25052.1; -.
DR HSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR0203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA: 60597 MW: FB53ECC2E66D4C92 CRC64:
      71.6%; Score 2613; DB 13; Length 534;
Query Match
Best Local Similarity 94.8%; Pred. No. 1.4e-149;
Matches 506; Conservative 13; Mismatches 11; Indels 4; Gaps 3;
QY 164 NLHDYGMLLPCGIDKFRGVFVCCPLAEESDVSADAEEDSDVMWGADIDVAGSDE 223
DB 3 NLHDYGMLLPCGIDKFRGVFVCCPLAEESDVSADAEEDSDVMWGADIDVAGSDE 62
QY 224 KYVEVAEEVAEEVEEEDDDDDGDEVEEEAEPEYEATERTISTATITTTTITE 281
DB 63 KYVEEOPDEDELTVVEDEDADD- DDDGDGI- ETEEEYEATERTISTATITTTITE 120
QY 282 SVSEVYKVTPTAASTPDVDKYLETPGDENEHAHFQKAKERLEAKHRKSKQVREWEA 341
DB 121 SVSEVYKVTPTAASTPDVDKYLETPGDENEHAHFQKAKERLEAKHRKSKQVREWEA 180
QY 342 EROAKNLPRADKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENY 401
DB 161 EROAKNLPRADKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENY 240
QY 402 ITALQAVPRPRHVFNNLKKYVRAEQKQKHILKHFPHVRYVDPKKAQIRSQVMTLRLV 461
DB 241 ITALQVTPPRHVFNNLKKYVRAEQKQKHILKHFPHVRYVDPKKAQIRSQVMTLRLV 300
QY 462 IYERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMP 521
DB 301 IYERMNSQLSLLYNPVPAVEEIQDEVDLQEQNYSDVLANMISEPRISYGNDAIMP 360
QY 522 LTETKTTVELLPVNGEFLDDLPWHSGFADSVPAANTEVEFPVDARPAADRGLTTRPGS 581
DB 361 LTETKTTVELLPVNGEFLDDLPWHSGFADSVPAANTEVEFPVDARPAADRGLTTRPGS 420
QY 582 GLTNKITEISRVKMDAEFRHDSGVEVHHQKLVFFAEVDGSKNGAIIGLMVGGVVIAIV 641
DB 421 GLTNKITEISRVKMDAEFRHDSGVEVHHQKLVFFAEVDGSKNGAIIGLMVGGVVIAIV 480
QY 642 VITLMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMQN 695
DB 481 VITLMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMQN 534
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GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.
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 Run on: October 2, 2003, 13:55:09 ; Search time 32.3333 Seconds
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 Perfect score: 3651
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 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 1107863 seqs, 158726573 residues
 Total number of hits satisfying chosen parameters: 1107863
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3651	100.0	697	21	Human APPSW-KK am
2	3651	100.0	697	22	Human amyloid prot
3	3651	100.0	697	22	Human amyloid prec
4	3651	100.0	697	22	Human amyloid prec
5	3651	100.0	697	22	Human amyloid prec
6	3651	100.0	697	22	Human amyloid prec
7	3651	100.0	697	23	Human APP695-SW-KK
8	3643	99.8	697	21	Human APP695-KK am
9	3643	99.8	697	22	Human amyloid prot

10	3643	99.8	697	22	AAE06865	Human amyloid prec
11	3643	99.8	697	22	AAU06609	Human amyloid prec
12	3643	99.8	697	22	AAU07208	Human beta-amyloid
13	3643	99.8	697	22	AAE02587	Human amyloid prec
14	3643	99.8	697	23	ABB78596	Human APP695-KK pr
15	3641	99.7	695	21	AAV88435	Human APP695-SW va
16	3641	99.7	695	22	AAE10633	Human amyloid prot
17	3641	99.7	695	22	AAE06863	Human amyloid prec
18	3641	99.7	695	22	AAU06607	Human amyloid prec
19	3641	99.7	695	22	AAU07206	Human beta-amyloid
20	3641	99.7	695	22	AAE02585	Human amyloid prec
21	3641	99.7	695	23	ABB78594	Human APP695-SW pr
22	3638	99.6	697	21	AAV88430	Human APP695-VF-KK
23	3638	99.6	697	22	AAE10637	Human amyloid prot
24	3638	99.6	697	22	AAE06867	Human amyloid prec
25	3638	99.6	697	22	AAU06611	Human amyloid prec
26	3638	99.6	697	22	AAU07210	Human beta-amyloid
27	3638	99.6	697	22	AAE02589	Human amyloid prec
28	3638	99.6	697	23	ABB78598	Human APP695-VF-KK
29	3636	99.6	695	18	AAW19504	APP695 mutant A-be
30	3636	99.6	695	18	AAW19490	Sequence of human
31	3633	99.5	695	9	AP81692	APP695. Homo sapi
32	3633	99.5	695	13	AAE26338	Human beta-amyloid
33	3633	99.5	695	19	AAV20233	Amyloid precursor
34	3633	99.5	695	20	AAV07221	Human APP695 amino
35	3633	99.5	695	21	AAV88434	Human beta amyloid
36	3633	99.5	695	21	AAV44705	Human wild-type am
37	3633	99.5	695	22	AAE10632	Human wild-type am
38	3633	99.5	695	22	AAE06862	Human amyloid prec
39	3633	99.5	695	22	AAU06606	Human amyloid prec
40	3633	99.5	695	22	AAE02584	Human amyloid prec
41	3633	99.5	695	23	ABG32721	Human APP695 prote
42	3633	99.5	695	23	ABB78593	Human amyloid prec
43	3633	99.5	695	23	AAE68315	Amino acid sequenc
44	3633	99.5	695	24	ABB9604	Human beta amyloid
45	3630	99.4	695	20	AAV49690	

ALIGNMENTS

RESULT 1
 AA88429
 ID AA88429 standard; Protein: 697 AA.
 AC AA88429;
 DC 03-AUG-2000 (first entry)
 DE Human APPSW-KK amino acid sequence.
 XX
 XX Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
 KW Alzheimer's disease; beta secretase site; APPSW-KK.
 XX
 XX Homo sapiens.
 XX
 XX WO200017369-A2.
 XX
 XX 30-MAR-2000.
 XX
 XX 23-SEP-1999; 99WO-US20881.
 XX
 XX 24-SEP-1998; 98US-0101594.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yar R;
 DR WPI: 2000-303209/26.
 DR N-PSDB; AAA15666.
 XX
 XX New enzyme designated human aspartase useful in research into
 PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

the beta secretase site to produce amyloid beta peptide -
Claim 133; Page 143-147; 183pp; English.

This sequence represents a modified version of the human amyloid precursor protein (APP) amino acid sequence. The sequence is used in an example of the method of the invention, to show that modification of APP increases beta amyloid protein processing. The invention relates to a protease (e.g. Aspl) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acid sequence DTG and a sequence encoding DTG or DTG separated by 100-300 amino acids. When mutated the APP gene causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single C-terminal transmembrane domain. Proteolytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease. The invention includes a nucleotide sequence encoding the protease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying inhibitors of the protease, are useful in the treatment of and research in to Alzheimer's disease.

XX SQ Sequence 697 AA;
Query Match 100.0%; Score 3651; DB 21; Length 697;
Best Local Similarity 100.0%; Pred. No. 1,40-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAPQIAMFCGRINMNMVONGKWSDFSGTK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAPQIAMFCGRINMNMVONGKWSDFSGTK 60

QY 61 TCIDTKERILQCOEYVPELQITNNVEANQVTONMCKRGKCKTSPHEVPIRYCLVG 120
DB 61 TCIDTKERILQCOEYVPELQITNNVEANQVTONMCKRGKCKTSPHEVPIRYCLVG 120

QY 121 EFVSDALLVPDKCKTLHQRMDVOCETHLHWHVAKETCSKSTNLHDYGMILPGGIDKFR 180
DB 121 EFVSDALLVPDKCKTLHQRMDVOCETHLHWHVAKETCSKSTNLHDYGMILPGGIDKFR 180

QY 181 GVEFFVCCPLAESDNDVSDADESDVWNGCADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFFVCCPLAESDNDVSDADESDVWNGCADTDYADGSEDKVVEAEVEAEVEE 240

QY 241 EADDDDEDDGDEVEEAPEYEEATERTSTIATTTTTSVEEVVRVPTTAASIPFV 300
DB 241 EADDDDEDDGDEVEEAPEYEEATERTSTIATTTTTSVEEVVRVPTTAASIPFV 300

QY 301 DKYLETPGDENHAFQKAKEHLEAKHREMSQVNRKEEAFQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENHAFQKAKEHLEAKHREMSQVNRKEEAFQAKNLPKADKAVIQHF 360

QY 361 QKVESLEQEAANERCOLVETHMARVEAMLDNRRLALENTTALQAVPPRPHVFNKJK 420
DB 361 QKVESLEQEAANERCOLVETHMARVEAMLDNRRLALENTTALQAVPPRPHVFNKJK 420

QY 421 KYVRAEQDKRQHTLKHFEHVRVMDPKKAAQIRSQVMTHLRVYERKMSLSLLNVPAVA 480
DB 421 KYVRAEQDKRQHTLKHFEHVRVMDPKKAAQIRSQVMTHLRVYERKMSLSLLNVPAVA 480

QY 481 ESTQDEVDLQKQNYSDQVLANMISEPRISYGNALMPLSLETETVELLPNGEFL 540
DB 481 ESTQDEVDLQKQNYSDQVLANMISEPRISYGNALMPLSLETETVELLPNGEFL 540

QY 541 DDLQPHSFGADSVPAANTEVEPVDARPAADRGITTRPGSGELNKTKEEISEVNLKAEF 600
DB 541 DDLQPHSFGADSVPAANTEVEPVDARPAADRGITTRPGSGELNKTKEEISEVNLKAEF 600

QY 601 RHDGSGVEVHQKLVFAEDVGSNGKGAITGLMVGGVVIATVITLVMKKQYTSIHGV 660
DB 601 RHDGSGVEVHQKLVFAEDVGSNGKGAITGLMVGGVVIATVITLVMKKQYTSIHGV 660

QY 661 VEVDAAVTPEERHLKSMQONGYENPTYKFFEQMNKK 697
PS |||||
XX 661 VEVDAAVTPEERHLKSMQONGYENPTYKFFEQMNKK 697
DB |||||

RESULT 2
AAE10536
ID AAE10536 standard; Protein: 697 AA.
XX
AC AAE10536:
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid protein precursor 695-Sw-KK (APP695-Sw-KK) isoform.
XX
KW Human; aspartyl protease 1; Aspl; amyloid precursor protein;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neuroprotective;
KW APP695-Sw-KK; mutant; muten.
XX
CS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 595 /note= "Wild-type Lys substituted with Asn"
FT Misc-difference 596 /note= "Wild-type Met substituted with Leu"
FT
XX GB2357767-A.
XX 04-JUL-2001.
XX 22-SEP-2000; 2000GB-0023315.
XX 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99MO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX
XX Bieskowksi MJ, Gurney M;
WP1: 2001-44208/48.
DR N-PSDB; AAD17872.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
XX Example 6; Page 117-119; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-Sw-KK (APP695-Sw-KK) isoform which is obtained
CC by the addition of two lysine residues (KK motif) at the C-terminal
CC of App695-Sw isoform which is generated by the Swedish mutation
CC APP695, where Lys at position 595 is replaced with Asn and Met at

CC	position 595 is replaced with Leu. APP695-Sw-KK isoform is useful for assaying the beta-secretase activity of human aspartyl protease 2a (Hu-Asp2a) protein.	
XX		
SQ	Sequence 697 AA:	
	Query Match 100.0%; Score 3651; DB 22; Length 697;	
	Best Local Similarity 100.0%; Pred. No. 1.4e-256;	
	Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHNMYNQNGKWDSPSGTK 60	
DB	1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHNMYNQNGKWDSPSGTK 60	
QY	61 TCIDTKEGILQYCEVPELQITNNVEANOPVTIONWCKRGRKQCKTHPHFVTPYRC:VG 120	
DB	61 TCIDTKEGILQYCEVPELQITNNVEANOPVTIONWCKRGRKQCKTHPHFVTPYRC:VG 120	
QY	121 EFVSDALLVPDKCFELHQRMDVCEITHLHWRTVAKETCEKSTNLHRYGMLLPCCGIDKFR 180	
DB	121 EFVSDALLVPDKCFELHQRMDVCEITHLHWRTVAKETCEKSTNLHRYGMLLPCCGIDKFR 180	
QY	181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTGYADGSEDKYVEVAEEFEVVEE 240	
DB	181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTGYADGSEDKYVEVAEEFEVVEE 240	
QY	241 EADDDEDDEDGEVEEAEPEEAEATERTTSTIAITTTTTIESVEVVRVP:TTAASTPDAV 300	
DB	241 EADDDEDDEDGEVEEAEPEEAEATERTTSTIAITTTTTIESVEVVRVP:TTAASTPDAV 300	
QY	301 DXYLETDPDENEFAHFQAKERLEAKHRMSQVNRWPEAKRQAKNLPKADKKAV:CHF 360	
DB	301 DXYLETDPDENEFAHFQAKERLEAKHRMSQVNRWPEAKRQAKNLPKADKKAV:CHF 360	
QY	361 QEKVESLEQEAANERQQLVETIHARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420	
DB	361 QEKVESLEQEAANERQQLVETIHARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420	
QY	421 KYVRAEQDKRQHTLKHFEHVRVYDPKAAQIRSQVMTILRV:YERMGSLSLLYNYPVA 480	
DB	421 KYVRAEQDKRQHTLKHFEHVRVYDPKAAQIRSQVMTILRV:YERMGSLSLLYNYPVA 480	
QY	481 BEIQDEVDLLOKEQNSDDVLANNISPRISYGNDAKLPSTLTKTVELLPVNGE:SL 540	
DB	481 BEIQDEVDLLOKEQNSDDVLANNISPRISYGNDAKLPSTLTKTVELLPVNGE:SL 540	
QY	541 DDLQPMHSGADSVFANTENEPVDPADPAADRGTLTPGSGLTNFKTEESSEVNDLAEF 600	
DB	541 DDLQPMHSGADSVFANTENEPVDPADPAADRGTLTPGSGLTNFKTEESSEVNDLAEF 600	
QY	601 RHDSGYEVHHQKLVFEAFEDVGSNGKGAIGLVGVVVIATVITLVMKKGYT:SIHHGV 660	
DB	601 RHDSGYEVHHQKLVFEAFEDVGSNGKGAIGLVGVVVIATVITLVMKKGYT:SIHHGV 660	
QY	661 VEVDAAVTPPEHRLSKMQNGYENPTYKFFEQMNKK 697	
DB	661 VEVDAAVTPPEHRLSKMQNGYENPTYKFFEQMNKK 697	
RESULT 3		
AAE06866		
ID	AAE06866 standard; Protein; 697 AA.	
XX		
AC	AAE06866;	
XX		
DT	23-OCT-2001 (first entry)	
XX		
DE	Human amyloid precursor protein 695-Sw-KK (APP695-Sw-KK) isoform.	
XX		
KW	Human: aspartyl protease; Asp; beta-amyloid precursor protein 695-Sw-KK;	
KW	beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;	
KW	neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;	
KW	neuroprotective; antisense therapy; gene therapy; APP695-Sw-KK; mutant;	

KW	muteln.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
PH	Key Location/Qualifiers	
FT	Misc-difference 595	
FT	/note= "Wild type Lys substituted with Asn"	
FT	Misc-difference 596	
FT	/note= "Wild type Met substituted with Leu"	
XX		
XX	WO200150829-A2.	
XX	19-JUL-2001.	
XX	09-MAY-2001; 2001WO-IB00799.	
XX	09-MAY-2001; 2001WO-IB00799.	
XX	(BIEN/) BIENKOWSKI M J.	
PA	(GURN/) GURNEY M E.	
PA	(HEIN/) HEINRIKSON R L.	
PA	(PARO/) PARODI L A.	
PA	(YANK/) YAN R.	
PI	Fienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;	
DR	WPI; 2001-483072/52.	
DR	N-PSDB; AAD13028.	
XX		
PI	Novel purified polypeptide comprising fragment of mammalian aspartyl	
PI	protease 2, lacking Asp2 transmembrane domain and retaining beta	
PI	secretase activity of Asp2 useful for identifying inhibitors of Asp2	
PI	activity	
XX		
PS	Example 6; Page 147-149; 185pp; English.	
XX		
CC	The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid	
CC	precursor protein (APP) isoforms and their corresponding DNA molecules.	
CC	Human aspartyl proteases can act as beta-secretase proteases useful for	
CC	treating Alzheimer's disease. APP isoforms are useful for identifying	
CC	modulators of amyloid-beta peptide production, for use in designing	
CC	therapeutics for the treatment and prevention of Alzheimer's disease,	
CC	dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis	
CC	and neuronal loss. APP isoforms are also used in methods for identifying	
CC	inhibitors and modulators of human Asp2 activity. The invention relates	
CC	to a method for identifying agents that modulate the activity of human	
CC	aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used	
CC	as a means to screen in cellular assays for the inhibitors of beta- and	
CC	gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in	
CC	polymerase chain reactions (PCR). The probes are useful for detecting	
CC	Hu-Asp nucleic acids in in vitro assays and in Northern and Southern	
CC	blots. The present sequence is modified human amyloid precursor	
CC	protein 695-Swedish (APP695-Sw-KK) isoform. APP695-Sw-KK isoform is	
CC	obtained by addition of two Lys residues (KK motif) at the C-terminal	
CC	end of APP695-Sw isoform. APP695-Sw isoform is obtained by Swedish KM-NL	
CC	mutation in APP695 isoform, where Lys at position 595 is replaced with	
CC	Asn. Met at position 596 is replaced with Leu. APP695-Sw-KK isoform is	
CC	useful for assaying the beta-secretase activity of human aspartyl	
CC	protease 2a (Hu-Asp2a) protein.	
XX		
SQ	Sequence 697 AA;	
	Query Match 100.0%; Score 3651; DB 22; Length 697;	
	Best Local Similarity 100.0%; Pred. No. 1.4e-256;	
	Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHNMYNQNGKWDSPSGTK 60	
DB	1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAFMCGRLNMHNMYNQNGKWDSPSGTK 60	
QY	61 TCIDTKEGILQYCEVPELQITNNVEANOPVTIONWCKRGRKQCKTHPHFVTPYRC:VG 120	

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Db 61 TCIDKSGILQYQCVYVPELQITNVVEANGPVTIQNWCKYGRKQCKTHPEVPIYRCLVG 120
Qy 121 EFVSDALLVPCKKFLHQERMDVCEIHJHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 122 EFVSDALLVPCKKFLHQERMDVCEIHJHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Qy 181 GVRVCCPLAESDNVDSADAEDSDVWVGSGADTDYADGSDKVVVEAEVEEVEEVEE 240
Db 181 GVRVCCPLAESDNVDSADAEDSDVWVGSGADTDYADGSDKVVVEAEVEEVEEVEE 240
Qy 241 EADDEDEDGDEVEEAEPEYEATERTTSTATTITTESVEEVVVTAASTPDVAV 300
Db 241 EADDEDEDGDEVEEAEPEYEATERTTSTATTITTESVEEVVVTAASTPDVAV 300
Qy 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMEKEAECAKNLPKADKKAVIQEF 360
Db 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMEKEAECAKNLPKADKKAVIQEF 360
Qy 361 QEKVESLEQEAANERQOLVETHMARVEAMINRRRLALENYITALQAVTPRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQOLVETHMARVEAMINRRRLALENYITALQAVTPRPHVFNMLK 420
Qy 421 KYVRAEQDKRQHTLKHFEHVVMVDPKKAQIRSOVMTHLRVIVYERMNQSLSLYNNPVA 480
Db 421 KYVRAEQDKRQHTLKHFEHVVMVDPKKAQIRSOVMTHLRVIVYERMNQSLSLYNNPVA 480
Qy 481 EEOIDEVDELLQKQNSYSDVLANMISEPRISVGNDAIMHSLTETKTIVLLPVNGEFS 540
Db 481 EEOIDEVDELLQKQNSYSDVLANMISEPRISVGNDAIMHSLTETKTIVLLPVNGEFS 540
Qy 541 DDLPQWHSFGADSVPAANTEVEVPDARPAADRGLTTRPGSGLTNITKEISEVNLDAEF 600
Db 541 DDLPQWHSFGADSVPAANTEVEVPDARPAADRGLTTRPGSGLTNITKEISEVNLDAEF 600
Qy 601 RHDGSEYVHQKLYFPREDVGSNGKAIIGLMGVGVATVIVITVLMKKKQYTSIHGV 660
Db 601 RHDGSEYVHQKLYFPREDVGSNGKAIIGLMGVGVATVIVITVLMKKKQYTSIHGV 660
Qy 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPERHLSKMQQNGYENPTYKFFEQMNKK 697

RESULT 4
AAU06610
ID AAU06610 standard; Protein: 697 AA.
AC AAU06610;
XX
XX 24-OCT-2001 (first entry)
XX Human Amyloid precursor protein mutant, APP695-SW-KK.
XX
XX Human: Aspartyl protease; Asp2b; beta-secretase; nototropic;
XX neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
XX amyloid-beta; Abeta; APP695-SW-KK; Mutant; mutant.
XX
XX Homo sapiens.
XX
XX Key Location/Q: modifiers
XX
XX Misc-difference 595..596
XX
XX FT /note- "Wild-type Lys-Met substituted by Asn-Leu"
XX
XX FT Misc-difference 696..697
XX
XX FT /note- "2 Extra Lys residues added compared to
XX wild-type APP695"
XX
XX W0200-49038-A2.
XX
XX PD 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-1B00798.
XX
XX 09-MAY-2001; 2001WO-1B00798.

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XX
PA (RIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANK/) YAN R.
XX
XX Bienkowski MZ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WPI; 2001-502549/55.
XX N-PSDB: AAS11524.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity
XX
XX Example 6: Page 147-149; 185pp; English.
XX
XX The invention relates to a purified polypeptide comprising a fragment of
XX mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
XX transmembrane domain and the Asp2 protein, and where the polypeptide and
XX the fragment retain the beta-secretase activity of the mammalian Asp2
XX protein. The invention also details polynucleotides for the Asp
XX proteins and vectors expressing them, and a polypeptide (isoform of
XX amyloid protein precursor (APP)) comprising the amino acid sequence of an
XX APP or its fragment containing an APP cleavage site recognizable by a
XX mammalian beta-secretase, and further comprising two lysine residues at
XX the carboxyl terminus of the amino acid sequence of the mammalian APP or
XX APP fragment. Also included in the invention are methods of identifying
XX modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
XX useful for treating Alzheimer's disease. APP is useful in methods for
XX identifying inhibitors or modulators of human Asp2 activity and
XX amyloid-beta (Abeta) peptide production. APP is also useful in designing
XX therapeutics for the treatment or prevention of Alzheimer's disease.
XX APP comprising the APP-SW-beta-secretase peptide sequence (NDA), which
XX is associated with increased levels of Abeta processing is useful in
XX assays relating the Alzheimer's research. The expression vector is useful
XX for recombinantly expressing APP. Nucleic acids that hybridize to
XX Asp oligonucleotides are useful as probes or primers. The probes are
XX useful for detecting Hu-Asp nucleic acids in vitro assays and in
XX Northern and Southern blots. The present sequence is the human
XX APP695 mutant, APP695-SW-KK which has 2 extra Lys residues added at
XX the C-terminus compared to the APP695-SW mutant. The mutation alters the
XX specificity of the APP gamma-secretase activity and increases the rate
XX of processing of the amyloid Abeta peptide.
XX
XX Sequence 697 AA:

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Query Match 100.0%; Score 3651; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.4e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLFGLALLLAATAWTALEVPDGNAGLAEQIAFMFCORLNHNMNVQNGKWDSPSGTK 60
Db 1 MLFGLALLLAATAWTALEVPDGNAGLAEQIAFMFCORLNHNMNVQNGKWDSPSGTK 60
Qy 62 TCIDTKEGILQYQCVYVPELQITNVVEANGPVTIQNWCKYGRKQCKTHPEVPIYRCLVG 120
Db 62 TCIDTKEGILQYQCVYVPELQITNVVEANGPVTIQNWCKYGRKQCKTHPEVPIYRCLVG 120
Qy 121 EFVSDALLVPCKKFLHQERMDVCEIHJHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPCKKFLHQERMDVCEIHJHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEDSDVWVGSGADTDYADGSDKVVVEAEVEEVEEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVWVGSGADTDYADGSDKVVVEAEVEEVEEVEE 240
Qy 241 EADDEDEDGDEVEEAEPEYEATERTTSTATTITTESVEEVVVTAASTPDVAV 300
Db 241 EADDEDEDGDEVEEAEPEYEATERTTSTATTITTESVEEVVVTAASTPDVAV 300

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301	Qy	DKYLETGDSNEHAHFQAKERLEAKHERMSQVMREZEAEQRQAKNLPKADUKKAVICGF	360
301	Dd	DKYLETGDSNEHAHFQAKERLEAKHERMSQVMREZEAEQRQAKNLPKADUKKAVICGF	360
361	Qy	QEKVESLEQEAANEQQOLVETHMARVEAMLNDRRLALENYITACAVPPRPFRHVNMLK	420
361	Dd	QEKVESLEQEAANEQQOLVETHMARVEAMLNDRRLALENYITACAVPPRPFRHVNMLK	420
421	Qy	KYVRAEQKDRQHTLKHFEHVRWVDPKKAQIRSQVYTHLRVYERMNOSLSLYLVNPAVA	480
421	Dd	KYVRAEQKDRQHTLKHFEHVRWVDPKKAQIRSQVYTHLRVYERMNOSLSLYLVNPAVA	480
481	Qy	BEIQDEVDELLOKEQNYSDDVLANMISEPRISYGNDALMPS-TETKITVELLPVNGEFSL	540
481	Dd	BEIQDEVDELLOKEQNYSDDVLANMISEPRISYGNDALMPS-TETKITVELLPVNGEFSL	540
541	Qy	DDLQPHWSFGADSPVANTENEVEPVDAPAAQDGTTRPGSLGTLNITKEEISEVNLDAEF	600
541	Dd	DDLQPHWSFGADSPVANTENEVEPVDAPAAQDGTTRPGSLGTLNITKEEISEVNLDAEF	600
601	Qy	RHDSGYEVHHQKLVFAEDVGSNKGAIGLWGGVVATVIVITLVMKKKQYTSIHGV	660
601	Dd	RHDSGYEVHHQKLVFAEDVGSNKGAIGLWGGVVATVIVITLVMKKKQYTSIHGV	660
661	Qy	VEVDAANTPEERHLSKMGQNGYENTYKFFPEOMQNKK	697
661	Dd	VEVDAANTPEERHLSKMGQNGYENTYKFFPEOMQNKK	697

2015

RESUL. 5
A2107209

AAUC7209
ID AAUC7209 standard; Protein: 697 AA.

XX
AC

DT 24-OCT-2001 (first entry)

DE Human beta-amyloid protein precursor, App695-Sw-KK.

Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP; aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease; APP695-Sw-KK.

OS Homo sapiens.

Key	Location/Qualifiers
-----	---------------------

FT Misc-difference 595

FT /note= "Wild type Lys substituted by Asn"

F⁷¹ Misc-difference 596

FT /note "Wild type Met substituted by Leu"

PN WC200149097-A2.

PD 22-JUL-2001.

PF 09-MAY-2001; 2001WO-IB00797.

PR 09-MAY-2001; 2001WO-IBC0797.

AA (BIEN/) BIENKOWSKI M J.

PA (BIEN/) PIENKOWSKI M J.
PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

PI Bienkowski MJ, Gurney ME, Henrikson RL, Parodi LA, Yan R;

DR WPI; 2001-502548/55.

DR N-PSDB; AAS11709.

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2

QY 501 RHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGCVIATVITVILVLMKKKKQYTSIHRSV 660
D5 601 RHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGCVIATVITVILVLMKKKKQYTSIHRSV 660
QY 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697
D5 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697

RESULT 6
AAE02588
ID AAE02588 standard; Protein: 697 AA.
AC AAE02588;
XX
DT 10-AUG-2001 (first entry)
DE Human amyloid precursor protein 695-Sw-KK (APP695-Sw-KK).
KW Human; alpha-secretase; amyloid precursor protein 695-Sw-KK; therapy;
KW APP695-Sw-KK; Alzheimer's disease; anti-Alzheimer's.
OS Homo sapiens.
OS Synthetic.
XX
PN W02001:23533 A2.
XX
PD C5-APR-2001.
XX
PF 22-SEP-2000; 2000NO-US26280.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99NO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-C169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
XX WPI: 2001-290516/30.
DR N-PSNR; AAD05746.
XX
PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease -
XX
PS Example 6; Page 146-148; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human APP695-Sw-KK. This
CC sequence contains a Sw mutation which is characterised by a K to N
CC alteration at positions 595-596 and two lysine residues at the
CC carboxyl-terminal end.
XX
SQ Sequence 697 AA;

Query Match 100.0%; Score 3651; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.4e-256;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOLAMFCGRLNMHNVQNGKWSDFSGTK 60
D5 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOLAMFCGRLNMHNVQNGKWSDFSGTK 60
QY 61 TCIDTKESGILQYQCEVPELQITNVVEANQPVTIQNCKRQCKQTHPHFVTPYKCVG 120
D5 61 TCIDTKESGILQYQCEVPELQITNVVEANQPVTIQNCKRQCKQTHPHFVTPYKCVG 120
QY 121 EFVSDALLVPDKCFLEHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLFCGIDKFR 180

D5 121 EFVSDALLVPDKCFLEHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLFCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEKVVVEAEVEEVAEVEE 240
D5 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEKVVVEAEVEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEAEATERTTSIATTTTITESTVEEVVVRPTTAASFPDAV 300
D5 241 EADDDDEDDGDEVEEAEPEAEATERTTSIATTTTITESTVEEVVVRPTTAASFPDAV 300
QY 301 DKYLETGPDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
D5 301 DKYLETGPDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
D5 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVMYDPPKKAACIRSOVMTHLRVYIYERMNQSLSLLYNPVAV 480
D5 421 KYVRAEQKDRQHTLKHFEHVMYDPPKKAACIRSOVMTHLRVYIYERMNQSLSLLYNPVAV 480
QY 481 SEIQDEYDELLQKQNYSDVLANMISEPRISYGNDALMPSLTETKITVELLPVNGEFSL 540
D5 481 SEIQDEYDELLQKQNYSDVLANMISEPRISYGNDALMPSLTETKITVELLPVNGEFSL 540
QY 541 DDLOPWHISFGADSVYPANTENEVEPVDARPAADRGITTRPGSGLTNKTEELISEVNLDAEF 600
D5 541 DDLOPWHISFGADSVYPANTENEVEPVDARPAADRGITTRPGSGLTNKTEELISEVNLDAEF 600
QY 601 RHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGCVIATVITVILVLMKKKKQYTSIHRSV 660
D5 601 RHDSGYEVHOKLVFFAEDVGSNKGALIGLMVGCVIATVITVILVLMKKKKQYTSIHRSV 660
QY 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697
D5 661 VEYDAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697

RESULT 7
ABB78597
ID ABB78597 standard; Protein: 697 AA.
XX
AC ABB78597;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human APP695-Sw-KK protein sequence SEQ ID NO:18.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic; amyloid precursor protein; APP.
XX
OS Homo sapiens.
XX
PN GB2367060-A.
XX
PD 27-MAR-2002.
XX
XX 29-OCT-2001; 2001GB-0025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99NO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-0023315.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
XX WPI: 2002-396337/43.
DR

Best Local Similarity 99.7%; Pred. No. 5.3e-256;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATARALETPTDGNAGLLAEQIAFMCGRLNHHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATARALETPTDGNAGLLAEQIAFMCGRLNHHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCOEYVPEQITNVYANOPTVIONCKRGKCKTHPHFVPIRCLVG 120
DB 61 TCIDTKEGILQCOEYVPELOITNVYANOPTVIONCKRGKCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR 180
QY 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEKVVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEKVVVEAEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEEPEEATERTTSTATTITTESVEEVVRVPTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEEPEEATERTTSTATTITTESVEEVVRVPTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVNMLK 420
QY 421 KYVRAEQKORHTLKHFRVRYMDPKKAAQIRSOVNIHLRVIERNOSLSLLYNPAVA 480
DB 421 KYVRAEQKORHTLKHFRVRYMDPKKAAQIRSOVNIHLRVIERNOSLSLLYNPAVA 480
QY 481 EETODEVELLOKEQNSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSJ 540
DB 481 EETODEVELLOKEQNSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSJ 540
QY 541 DLQOPHRSFGADSVANTENEVEPDARPAADRLTRPGSLTNIKTEIESEVNIADCF 600
DB 541 DLQOPHRSFGADSVANTENEVEPDARPAADRLTRPGSLTNIKTEIESEVNIADCF 600
QY 601 RHDGSEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVITLVMKKKYTSIHGV 660
DB 601 RHDGSEVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVITLVMKKKYTSIHGV 660
QY 661 VEYDAAVIPEERHLSKMOQNGYENPTYKFEQMONKK 697
DB 661 VEYDAAVIPEERHLSKMOQNGYENPTYKFEQMONKK 697

RESULT 9
AAE10635
ID AAE10635 standard; Protein; 697 AA.
XX
AC AAE10635;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX
KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective.
OS Homo sapiens.
OS Synthetic.
XX GB237767-A.
XX
XX 04-JUL-2001.
XX

PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WC-US20881.
PR 23-SEP-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX (PHAA) PHARMACIA & UPJOHN CO.
XX Bienkowski MJ, Gurney M;
XX WPI: 2001-444208/48.
XX N-PSDB; AAD17871.
XX Polypeptide comprising fragments of human aspartyl protease with
XX amyloid precursor protein processing activity and alpha-secretase
XX activity, for identifying modulators useful in treating Alzheimer's
XX disease.
XX Example 6; Page 114-116; 187pp; English.
XX The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
XX Aspl proteins which lack transmembrane domain or amino terminal
XX domain or cytoplasmic domain and retains alpha-secretase activity
XX and amyloid protein precursor (APP) processing activity. The proteins
XX of the invention are useful for assaying hu-Aspl alpha-secretase
XX activity, which in turn is useful for identifying modulators of
XX hu-Aspl alpha-secretase activity, where modulators that increase
XX hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
XX disease (AD) which causes progressive dementia with consequent
XX neuronal loss. Hu-Aspl protease substrate is useful for assaying
XX hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
XX the substrate under acidic conditions and determining the level of
XX hu-Aspl proteolytic activity. The present sequence is human amyloid
XX protein precursor 695-KK (APP695-KK) isoform which is obtained by
XX the addition of two Lys residues (KK motif) at the C-terminus of
XX APP695 protein.
XX Sequence 697 AA;
SQ
Query Match 99.8%; Score 3643; DB 22; Length 697;
Best Local Similarity 99.7%; Pred. No. 5.3e-256;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATARALETPTDGNAGLLAEQIAFMCGRLNHHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATARALETPTDGNAGLLAEQIAFMCGRLNHHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCOEYVPELOITNVYANOPTVIONCKRGKCKTHPHFVPIRCLVG 120
DB 61 TCIDTKEGILQCOEYVPELOITNVYANOPTVIONCKRGKCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHHHTVAKETCSKSTNLHDYGMILPGCIDKFR 180
QY 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEKVVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEKVVVEAEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEEPEEATERTTSTATTITTESVEEVVRVPTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEEPEEATERTTSTATTITTESVEEVVRVPTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVNMLK 420

QY 421 KYVRAEQKDRQHTLKHFHVMKDPKAAQIRSOVMTHLRVYERKNQSLSLYNNPVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVMKDPKAAQIRSOVMTHLRVYERKNQSLSLYNNPVA 480
 QY 481 ERIQDEVDELLOKQNYSDOVLANKMISEPRISYNDALMPSLTETKTTVELLVNGEESL 540
 DB 481 ERIQDEVDELLOKQNYSDOVLANKMISEPRISYNDALMPSLTETKTTVELLVNGEESL 540
 QY 541 DDLQPHWSFGADSVDPANTENEVEVDPAADRLITRPGSLGNINTEISEVKNLDAEP 600
 DB 541 DDLQPHWSFGADSVDPANTENEVEVDPAADRLITRPGSLGNINTEISEVKNLDAEP 600
 QY 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGQVIAIVITLVMLKKQYTSIHGV 660
 DB 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGQVIAIVITLVMLKKQYTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 10
 AAU06865
 ID AAU06865 standard; Protein: 697 AA.
 XX AAU06865;
 AC AAU06865;
 XX 23-OCT-2001 (first entry)
 XX Human amyloid precursor protein 695-KK (AP695-KK) isoform.
 DE Human amyloid precursor protein 695-KK (AP695-KK) isoform.
 XX Human: aspartyl protease; Asp; beta-amyloid precursor protein 695-KK;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; glycosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotrophic;
 KW neuroprotective; antisense therapy; gene therapy; AP695-KK; mutant;
 KW mutain.
 OS Homo sapiens.
 XX W0320150829-A2.
 PN 19-JUL-2001.
 XX 09-MAY-2001; 2001WO-IB00799.
 PF 09-MAY-2001; 2001WO-IB00799.
 PR 09-MAY-2001; 2001WO-IB00799.
 XX (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 PI WPI; 2001-483072/52.
 DR N-PSDB; AAD13027.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX Example 6; Page 144-146; 195pp; English.
 PS The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 XX precursor protein (APP) isoforms and their corresponding DNA molecules.
 CC Human aspartyl proteases can act as beta-secretase proteases useful for
 CC treating Alzheimer's disease. APP isoforms are useful for identifying
 CC modulators of amyloid-beta peptide production, for use in designing
 CC therapeutics for the treatment and prevention of Alzheimer's disease.
 CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis

CC and neuronal loss. APP isoforms are also used in methods for identifying
 CC inhibitors and modulators of human Asp2 activity. The invention relates
 CC to a method for identifying agents that modulate the activity of human
 CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
 CC as a means to screen in cellular assays for the inhibitors of beta- and
 CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
 CC polymerase chain reactions (PCR). The probes are useful for detecting
 CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
 CC blots. The present sequence is modified human amyloid precursor
 CC protein 695-KK (APP695-KK) isoform. APP695-KK isoform is obtained by
 CC addition of two Lys residues (KK motif) at the C-terminal end of APP695
 CC isoform.
 XX

Sequence 697 AA;

Query Match 99.8%; Score 3643; DB 22; Length 697;
 Best Local Similarity 99.7%; Pred. No. 5.3e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGALALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNHHMNVQNGKWDSPSGTK 60
 DB 1 MLPGALALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLNHHMNVQNGKWDSPSGTK 60
 QY 61 TC-DTKEGILQYCOEYVPELQITNVVEANOPTVIONWCKRCKOCKTHPHFVPIVRCIVG 120
 DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPTVIONWCKRCKOCKTHPHFVPIVRCIVG 120
 QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETCEKSTLNLDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHTVAKETCEKSTLNLDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESNVNDSADAEEDSDVWVGADTDYAGSDEKVVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAESNVNDSADAEEDSDVWVGADTDYAGSDEKVVVEAEVEAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEYEAETERTTSIATTTTTSVESVEVVRVPTTAASPTDAV 300
 DB 241 EADDDDEDDGDEVEEAEPEYEAETERTTSIATTTTTSVESVEVVRVPTTAASPTDAV 300
 QY 301 DKYLETPGDENEHAFQKAKERLEAKHREKMSQVREWEAEERQAKNLPKADKAVIQHF 360
 DB 301 DKYLETPGDENEHAFQKAKERLEAKHREKMSQVREWEAEERQAKNLPKADKAVIQHF 360
 QY 361 QEKVESLEGEAANERQQLVETIHARVEAMLDNRRLALENYITALQAVPPRRHHVFNMLK 420
 DB 361 QEKVESLEGEAANERQQLVETIHARVEAMLDNRRLALENYITALQAVPPRRHHVFNMLK 420
 QY 421 KYVRAEQKDRQHTLKHFHVMKDPKAAQIRSOVMTHLRVYERKNQSLSLYNNPVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVMKDPKAAQIRSOVMTHLRVYERKNQSLSLYNNPVA 480
 QY 481 ERIQDEVDELLOKQNYSDOVLANKMISEPRISYNDALMPSLTETKTTVELLVNGEESL 540
 DB 481 ERIQDEVDELLOKQNYSDOVLANKMISEPRISYNDALMPSLTETKTTVELLVNGEESL 540
 QY 541 DDLQPHWSFGADSVDPANTENEVEVDPAADRLITRPGSLGNINTEISEVKNLDAEP 600
 DB 541 DDLQPHWSFGADSVDPANTENEVEVDPAADRLITRPGSLGNINTEISEVKNLDAEP 600
 QY 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGQVIAIVITLVMLKKQYTSIHGV 660
 DB 601 RHDGSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGQVIAIVITLVMLKKQYTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 1:
 AAU06609
 ID AAU06609 standard; Protein: 697 AA.
 XX AAU06609;
 AC AAU06609;

XX DT 24-OCT-2001 (first entry)
 XX DE Human Amyloid precursor protein mutant, APP695-KK.
 XX KW Human; Aspartyl protease; Asp2b; beta-secretase; neurotropic;
 XX KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 XX KW amyloid-beta; Abeta; APP695-KK; mutant; mature.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 695..697
 XX FT /note="2 Extra Lys residues added compared to
 XX FT wild-type APP695"
 XX PN WO200145098-A2.
 XX PD 12-JUL-2001.
 XX XX 09-MAY-2001; 2001WO-1B00798.
 XX PR 09-MAY-2001; 2001WO-1B00798.
 XX PA (BIEN/) BIENKOWSKI M J.
 XX PA (GURNEY/) GURNEY M E.
 XX PA (HEIN/) HEINRIKSON R L.
 XX PA (PARODI/) PARODI L A.
 XX PA (YANK/) YANK R.
 XX PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yank R;
 XX DR WPI: 2001-502545/55.
 XX DR N-PSDB: AAS11523.
 XX XX Novel purified polypeptide comprising fragment of mammalian aspartyl-
 XX PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 XX PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 XX PT activity -
 XX XX Example 5; Page 144-146; 185pp; English.
 XX CC The invention relates to a purified polypeptide comprising a fragment of
 XX CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 XX CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 XX CC the fragment retain the beta-secretase activity of the mammalian Asp2
 XX CC protein. The invention also details polynucleotides for the Asp
 XX CC proteins and vectors expressing them, and a polypeptide (isoform of
 XX CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 XX CC APP or its fragment containing an APP cleavage site recognizable by a
 XX CC mammalian beta-secretase, and further comprising two lysine residues at
 XX CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 XX CC APP fragment. Also included in the invention are methods of identifying
 XX CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 XX CC useful for treating Alzheimer's disease. APP is useful in methods for
 XX CC identifying inhibitors or modulators of human Asp2 activity and
 XX CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
 XX CC therapeutics for the treatment or prevention of Alzheimer's disease.
 XX CC APP comprising the APP-Sw-beta-secretase peptide sequence (NDA), which
 XX CC is associated with increased levels of Abeta processing is useful in
 XX CC assays relating to the Alzheimer's research. The expression vector is useful
 XX CC for recombinantly expressing APP. Nucleic acids that hybridize to
 XX CC Asp oligonucleotides are useful as probes or primers. The probes are
 XX CC useful for detecting Hu-Asp nucleic acids in *in vitro* assays and in
 XX CC Northern and Southern blots. The present sequence is the human
 XX CC APP695 mutant. APP695-KK which has 2 extra Lys residues added at
 XX CC the C-terminus compared to the wild-type APP695. The mutation alters the
 XX CC specificity of the APP gamma-secretase activity and increases the rate
 XX CC of processing of the amyloid Abeta peptide.

SQ Sequence 697 AA; Query Match 99.8%; Score 3643; DB 22; Length 697;

Best Local Similarity 99.7%; Pred. No. 5.3e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPDIAFCGRNLNHHMNVQNGKWDSDSGTK 60
 DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPDIAFCGRNLNHHMNVQNGKWDSDSGTK 60
 QY 61 TCIDTKGILQYCOEYVPELQITNNVEANQPV71QNMCKRGRKQCKTHPHFV1PYRCLVG 120
 DB 61 TCIDTKGILQYCOEYVPELQITNNVEANQPV71QNMCKRGRKQCKTHPHFV1PYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCE71HLHWH7VAKETCSEKSTN1LHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCE71HLHWH7VAKETCSEKSTN1LHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVDSADAEDSDVMMVGADTDYADGSEDKVVEVAEEVEEVEE 240
 DB 181 GVEFVCCPLAESDNVDSADAEDSDVMMVGADTDYADGSEDKVVEVAEEVEEVEEVEE 240
 QY 241 EADDDDEDDGDEVEHEAEPEYEATERTIS1ATTTTITTESVEEVVVP7TAASTPDAY 300
 DB 241 EADDDDEDDGDEVEHEAEPEYEATERTIS1ATTTTITTESVEEVVVP7TAASTPDAY 300
 QY 301 DKYLETPGDSNEHAHFQKAKERLEAKHRRSMQVMEWEAEAEQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDSNEHAHFQKAKERLEAKHRRSMQVMEWEAEAEQAKNLPKADKKAVIQHF 360
 QY 361 QEKVESLEGEAANERQQLVETHKARVFAMLNDRRLALENYITALQAVPPRPHVNMUK 420
 DB 361 QEKVESLEGEAANERQQLVETHKARVFAMLNDRRLALENYITALQAVPPRPHVNMUK 420
 QY 421 KYVRAEQKDRQHTLKHFHEVVMYDPKKAAQIRSOVATHRV1YERNQSLSLLYNPVAVA 480
 DB 421 KYVRAEQKDRQHTLKHFHEVVMYDPKKAAQIRSOVATHRV1YERNQSLSLLYNPVAVA 480
 QY 481 EE-QDEYDELLQKPNYSDDVLANMISEPRISYGNALMPSLTFTKT7VELLPVNGEFS 540
 DB 481 EEIQDEYDELLQKPNYSDDVLANMISEPRISYGNALMPSLTFTKT7VELLPVNGEFS 540
 QY 541 DDLOPHSFSGADSVPAANTEVEVEVDARPAADRLTIRPGSLTN1KTEISEVNLDAAEF 600
 DB 541 DDLOPHSFSGADSVPAANTEVEVEVDARPAADRLTIRPGSLTN1KTEISEVNLDAAEF 600
 QY 561 RHDSGYEVHVKQLVFAEDYGSNKGAIIGDMVGWVIATVIV1LYMKKKQVTSIHGGV 660
 DB 561 RHDSGYEVHVKQLVFAEDYGSNKGAIIGDMVGWVIATVIV1LYMKKKQVTSIHGGV 660
 QY 661 VEVDAAVTPBERHLSKMQQNGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPBERHLSKMQQNGYENPTYKFFEQMONKK 697
 RESULT 12
 AAU07208
 ID AAU07208 standard; Protein; 697 AA.
 XX AC AALC07208;
 XX XX 24-OCT-2001 (first entry)
 XX DE Human beta-amyloid protein precursor, APP695-KK.
 XX KW Human; aspartyl protease 1; Asp-1; neurotropic; neuroprotective;
 XX KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 XX KW beta-secretase; Alzheimer's disease; APP695-KK.
 XX OS Homo sapiens.
 XX PN WO200145097-A2.
 XX PD 12-JUL-2001.
 XX XX 09-MAY-2001; 2001WO-1B00797.

XX PR 09-MAY-2001: 2001WO-1B00797.
 XX PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX BIENKOWSKI MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX WPI: 2001-502548/55.
 DR N-PSDB: AAS11108.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX Example 6: Page 144-146; 185pp; English.
 XX The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP),
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognizable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, APP695-KK,
 CC used in the method of the invention.
 XX Sequence 597 AA;
 SQ
 Query Match: 99.8%; Score 3643; LH 22; Length 697;
 Best Local Similarity 99.7%; Pred. No. 5.3e-256;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAATAARAEVPTDGNAGLLAEPOIAMFCGRLENNHNMVQNGKWDSPSGTK 60
 DB 1 MLPGLALLLAATAARAEVPTDGNAGLLAEPOIAMFCGRLENNHNMVQNGKWDSPSGTK 60
 QY 61 TCIDTREGILQYCEVYFELQIINVEANQPTVIQNKCKRGRKQCKTHPHFVYPRCLVG 120
 DB 61 TCIDTREGILQYCEVYFELQIINVEANQPTVIQNKCKRGRKQCKTHPHFVYPRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCEPHLHWHVYAKETCSKSTNLHDYGNLLPCGIDKPR 180
 DB 121 EFVSDALLVPDKCKFLHQRMDVCEPHLHWHVYAKETCSKSTNLHDYGNLLPCGIDKPR 180
 QY 181 GVEFVCCPLAEESDNDSDAEDDDSDVWGGADTDYADGSEDKVVEAESEVAEVEE 240
 DB 181 GVEFVCCPLAEESDNDSDAEDDDSDVWGGADTDYADGSEDKVVEAESEVAEVEE 240
 QY 241 EADDDEDDGDEVEEAPEEATERTISTATITTTTIESVEEVVPTTAASTPDAY 300
 DB 241 EADDDEDDGDEVEEAPEEATERTISTATITTTTIESVEEVVPTTAASTPDAY 300
 QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMRMSQVMREWEAEARQAKNLFKADKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRMRMSQVMREWEAEARQAKNLFKADKAVIQHF 360

CY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK 420
 DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK 420
 QY 421 KYVRAEKDRQHTLKHFEHVRVMDPKKAAQIISQVMTHLRVIVYERMNSLNLNVPFAVA 480
 DB 421 KYVRAEKDRQHTLKHFEHVRVMDPKKAAQIIRSOVMTHLRVIVYERMNSLNLNVPFAVA 480
 QY 481 FEIDQDEVELIQKQDNYSDDVLANMISEPRISYGNDAIMPFLSETKTIVTEILPYNGEFSL 540
 DB 481 ESIQDEVELIQKQDNYSDDVLANMISEPRISYGNDAIMPFLSETKTIVTEILPYNGEFSL 540
 QY 541 DDLQPMHSFGADSVDPANTENEVEPVDARPAADRLITRPGSGLTNINIKETISEVNLDAEF 600
 DB 541 DDLQPMHSFGADSVDPANTENEVEPVDARPAADRLITRPGSGLTNINIKETISEVNLDAEF 600
 QY 601 RHDGSEYVHHOKLVFFAEDVGSNGKGAIGLWVGWGIATVIVITLVMLKKQYTSIHGV 660
 DB 601 RHDGSEYVHHOKLVFFAEDVGSNGKGAIGLWVGWGIATVIVITLVMLKKQYTSIHGV 660
 QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMONKK 697
 RESULT 13
 AAEE02587
 ID AAE02587 standard; Protein: 697 AA.
 AC AAE02587;
 DT 10-AUG-2001 (first entry)
 DE Human amyloid precursor protein 695-KK (APP695-KK).
 KW Human; alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
 KW therapy; Alzheimer's disease; antialzheimer's.
 OS Homo sapiens.
 CS Synthetic.
 XX WO200123533-A2.
 XX 05-APR-2001.
 XX 22-SEP-2000; 2000WO-US26080.
 XX 23-SEP-1999; 99US-0155493.
 XX 23-SEP-1999; 99WO-US20881.
 XX 13-OCT-1999; 99US-0416901.
 XX 06-DEC-1999; 99US-0169232.
 XX (PIAA) PHARMACIA & UPJOHN CO.
 XX Gurney M, Bienkowski MJ;
 XX WPI: 2001-290516/30.
 DR N-PSDB: AAD06745.
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.
 XX Example 6: Page 143-145; 189pp; English.
 XX The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-KK. This
 CC sequence contains two carboxy-terminal lysine residues.

Seq	Sequence	697 AA;
Query Match	99.8%; Score 3643; DB 23; Length 697;	
Best Local Similarity	99.7%; Pred. No. 5.3e-256;	
Matches 695; Conservative	1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRINMNMVQNGKWDSPSGTK 60	
Db	1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRINMNMVQNGKWDSPSGTK 60	
Qy	61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120	
Db	61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120	
Qy	121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCGIDKFR 180	
Db	121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCGIDKFR 180	
Qy	181 GVEFYCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEVEAEVEE 240	
Db	181 GVEFYCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEVEAEVEE 240	
Qy	241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTTSVEEVVVRVPTTAASPDAY 300	
Db	241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTTSVEEVVVRVPTTAASPDAY 300	

RESULT 14	ABR78596	
ID	ABR78596	
XX	ABR78596 standard; Protein; 697 AA.	
XX	ABR78596;	
XX	16-JUL-2002 (first entry)	
XX	Human APP695-KK protein sequence SEQ ID NO:16.	
XX	Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;	
XX	proteolytic; amyloid precursor protein; APP.	
XX	Homo sapiens.	
XX	GB2367060-A.	
XX	27-MAR-2002.	

XX	29-OCT-2001; 2001GB-0025934.	
XX	23-SEP-1999; 99US-155493P.	
XX	23-SEP-1999; 99US-0404133.	
XX	23-SEP-1999; 99WO-US20881.	
XX	13-OCT-1999; 99US-0416901.	
XX	06-DEC-1999; 99US-169232P.	
XX	22-SEP-2000; 2000GB-0023315.	
XX	(PHAA) PHARMACIA & UPJOHN CO.	
XX	Bienkowski MJ, Gurney M.	
XX	WPI: 2002-396337/43.	
XX	N-PSDB: AB152463.	
PT	Human aspartyl protease 1 substrates useful in assays to detect	
PT	aspartyl protease activity, e.g. for the diagnosis of Alzheimer's	
PT	disease.	
XX	Example 6: Page 114-116; 182pp; English.	
XX	The present invention describes a human aspartyl protease 1 (hu-Asp1)	
CC	substrate (I) which comprises a peptide of no more than 50 amino acids,	
CC	and which comprises the 6 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-	
CC	Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1	
CC	proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with	
CC	(1) under acidic conditions; and (b) determining the level of hu-Asp1	
CC	proteolytic activity; (2) a purified polynucleotide (III) comprising a	
CC	nucleotide sequence that hybridises under stringent conditions to the	
CC	non-coding strand complementary to a defined 1804 nucleotide sequence	
CC	(see AB152456) where the nucleotide sequence encodes a polypeptide having	
CC	Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane	
CC	domain; (3) a purified polynucleotide (III') comprising a sequence that	
CC	hybridises under stringent conditions to (III) (the nucleotide sequence	
CC	encodes a polypeptide further lacking a pro-peptide domain corresponding	
CC	to amino acids 23-62 of hu-Asp1 (see ABR78596); (4) a vector (IV)	
CC	comprising (III) or (III'); and (5) a host cell (V) transformed or	
CC	transfected with (III), (III') and/or (IV). The hu-Asp1 protease	
CC	aspartyl protease activity, (II) and therefore substrate in assays to detect	
CC	associated with aberrant hu-Asp1 expression and activity such as	
CC	Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21. While	
CC	hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present	
CC	sequence represents human amyloid precursor protein APP695-KK, which is	
CC	given in an example from the present invention.	
XX	Sequence 697 AA;	

Query Match	99.8%; Score 3643; DB 23; Length 697;	
Best Local Similarity	99.7%; Pred. No. 5.3e-256;	
Matches 695; Conservative	1; Mismatches 1; Indels 0; Gaps 0;	
Qy	1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRINMNMVQNGKWDSPSGTK 60	
Db	1 MLPLGALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRINMNMVQNGKWDSPSGTK 60	
Qy	61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120	
Db	61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITONMCKRGRKQCKTHPHFVPIYRCLVG 120	
Qy	121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCGIDKFR 180	
Db	121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHRTVAKETCSEKSTNLDHYGMLLPCGIDKFR 180	
Qy	181 GVEFYCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEVEAEVEE 240	
Db	181 GVEFYCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEVEAEVEE 240	
Qy	241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTTSVEEVVVRVPTTAASPDAY 300	
Db	241 EADDDEDDGDEVEEAEPEYEATEERTTSIATTTTTSVEEVVVRVPTTAASPDAY 300	

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QY 301 DKYLETGCDENEHAHFYKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETGCDENEHAHFYKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLLLYNPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLLLYNPAVA 480
QY 481 BEIODEVDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSELYNPAVA 540
DB 481 BEIODEVDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSELYNPAVA 540
QY 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTRPGSGLTNIKTEISEVNLDAEF 600
DB 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTRPGSGLTNIKTEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 15
RAY88435
ID AAY88435 standard; Protein: 695 AA.
XX
AC AAY88435;
XX
DI 03-AUG-2000 (first entry)
XX
DE Human APP695-sw variant amino acid sequence.
XX
KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
XX Alzheimer's disease; beta secretase site.
XX Homo sapiens.
XX
PN WO200017369-A2.
XX
PD 30-MAR-2000.
XX
PF 23-SEP-1999; 59WO-US20881.
XX
PR 24-SEP-1998; 98US-0101594.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;
XX
XX WPI: 2000-303209/26.
DR N-PSDB; AAA15672.
XX
XX New enzyme designated human aspartase useful in research into
PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at:
PT the beta secretase site to produce amyloid beta peptide -
XX
PS Example 6; Page 125-129; 183pp; English.
XX
XX This sequence represents a human amyloid precursor protein 695 (APP695)
CC variant amino acid sequence. The sequence is used in an example of the
CC invention, showing that modification of APP can increase beta amyloid
CC peptide processing. The invention relates to a protease (e.g. Asp2)
CC capable of cleaving the beta secretase site of amyloid precursor protein
CC (APP). The protease contains a sequence encoding the amino acid sequence
CC DTG and a sequence encoding DSG or DTG separated by 100-300 amino acids.
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CC When mutated the APP gene causes an autosomal dominant form of
CC Alzheimer's disease. APP localises to the cell surface membrane and have
CC a single C-terminal transmembrane domain. Proteolytic processing of APP
CC produces the amyloid beta protein, which is possibly very important in
CC Alzheimer's disease. The invention includes a nucleotide sequence
CC encoding the protease, a vector containing the nucleotide sequence, and a
CC cell line comprising the vector. Methods for screening for inhibitors of
CC beta secretase activity are also given in the invention. The human
CC aspartase protein and nucleotide sequences and the methods for
CC identifying inhibitors of the protease, are useful in the treatment of
CC and research in to Alzheimer's disease.
XX
SQ Sequence 695 AA;
```

```
Query Match: 99.7%; Score 3641; DB 21; Length 695;
Best local Similarity 100.0%; Pred. No. 7.4e-256;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGCLALLLLAAATARALEVPTDGNAGLLAEPOIAMEFCGRLNHMNMVQNGKWDSPSGTK 60
DB 1 MLPGCLALLLLAAATARALEVPTDGNAGLLAEPOIAMEFCGRLNHMNMVQNGKWDSPSGTK 60
QY 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIQNMCKRGRKOCKTHPHFVPRCLVG 120
DB 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIQNMCKRGRKOCKTHPHFVPRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTYAKETCSKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTYAKETCSKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVEE 240
QY 241 EAUDDEDDEGDEVEEAEPEYEATEKITTSIATTTTTTTSVEEVVRVP:TAASITPDV 300
DB 241 EAUDDEDDEGDEVEEAEPEYEATEKITTSIATTTTTTTSVEEVVRVP:TAASITPDV 300
QY 301 DKYLETGCDENEHAHFYKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETGCDENEHAHFYKAKERLEAKHHRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLLLYNPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLLLYNPAVA 480
QY 481 BEIODEVDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSELYNPAVA 540
DB 481 BEIODEVDELLOKSONYSDOVLANNISEPRISYNDALMPSLTETKTIVSELYNPAVA 540
QY 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTRPGSGLTNIKTEISEVNLDAEF 600
DB 541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGTTTRPGSGLTNIKTEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMLKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMON 695
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Search completed: October 2, 2003, 13:58:59
Job time : 40.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:59 : Search time 14 Seconds
(without alignments)
1638.370 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
Sequence: 1 MLPGLALLLAANTARALEV.....QQNGVNPYYKPPQMOKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA: *
1: /cgn2.6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2.6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2.6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2.6/ptodata/1/1aa/PCIU.COMB.pep: *
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3651	100.0	697	4	US-09-548-372D-18
2	3651	100.0	697	4	US-09-548-367D-18
3	3651	100.0	697	4	US-09-551-853D-18
4	3643	99.8	697	4	US-09-548-372D-16
5	3643	99.8	697	4	US-09-548-367D-16
6	3643	99.8	697	4	US-09-551-853D-16
7	3641	99.7	695	4	US-09-548-372D-12
8	3641	99.7	695	4	US-09-548-367D-12
9	3641	99.7	695	4	US-09-551-853D-12
10	3638	99.6	697	4	US-09-548-372D-20
11	3638	99.6	697	4	US-09-548-367D-20
12	3638	99.6	697	4	US-09-551-853D-20
13	3633	99.5	695	1	US-09-123-702-2
14	3633	99.5	695	2	US-08-104-165-1
15	3633	99.5	695	3	US-08-464-250-1
16	3633	99.5	695	4	US-08-464-250-1
17	3633	99.5	695	4	US-09-458-481A-7
18	3633	99.5	695	4	US-09-458-481B-8
19	3633	99.5	695	4	US-09-548-372D-10
20	3633	99.5	695	4	US-09-548-367D-10
21	3633	99.5	695	4	US-09-551-853D-10
22	3633	99.5	695	6	5218100-2
23	3628	99.4	695	4	US-09-548-372D-4
24	3628	99.4	695	4	US-09-548-367D-4
25	3628	99.4	695	4	US-09-551-853D-4
26	3627	99.3	694	1	US-08-339-152A-18
27	3627	99.3	694	2	US-08-007-999B-5

29	3627	99.3	694	2	US-08-689-276A-5
30	3621	99.2	695	1	US-08-371-930-27
31	3621	99.2	695	5	PCT-US94-01712-27
32	3609	98.8	695	1	US-08-339-152A-30
33	3604	98.7	753	4	US-09-548-372D-61
34	3604	98.7	753	4	US-09-548-367D-61
35	3594	98.4	753	1	US-09-551-853D-61
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42	3594	98.4	751	4	US-08-832-867-5
43	3594	98.4	751	4	US-09-548-372D-57
44	3594	98.4	751	4	US-09-548-367D-57
45	3594	98.4	751	6	US-09-551-853D-57

ALIGNMENTS

RESULT 1

US-09-548-372D-18
: Sequence 18, Application US/05548372D
: Patent No. 6420334
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
: FILE REFERENCE: 29315/62801
: CURRENT APPLICATION NUMBER: US/09/548.372D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 18
: TYPE: PRI
: ORGANISM: Homo sapiens
US-09-548-372D-18

Query Match	Best Local Similarity	Score	DB 4:	Length	697:
Matches 597:	Conservative	0:	Mismatches	0:	Gaps
QY	1	MLPGLALLLAANTARALEVPTDGNAGLLAEQIAFCGRLLNMHNVQNGKWDSPSSTK	60		
DB	1	MLPGLALLLAANTARALEVPTDGNAGLLAEQIAFCGRLLNMHNVQNGKWDSPSSTK	60		
QY	61	TCIDTKRG:LOYCQEVPELOITNVVEANQVPTONMCKRGKCKKTHPHVPIYRCLVG	120		
DB	61	TCIDTKRG:LOYCQEVPELOITNVVEANQVPTONMCKRGKCKKTHPHVPIYRCLVG	120		
QY	121	EFVSDALLVPDKCFPHOERMDVCTHLLHMTVAKCTSEKSTNLHDYGMLLPGIDKFR	180		
DB	121	EFVSDALLVPDKCFPHOERMDVCTHLLHMTVAKCTSEKSTNLHDYGMLLPGIDKFR	180		
QY	181	GVFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEKVKVEAEVEEVEE	240		
DB	181	GVFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEKVKVEAEVEEVEE	240		
QY	241	EADDEDDGDEVEEAEPEEATERTTSTATTITTTTSTESVEEVVPTTAASTPDV	300		
DB	241	EADDEDDGDEVEEAEPEEATERTTSTATTITTTTSTESVEEVVPTTAASTPDV	300		

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QY 301 DKYLETPGDNENHAHFQKAKERLEAKHRRMSQVREWEAEARQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDNENHAHFQKAKERLEAKHRRMSQVREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVMTHLRVYIERNQSLSLLYNPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVMTHLRVYIERNQSLSLLYNPAVA 480
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DB 481 BEIQDEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
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DB 541 DDLOPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKQYTSIHGGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKQYTSIHGGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697

RESULT 2
US-09-548-367D-18
; Sequence 18, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/628CH
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 03/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/24881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-18

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 3,1e+255;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCOEYVPELQITNVVEANQPVTIQNCKRGRKQCKTHPHFVPIRCLVG 120
DB 61 TCIDTKEGILQCOEYVPELQITNVVEANQPVTIQNCKRGRKQCKTHPHFVPIRCLVG 120
QY 121 EFVSDALLVPDKCKFLQERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLQERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLPCGIDKFR 180
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DB 181 GYFVCCPLAEESDNVSDADAEUDSDVWVGADTDYADGSEDKVYVEAEVEEVAEVEER 240
QY 241 EADDEDDEDGDEVEEAEPEEYEEATERITTSIATTTTTSVEEVRVPTTAASTPDVAV 300
DB 241 EADDEDDEDGDEVEEAEPEEYEEATERITTSIATTTTTSVEEVRVPTTAASTPDVAV 300
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DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVMTHLRVYIERNQSLSLLYNPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVMTHLRVYIERNQSLSLLYNPAVA 480
QY 481 BEIQDEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
DB 481 BEIQDEVDELLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
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DB 541 DDLOPHSFGADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTIEISEVNLDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKQYTSIHGGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMLKKQYTSIHGGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMKNK 697

RESULT 3
US-09-551-853D-18
; Sequence 18, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, SECRETASE, APP SUBSTRATES THEREFOR AND
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-18

Query Match 100.0%; Score 3651; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 3,1e+265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCOEYVPELQITNVVEANQPVTIQNCKRGRKQCKTHPHFVPIRCLVG 120
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Db 6: TCIDTKGILQYCEVYPELOITNVVEANOPVTIONNCKRGKCKTTHPHVPIYRCILVG 120
QY 121 EFVSALLVPKCKFLHGRMDVCETHLHMTVAKETSEKSTNHDYGMILPGSIDKFR 180
Db 121 EFVSALLVPKCKFLHGRMDVCETHLHMTVAKETSEKSTNHDYGMILPGSIDKFR 180
QY 181 GVEFVCCPLAESNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEAEVEE 240
Db 181 GVEFVCCPLAESNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEEAEPEYEATERTTSTIAATTTTTTETSEVEEVVPTTAASTPDV 300
Db 241 EADDDDEDDGDEVEEEAEPEYEATERTTSTIAATTTTTTETSEVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
Db 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKL 420
Db 361 QEKVESLQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKL 420
QY 421 KYVRAEQDRQHTLKHFEHVRVDPKKAQIRSOVTHLRYIYERMNQSLSLLYNPVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRVDPKKAQIRSOVTHLRYIYERMNQSLSLLYNPVA 480
QY 481 EBIQDEVDLLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLPVNGEFS 540
Db 481 EBIQDEVDLLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLPVNGEFS 540
QY 541 DDLQPHWSFGADSVDPANTENEVEPVDPADPAADRGLTTPGSLTNIKTEEISEVNLDAEF 600
Db 541 DDLQPHWSFGADSVDPANTENEVEPVDPADPAADRGLTTPGSLTNIKTEEISEVNLDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIHGV 660
Db 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFEQMONKK 697
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFEQMONKK 697
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RESULT 4
US-09-548-372D-16
; Sequence 16, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-16
Query Match 99.8%; Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.2e-264;
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Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MIPGJALLLLAAWTAARALEVPTDGNAGLLAPFOATMPGGRLLNMHMNVONGKWDSDPSGTK 60
Db 1 MIPGJALLLLAAWTAARALEVPTDGNAGLLAPFOATMPGGRLLNMHMNVONGKWDSDPSGTK 60
QY 61 TCIDTKGILQYCEVYPELOITNVVEANOPVTIONNCKRGKCKTTHPHVPIYRCILVG 120
Db 61 TCIDTKGILQYCEVYPELOITNVVEANOPVTIONNCKRGKCKTTHPHVPIYRCILVG 120
QY 121 EFVSALLVPKCKFLHGRMDVCETHLHMTVAKETSEKSTNHDYGMILPGSIDKFR 180
Db 121 EFVSALLVPKCKFLHGRMDVCETHLHMTVAKETSEKSTNHDYGMILPGSIDKFR 180
QY 181 GVEFVCCPLAESNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEAEVEE 240
Db 181 GVEFVCCPLAESNVDSADAEEDSDVMWGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEEAEPEYEATERTTSTIAATTTTTTETSEVEEVVPTTAASTPDV 300
Db 241 EADDDDEDDGDEVEEEAEPEYEATERTTSTIAATTTTTTETSEVEEVVPTTAASTPDV 300
QY 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
Db 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIOHF 360
QY 361 QEKVESLQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKL 420
Db 361 QEKVESLQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKL 420
QY 421 KYVRAEQDRQHTLKHFEHVRVDPKKAQIRSOVTHLRYIYERMNQSLSLLYNPVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRVDPKKAQIRSOVTHLRYIYERMNQSLSLLYNPVA 480
QY 481 EBIQDEVDLLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLPVNGEFS 540
Db 481 EBIQDEVDLLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLPVNGEFS 540
QY 541 DDLQPHWSFGADSVDPANTENEVEPVDPADPAADRGLTTPGSLTNIKTEEISEVNLDAEF 600
Db 541 DDLQPHWSFGADSVDPANTENEVEPVDPADPAADRGLTTPGSLTNIKTEEISEVNLDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIHGV 660
Db 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFEQMONKK 697
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFEQMONKK 697
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RESULT 5
US-09-548-367D-16
; Sequence 16, Application Us/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR ANI
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
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; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-16

Query Match      99.8%  Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%  Pred. No. 1.2e-264;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPQIAFMFCGRLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPQIAFMFCGRLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCYQEVPELOITNVVEANQPVTTQNMCKRGRKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQCYQEVPELOITNVVEANQPVTTQNMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCFLQHERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCFLQHERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESNVDSADAEEDSDVVMGGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESNVDSADAEEDSDVVMGGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
DB 241 EADDEDEDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMKEEAEFRQKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMKEEAEFRQKNLPKADKKAVIQHF 360
QY 361 QKVESLEQEAANERQOVLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QKVESLEQEAANERQOVLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYERMNQSLILYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYERMNQSLILYNVPAVA 480
QY 481 EIQDEVDLLOKEQNSYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
DB 481 EIQDEVDLLOKEQNSYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
QY 541 DDLQPMHSEFGADSVPAKNTENEVEPVDARPAADRGLTTPGSGLTNKTETSEIYKMDARF 600
DB 541 DDLQPMHSEFGADSVPAKNTENEVEPVDARPAADRGLTTPGSGLTNKTETSEIYKMDARF 600
QY 601 RHDSGYEVHHQKLVFFAEEDVGSNGKGAIGLMVGGVVIATVITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEEDVGSNGKGAIGLMVGGVVIATVITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697

RESULT 6
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551.853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
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; PRIOR APPLICATION NUMBER: PCI/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-16

Query Match      99.8%  Score 3643; DB 4; Length 697;
Best Local Similarity 99.7%  Pred. No. 1.2e-264;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPQIAFMFCGRLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPQIAFMFCGRLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQCYQEVPELOITNVVEANQPVTTQNMCKRGRKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQCYQEVPELOITNVVEANQPVTTQNMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCFLQHERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCFLQHERMDVCETHLHWITVAKETCSKSTNLHDYGMLLPGGIDKFR 180
QY 181 GVEFVCCPLAESNVDSADAEEDSDVVMGGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAESNVDSADAEEDSDVVMGGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
DB 241 EADDEDEDGDEVEEAEPEYEATERTTISATTTTITTESVEEVVVPVTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMKEEAEFRQKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVMKEEAEFRQKNLPKADKKAVIQHF 360
QY 361 QKVESLEQEAANERQOVLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QKVESLEQEAANERQOVLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYERMNQSLILYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYERMNQSLILYNVPAVA 480
QY 481 EIQDEVDLLOKEQNSYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
DB 481 EIQDEVDLLOKEQNSYSDVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSI 540
QY 541 DDLQPMHSEFGADSVPAKNTENEVEPVDARPAADRGLTTPGSGLTNKTETSEIYKMDARF 600
DB 541 DDLQPMHSEFGADSVPAKNTENEVEPVDARPAADRGLTTPGSGLTNKTETSEIYKMDARF 600
QY 601 RHDSGYEVHHQKLVFFAEEDVGSNGKGAIGLMVGGVVIATVITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEEDVGSNGKGAIGLMVGGVVIATVITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMONKK 697

RESULT 7
US-09-548-372D-12
; Sequence 12, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
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FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US 09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20681
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-12

Query Match
Best Local Similarity 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCLVG 120
QY 121 EFVSALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPCGIDKFR 180
DB 121 EFVSALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSTATTTTTTTSVEEVVVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSTATTTTTTTSVEEVVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVNRHEEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVNRHEEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
QY 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLPVNGEFSL 540
DB 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLPVNGEFSL 540
QY 541 DDLQPHWSEFGADSVPAANTENEVEPVDARPAADRGITTRPGSGLTNKITEEISEVNLDAEF 600
DB 541 DDLQPHWSEFGADSVPAANTENEVEPVDARPAADRGITTRPGSGLTNKITEEISEVNLDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMN 695

US-09-548-372D-12

Query Match
Best Local Similarity 99.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPVITQNMCKRGKQCKTHPHFVIPYRCLVG 120
QY 121 EFVSALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPCGIDKFR 180
DB 121 EFVSALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCEKSTNLHDYGMILLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSTATTTTTTTSVEEVVVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSTATTTTTTTSVEEVVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVNRHEEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRMSQVNRHEEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVPSLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLYNVPAVA 480
QY 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLPVNGEFSL 540
DB 481 EEIQDEVDLLOKEQNSDDVLANMISEPRISYGNALMPSLTETKTIVELLPVNGEFSL 540
QY 541 DDLQPHWSEFGADSVPAANTENEVEPVDARPAADRGITTRPGSGLTNKITEEISEVNLDAEF 600
DB 541 DDLQPHWSEFGADSVPAANTENEVEPVDARPAADRGITTRPGSGLTNKITEEISEVNLDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMN 695
DB 661 VEVDAAVTPEERHLSKMQNGYENPTYKFFEQMN 695

RESULT 8
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QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695
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DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695

RESULT 9
US-09-551-853D-12
: Sequence 12, Application US/09551853D
: Patent No. 6500667
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
: FILE REFERENCE: 29915/6280L
: CURRENT APPLICATION NUMBER: US/09/551-853D
: CURRENT FILING DATE: 2000-04-18
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 69/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 12
: LENGTH: 695
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-551-853D-12

Query Match 59.7%; Score 3641; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPGLALLAAWTAHARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
DB 1 MHPGLALLAAWTAHARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONNCKRGRKCKTTPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONNCKRGRKCKTTPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCFPLHQERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCFPLHQERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTESVEEVVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTESVEEVVPTTAASTPDV 300

QY 301 DKYLETPGDENEHAFQKAKERLEAKHREMSQVREWEAEERQAKNLPKADKKAVIOHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHREMSQVREWEAEERQAKNLPKADKKAVIOHF 360

QY 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPRHVENMLK 420

QY 421 KYVRAEQDRQHTLKHFSHVRWDPKKAQIRSQVNTHLRVIYERMNQSLSLYNVPAVA 480
DB 421 KYVRAEQDRQHTLKHFSEHVRWDPKKAQIRSQVNTHLRVIYERMNQSLSLYNVPAVA 480

QY 481 BEIQDEVDLLOKEQNSDDVLANMISEPRISYNDALMPSLTETKTIVELLFVNGEFSL 540
DB 481 BEIQDEVDLLOKEQNSDDVLANMISEPRISYNDALMPSLTETKTIVELLFVNGEFSL 540
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QY 541 DDLQPMHSEFADSVDPANTENEVEPVDARPAADRGLTTRPGSGITNKTETEEISEVNLDAEF 600
|||||
DB 541 DDLQPMHSEFADSVDPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVNLDAEF 600

QY 601 RUDSGYEVHROKLVFAEDVGSNKGAIIGLMVGGVVVATVITLVMLKKQYTSIHGCV 660
|||||
DB 601 RUDSGYEVHROKLVFAEDVGSNKGAIIGLMVGGVVVATVITLVMLKKQYTSIHGCV 660

QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695
|||||
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMGN 695

RESULT 10
US-09-548-372D-20
: Sequence 20, Application US/09548372D
: Patent No. 6420534
: GENERAL INFORMATION:
: APPLICANT: GURNEY ET AL.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
: FILE REFERENCE: 29915/6280I
: CURRENT APPLICATION NUMBER: US/09/548-372D
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: US 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: US 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-548-372D-20

Query Match 59.6%; Score 3638; DB 4; Length 697;
Best Local Similarity 99.6%; Pred. No. 2.9e-264;
Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHPGLALLAAWTAHARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
DB 1 MHPGLALLAAWTAHARALEVPTDGNAGLLAEPOIAMFCGRLLNMHMNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONNCKRGRKCKTTPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIONNCKRGRKCKTTPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCFPLHQERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGGIDKFR 180
DB 121 EFVSDALLVPDKCFPLHQERMDVCETHLHHHTVAKETCSEKSTNLHDYGMLLPGGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTESVEEVVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTESVEEVVPTTAASTPDV 300

QY 301 DKYLETPGDENEHAFQKAKERLEAKHREMSQVREWEAEERQAKNLPKADKKAVIOHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHREMSQVREWEAEERQAKNLPKADKKAVIOHF 360

QY 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPRHVENMLK 420

QY 421 KYVRAEQDRQHTLKHFSEHVRWDPKKAQIRSQVNTHLRVIYERMNQSLSLYNVPAVA 480
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DB 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQINSQVYTHLRYEYRNMOSLSLLYNVPAVA 480
QY 481 EBIQEVDELQKEQYNSDVLNMISEPRISYNDALMKNSTETKTIVELAPVNEFSL 540
DB 481 EBIQEVDELQKEQYNSDVLNMISEPRISYNDALMKNSTETKTIVELAPVNEFSL 540
QY 541 DDLQPHSFGAUSVPANTENEVEPVDPARPAADRGTLTRPGSGLNKTETSESEVNLDAEF 600
DB 541 DDLQPHSFGAUSVPANTENEVEPVDPARPAADRGTLTRPGSGLNKTETSESEVNLDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 11

US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US 09/548,367D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 99.6%; Score 3638; DB 4; Length 697;

Best Local Similarity 99.6%; Pred. No. 2,9e-264;

Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVONGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVVEANQPTVTONMCKRGKCKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCEVYPELOITNVVEANQPTVTONMCKRGKCKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPCKFLHOERMDVCETHLHWHTVAKETCSEKSNLHDYGMILLPCGIDKFR 180
DB 121 EFVSDALLVPCKFLHOERMDVCETHLHWHTVAKETCSEKSNLHDYGMILLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWCGADTDYADGSDKVVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWCGADTDYADGSDKVVVEAEVEAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEEAEIERTTSTATTTTTFESVEVVRVPTIAASTPDV 360
DB 241 EADDDEDDGDEVEEAEPEEAEIERTTSTATTTTTFESVEVVRVPTIAASTPDV 360
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMSQVNRWEBAERQAKNLPKADKKAVIGHF 360

DB 301 DKYLETPGDENEHAFQKAKERLEAKHRMSQVNRWEBAERQAKNLPKADKKAVIGHF 360
QY 361 QEKVESLEQEAANERQQLVETIMAKVEAMLNDRRLALENTTALQAVPPRRHVFENMLK 420
DB 361 QEKVESLEQEAANERQQLVETIMAKVEAMLNDRRLALENTTALQAVPPRRHVFENMLK 420
QY 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSQVMTHLRVLYERKMOSLSLLYNVPAVA 480
DB 421 KYVRAEQDRQHTLKHFEHVRWVDPKAAQIRSQVMTHLRVLYERKMOSLSLLYNVPAVA 480
QY 481 EBIQEVDELQKEQYNSDVLNMISEPRISYNDALMKNSTETKTIVELAPVNEFSL 540
DB 481 EBIQEVDELQKEQYNSDVLNMISEPRISYNDALMKNSTETKTIVELAPVNEFSL 540
QY 541 DDLQPHSFGAUSVPANTENEVEPVDPARPAADRGTLTRPGSGLNKTETSESEVNLDAEF 600
DB 541 DDLQPHSFGAUSVPANTENEVEPVDPARPAADRGTLTRPGSGLNKTETSESEVNLDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIITGLMVGGVVIAIVITLVMKKKCYTTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 12

US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES THEREOF
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US 09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20891
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match 99.6%; Score 3638; DB 4; Length 697;

Best Local Similarity 99.6%; Pred. No. 2,9e-264;

Matches 694; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVONGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVYPELOITNVVEANQPTVTONMCKRGKCKCKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCEVYPELOITNVVEANQPTVTONMCKRGKCKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPCKFLHOERMDVCETHLHWHTVAKETCSEKSNLHDYGMILLPCGIDKFR 180
DB 121 EFVSDALLVPCKFLHOERMDVCETHLHWHTVAKETCSEKSNLHDYGMILLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWCGADTDYADGSDKVVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWCGADTDYADGSDKVVVEAEVEAEVEE 240

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QY 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
DB 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKKAVICHF 360
DB 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKKAVICHF 360
QY 361 QKVSLEQEAANERQQLVETHMARVEAMLDNRRLALENYITAIQAAPPPEPRVFNMLK 420
DB 361 QKVSLEQEAANERQQLVETHMARVEAMLDNRRLALENYITAIQAAPPPEPRVFNMLK 420
QY 421 KYVRAEQKDROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPAPA 480
DB 421 KYVRAEQKDROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPAPA 480
QY 481 BEIQDEVELLOKEQYSDVLANMISEPRISYNDALMPSLCTETKTIVELLPVNGEFSL 540
DB 481 BEIQDEVELLOKEQYSDVLANMISEPRISYNDALMPSLCTETKTIVELLPVNGEFSL 540
QY 541 DLOPWHSGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEIYVNDIAEF 600
DB 541 DLOPWHSGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEIYVNDIAEF 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNKGAITGLMVGGVVIATVITLVMLKKQNTSIIHGV 660
DB 601 RHDSGYEVHHQKLVFAEDVGSNKGAITGLMVGGVVIATVITLVMLKKQNTSIIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMKNK 695
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMKNK 695

RESULT 13
US-08-123-702-2
: Sequence 2, Application US/09123702
: Patent No. 5604131
: GENERAL INFORMATION:
: APPLICANT: Wadsworth, Samuel
: APPLICANT: Snyder, Benjamin
: APPLICANT: Reddy, Vermuri, B.
: APPLICANT: Wei, Chamer
: TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding ABP770
: Patent No. 5604131
: TITLE OF INVENTION: Containing a Genomic DNA Insert of the Kf and CX-2 Regions
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Patrea L. Pabst
: STREET: 2800 One Atlantic Center
: STREET: 1201 West Peachtree Street
: CITY: Atlanta
: STATE: GA
: COUNTRY: USA
: ZIP: 30309-3450
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/123,702
: FILING DATE: 17-SEPT-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: TS1121
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404)-873-8794
: TELEFAX: (404)-873-8795
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:

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: LENGTH: 695 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-123-702-2

Query Match: 99.5%; Score 3633; DB 1; Length 695;
Rest Local Similarity 99.7%; Pred. No. 6.9e-264;
Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MLPGALLLLAAWTAARALEVPTDGNAGILARPOTIAMFCGRLLNMHNVONGKWDSDPSGTK 60
DB 2 MLPGALLLLAAWTAARALEVPTDGNAGILARPOTIAMFCGRLLNMHNVONGKWDSDPSGTK 60
QY 61 TCTDTRKGTIOYCCQVEYVPELQITNVVEANQVPTIQNMCKRGKCKQCTHPIHPIYPRCLVG 120
DB 61 TCTDTRKGTIOYCCQVEYVPELQITNVVEANQVPTIQNMCKRGKCKQCTHPIHPIYPRCLVG 120
QY 121 EFVSADALLVPDKCKFLHQRMDVCEHLHWHYVAKETCEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSADALLVPDKCKFLHQRMDVCEHLHWHYVAKETCEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAFESDNVDSADAEEDSDVVMGGADTDYADGSEDKYVEVAEEVEE 240
DB 181 GVEFVCCPLAFESDNVDSADAEEDSDVVMGGADTDYADGSEDKYVEVAEEVEE 240
QY 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
DB 241 EADDDEDDGDEVEEAEPEYEATERITSIATITTTTTSVEEYVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKKAVICHF 360
DB 301 DKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKKAVICHF 360
QY 361 QKVSLEQEAANERQQLVETHMARVEAMLDNRRLALENYITAIQAAPPPEPRVFNMLK 420
DB 361 QKVSLEQEAANERQQLVETHMARVEAMLDNRRLALENYITAIQAAPPPEPRVFNMLK 420
QY 421 KYVRAEQKDROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPAPA 480
DB 421 KYVRAEQKDROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNOSLSLLYNPAPA 480
QY 481 BEIQDEVELLOKEQYSDVLANMISEPRISYNDALMPSLCTETKTIVELLPVNGEFSL 540
DB 481 BEIQDEVELLOKEQYSDVLANMISEPRISYNDALMPSLCTETKTIVELLPVNGEFSL 540
QY 541 DLOPWHSGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEIYVNDIAEF 600
DB 541 DLOPWHSGADSVFANTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEIYVNDIAEF 600
QY 601 RHDSGYEVHHQKLVFAEDVGSNKGAITGLMVGGVVIATVITLVMLKKQNTSIIHGV 660
DB 601 RHDSGYEVHHQKLVFAEDVGSNKGAITGLMVGGVVIATVITLVMLKKQNTSIIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMKN 695
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMKN 695

RESULT 14
US-08-104-165-1
: Sequence 1, Application US/08104165
: Patent No. 5877015
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: GATE, Alison Mary
: APPLICANT: MULLAN, Michael John
: APPLICANT: CHARTIER-HARLIN, Marie-Christine
: APPLICANT: OWEN, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew

```



```

: STREET: 379 Lytton Avenue
: City: Palo Alto
: State: California
: Country: US
: ZIP: 94301
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/104,165
: FILING DATE: 21-JAN-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 9101307.8
: FILING DATE: 21-JAN-1991
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-104-165-1
:
: Query Match 99.5%; Score 3633; DB 2; Length 695;
: Best Local Similarity 99.7%; Pred. No. 6.9e-264;
: Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
:
QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGKLNHMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLLAEPOIAMFCGKLNHMVQNGKWDSPSGTK 60
QY 61 TCIDTKGILQYCEVYPELQITNVVEANQPVITQNMCKRGRKQCKTHPEV:PYRCLVG 120
DB 61 TCIDTKGILQYCEVYPELQITNVVEANQPVITQNMCKRGRKQCKTHPEV:PYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSNLDYGMILPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSKSNLDYGMILPCGIDKFR 180
QY 181 GVEFVCCPLAESNVDSADAEEDSDVWGGACTDYADGSEKVKYVEVAEEEAVEREE 240
DB 181 GVEFVCCPLAESNVDSADAEEDSDVWGGADTYADGSEKVKYVEVAEEEAVEREE 240
QY 241 EADDEDDDEGVEEAEPEYBEATRTTSIAITTTTIESVEEVYVPTTAASTPDV 300
DB 241 EADDEDDDEGVEEAEPEYBEATRTTSIAITTTTIESVEEVYVPTTAASTPDV 300
QY 301 DKYLETPCDENEAHAFQKAKERLFAKIRMSQVMREWEAEARQANLPKAKKAVIQHF 360
DB 301 DKYLETPCDENEAHAFQKAKERLFAKIRMSQVMREWEAEARQANLPKAKKAVIQHF 360
QY 361 QEKVESLFOEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRSHVFNMLK 420
DB 361 QEKVESLFOEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRSHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHEFHVMDVDPKKAQAQIRSOVMTHFARVIERMKNQSLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHEFHVMDVDPKKAQAQIRSOVMTHFARVIERMKNQSLLYNPVAVA 480
QY 481 EEIQDEVDLLOKEQNSDDVLANNKISEPRISYGNDAKMLSLTKITVELLPVNGEFSI 540
DB 481 EEIQDEVDLLOKEQNSDDVLANNKISEPRISYGNDAKMLSLTKITVELLPVNGEFSI 540
:
: 541 DDLPWHISFGADSVPAENTENEVEPVDARPAADRLTRPGSLTNIKTEISEVNLDAEF 600
: 541 DDLPWHISFGADSVPAENTENEVEPVDARPAADRLTRPGSLTNIKTEISEVNLDAEF 600
: 601 RHDSGYEVHOKLVFFPAEDVGSNKGAIIGLMVGGVIAIVITLVMKKKKQVTSIHGV 660
: 601 RHDSGYEVHOKLVFFPAEDVGSNKGAIIGLMVGGVIAIVITLVMKKKKQVTSIHGV 660
: 661 VEVDAAVTPEERHLSKMQQNCYENPTYKFFEQMON 695
: 661 VEVDAAVTPEERHLSKMQQNCYENPTYKFFEQMON 695
:
: RESULT 15
: US-08-464-250-1
: Sequence 1. Application US/08/464250
: Patent No. 6107542
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: COATE, Alison Mary
: APPLICANT: MULLAN, Michael John
: APPLICANT: CHARTIER-HARTIN, Marie-Christine
: APPLICANT: OWEN, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464,250
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/104,165
: FILING DATE: 21-JAN-1992
: APPLICATION NUMBER: 9101307.8
: FILING DATE: 21-JAN-1991
: APPLICATION NUMBER: 9118445.7
: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
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: US-08-464-250-1
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: Query Match 99.5%; Score 3633; DB 3; Length 695;
: Best Local Similarity 99.7%; Pred. No. 6.9e-264;
: Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Search completed: October 2, 2003, 14:03:36
 Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: October 2, 2003, 14:00:39 : Search time 39 Seconds
(without alignments)
2827.550 Million cell updates/sec

Title: US-09-806-194-18
Perfect score: 3651
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Scoring table: RJSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 156212961 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3651	100.0	697	9	US-09-795-847-18
3	3651	100.0	697	9	US-09-794-743-18
4	3651	100.0	697	9	US-09-794-748-18
5	3651	100.0	697	9	US-09-794-925-18
6	3651	100.0	697	9	US-09-681-442-18
7	3651	100.0	697	11	US-09-869-414-18
8	3651	100.0	697	11	US-09-548-366-18
9	3643	99.8	697	9	US-09-794-927-16
10	3643	99.8	697	9	US-09-795-847-16
11	3643	99.8	697	9	US-09-794-743-16
12	3643	99.8	697	9	US-09-794-748-16
13	3643	99.8	697	9	US-09-794-925-16
14	3643	99.8	697	9	US-09-681-442-16
15	3643	99.8	697	11	US-09-869-414-16

16	3643	99.8	697	11	US-09-548-366-16	Sequence 16, Appl
17	3641	99.7	695	9	US-09-794-927-12	Sequence 12, Appl
18	3641	99.7	695	9	US-09-795-847-12	Sequence 12, Appl
19	3641	99.7	695	9	US-09-794-743-12	Sequence 12, Appl
20	3641	99.7	695	9	US-09-794-748-12	Sequence 12, Appl
21	3641	99.7	695	9	US-09-794-925-12	Sequence 12, Appl
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23	3641	99.7	695	11	US-09-869-414-12	Sequence 12, Appl
24	3641	99.7	695	11	US-09-548-366-12	Sequence 12, Appl
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43	3633	99.5	695	12	US-10-357-935-1	Sequence 1, Appl
44	3633	99.5	695	15	US-10-169-580-3	Sequence 3, Appl
45	3628	99.4	695	9	US-09-794-927-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-794-927-18
: Sequence 18, Application US/09794927
: Patent No. US20010016324A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/6280FG
: CURRENT APPLICATION NUMBER: US/09/794,927
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-927-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-795-847-18
: Sequence 18, Application US/09795847
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Van, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: FILE REFERENCE: 28341/6280DE
: CURRENT APPLICATION NUMBER: US/09/795,847
: PRIOR FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
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: PRIOR FILING DATE: 1999-09-23
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: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent in Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-795-847-18

Query Match 100.0% Score 3651; DB 9; Length 697;
Best Local Similarity 100.0% Pred No. 3 8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Van, Riqiang
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;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
;; TITLE OF INVENTION: USES
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 28341/6280BC
;; CURRENT APPLICATION NUMBER: US/09/794,743
;; CURRENT FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 18
;; LENGTH: 697
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-794-743-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228; Mismatches 0; Indels 0; Gaps 0;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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;; Sequence 18, Application US/09794748
;; Patent No. US20020037315A1
;; GENERAL INFORMATION:
;; APPLICANT: Gurney, Mark E.
;; APPLICANT: Bienkowski, Michael J.
;; APPLICANT: Heinrikson, Robert L.
;; APPLICANT: Parodi, Luis A.
;; APPLICANT: Yan, Riqiang
;; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A.
;; TITLE OF INVENTION: USES
;; TITLE OF INVENTION: THEREFOR
;; FILE REFERENCE: 28341/6280JL
;; CURRENT APPLICATION NUMBER: US/09/794,748
;; CURRENT FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 09/416,901
;; PRIOR FILING DATE: 1999-10-13
;; PRIOR APPLICATION NUMBER: 60/155,493
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 09/404,133
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: PCT/US99/20881
;; PRIOR FILING DATE: 1999-09-23
;; PRIOR APPLICATION NUMBER: 60/101,594
;; PRIOR FILING DATE: 1998-09-24
;; NUMBER OF SEQ ID NOS: 73
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 18
;; LENGTH: 697
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-794-748-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228; Mismatches 0; Indels 0; Gaps 0;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAFMCGRLNMHNVMNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAFMCGRLNMHNVMNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVPYELQITNVVEANQPVTTQNMCKRGKCKKTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEVPYELQITNVVEANQPVTTQNMCKRGKCKKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEAEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTISTATITTTTSTESVEEVVPTTAATPDV 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTISTATITTTTSTESVEEVVPTTAATPDV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
DB 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRYIERMNSLSLLYNPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRYIERMNSLSLLYNPVA 480

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481 BEIOEVDLQKEQNYSDVLANMISEPRISYGNALMPSLSETKTVLELLPVGESFL 540
481 BEIOEVDLQKEQNYSDVLANMISEPRISYGNALMPSLSETKTVLELLPVGESFL 540
541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVNLDAEF 600
541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVNLDAEF 600
601 RHDSGYEVHQLVFFAEVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 540
601 RHDSGYEVHQLVFFAEVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 540
661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 5
US-09-794-925-18
; Sequence 18, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heiorikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/628081
; CURRENT APPLICATION NUMBER: US/09794925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLPLGLALLLAATARALETVDGAGLAEFQIATMFCGRNLNMHNWONGKWDSDPSGK 60
DB 1 MLPLGLALLLAATARALETVDGAGLAEFQIATMFCGRNLNMHNWONGKWDSDPSGK 60
CY 61 TCIDTKEGTLQYCOEVPYELQITNVVEANQPVITONCKRGKCKTHPHVPIYRCLVG 120
DB 61 TCIDTKEGTLQYCOEVPYELQITNVVEANQPVITONCKRGKCKTHPHVPIYRCLVG 120
CY 121 EFVSDALLVPDKCKFLQHERMDVCEETHLHWHVAKETSEKSTNLHBYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLQHERMDVCEETHLHWHVAKETSEKSTNLHBYGMLLPGCIDKFR 180
CY 181 GVEFVCCPLAESDNVSDADAEEDSDVWVGADTDADGSEDKVVEAEVEE 240
DB 181 GVEFVCCPLAESDNVSDADAEEDSDVWVGADTDADGSEDKVVEAEVEE 240
CY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
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241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
301 DRYLETPGDENHAFQKAKERLEAKHRERMSQVMREWEAEQAQKNLPKADKXAVIQHF 360
301 DRYLETPGDENHAFQKAKERLEAKHRERMSQVMREWEAEQAQKNLPKADKXAVIQHF 360
361 QKVSLSLQEAANEHQVIVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK 420
361 QKVSLSLQEAANEHQVIVETHMARVEAMLNDRRLALENYITALQAVPPRHRVFNMLK 420
421 KYVRAEQDRQHTLKHFEHVRMWDPKAAQTRSQVMTHLRVIYERMGSLSLNVPAVA 480
421 KYVRAEQDRQHTLKHFEHVRMWDPKAAQTRSQVMTHLRVIYERMGSLSLNVPAVA 480
481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNALMPSLSETKTVLELLPVGESFL 540
481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNALMPSLSETKTVLELLPVGESFL 540
541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVNLDAEF 600
541 DDLQPHWSFGADSVDPANTENEVEPVDARPAADRGLTTPGSGLTNKTETSEVNLDAEF 600
601 RHDSGYEVHQLVFFAEVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
601 RHDSGYEVHQLVFFAEVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 6
US-09-681-442-18
; Sequence 18, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heiorikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES THEREFOR
; FILE REFERENCE: 28341/628081
; CURRENT APPLICATION NUMBER: US/09681442
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-18

Query Match 100.0%; Score 3651; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLPLGLALLLAATARALETVDGAGLAEFQIATMFCGRNLNMHNWONGKWDSDPSGK 60
DB 1 MLPLGLALLLAATARALETVDGAGLAEFQIATMFCGRNLNMHNWONGKWDSDPSGK 60
CY 61 TCIDTKEGTLQYCOEVPYELQITNVVEANQPVITONCKRGKCKTHPHVPIYRCLVG 120
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Db 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONWCKRGKQ/KTHPHEVYPCIVG 120
Qy 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLDYGM/LPGGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLDYGM/LPGGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Qy 241 EADDDDEDDGDEVEEAEPEEATEKTTS/ATTTTTTSVEEVVVPVTTAASTPDV 300
Db 241 EADDDDEDDGDEVEEAEPEEATEKTTS/ATTTTTTSVEEVVVPVTTAASTPDV 300
Qy 301 DKYLETPGDENEGHAFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAQVIOHF 360
Db 301 DKYLETPGDENEGHAFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAQVIOHF 360
Qy 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLLYNYPVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLLYNYPVA 480
Qy 481 EBIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 EBIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Qy 541 DDLQPHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNLD 600
Db 541 DDLQPHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNLD 600
Qy 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVM/LKKQYTSIRHG 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVM/LKKQYTSIRHG 660
Qy 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 7

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US-09-869-414-18
: Sequence 18, Application US/09869414
: Publication No. US20030077226A1
: GENERAL INFORMATION:
: APPLICANT: Beinowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
: FILE REFERENCE: 28341/6280A
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: US/09/869,414
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/416,901
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-869-414-18
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Query Match 100.0%; Score 3651; DB 11; length 697;
Best Local Similarity 100.0%; Pred. No. 3.8e-228;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLPGALLLLAANTARALEVPTOGNAGLLAEPRQ/AMFCCGLNMHMNVONGKWDSDPSGTR 60
Db 1 MLPGALLLLAANTARALEVPTOGNAGLLAEPRQ/AMFCCGLNMHMNVONGKWDSDPSGTR 60
Qy 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONWCKRGKQCKTHPHFVYPCIVG 120
Db 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONWCKRGKQCKTHPHFVYPCIVG 120
Qy 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLDYGM/LPGGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHGERMDVCETHLHWHTVAKETCSKSTNLDYGM/LPGGIDKFR 180
Qy 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKVVEVAEEVAEVEE 240
Qy 241 EADDDDEDDGDEVEEAEPEEATEKTTS/ATTTTTTSVEEVVVPVTTAASTPDV 300
Db 241 EADDDDEDDGDEVEEAEPEEATEKTTS/ATTTTTTSVEEVVVPVTTAASTPDV 300
Qy 301 DKYLETPGDENEGHAFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAQVIOHF 360
Db 301 DKYLETPGDENEGHAFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAQVIOHF 360
Qy 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Db 361 QKVESLEQEAEANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPHVFNMLK 420
Qy 421 KYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLLYNYPVA 480
Db 421 KYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERMNQSLSLLYNYPVA 480
Qy 481 EBIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Db 481 EBIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
Qy 541 DDLQPHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNLD 600
Db 541 DDLQPHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNLD 600
Qy 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVM/LKKQYTSIRHG 660
Db 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVM/LKKQYTSIRHG 660
Qy 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
Db 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 8

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US-09-548-366-18
: Sequence 18, Application US/09548366
: Publication No. US20030104365A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
: FILE REFERENCE: 28341/6280A
: CURRENT FILING DATE: 2000-04-12
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-348-366-18

Query Match
Best Local Similarity 100.0%; Score 3651; Db 11; Length 697;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLIAEPOIAFMCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLIAEPOIAFMCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQIINVEANOPVTIONWCKRGKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELQIINVEANOPVTIONWCKRGKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYAGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYAGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTITTESVEEVVRVPTAASTPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTITTESVEEVVRVPTAASTPDVAV 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEBVRWDPKKAQIRSOVMTHLRVIERMNSQSLLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEBVRWDPKKAQIRSOVMTHLRVIERMNSQSLLYNYPAVA 480
QY 481 EEIQDEVDLLOKEQYSDVLANMISEPRISYGNALMPSLTETKTIVVYNGEFSL 540
DB 481 EEIQDEVDLLOKEQYSDVLANMISEPRISYGNALMPSLTETKTIVVYNGEFSL 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTIRPGSGLTNKTEISEVNIADAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTIRPGSGLTNKTEISEVNIADAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMKKQYTSIHGGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMKKQYTSIHGGV 660
QY 661 VEYDAVTPERHLSKMQQNGYENPTYKFEQMONKK 697
DB 661 VEYDAVTPERHLSKMQQNGYENPTYKFEQMONKK 697

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RESULT 9

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US-09-794-927-16
; Sequence 16, Application US/09794927
; Patent No. US20010016324A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.

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; APPLICANT: Yae, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRAIES THEREFOR, AN
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-794-927-16

Query Match
Best Local Similarity 99.8%; Score 3643; Db 9; Length 697;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLIAEPOIAFMCGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLIAEPOIAFMCGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQIINVEANOPVTIONWCKRGKCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELQIINVEANOPVTIONWCKRGKCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHWHHTVAKETCSEKSTNLDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYAGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADTDYAGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTITTESVEEVVRVPTAASTPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSATTTTITTESVEEVVRVPTAASTPDVAV 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEBVRWDPKKAQIRSOVMTHLRVIERMNSQSLLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEBVRWDPKKAQIRSOVMTHLRVIERMNSQSLLYNYPAVA 480
QY 481 EEIQDEVDLLOKEQYSDVLANMISEPRISYGNALMPSLTETKTIVVYNGEFSL 540
DB 481 EEIQDEVDLLOKEQYSDVLANMISEPRISYGNALMPSLTETKTIVVYNGEFSL 540
QY 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTIRPGSGLTNKTEISEVNIADAEF 600
DB 541 DDLPQWHSFGADSVDPANTENEVEPVDARPAADRGLTIRPGSGLTNKTEISEVNIADAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMKKQYTSIHGGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITLVMKKQYTSIHGGV 660

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QY 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMONKK 697

RESULT 10
US-09-795-847-16
; Sequence 16, Application US/09795847
; Patent No. US20010018208A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280DE
; CURRENT APPLICATION NUMBER: US/09/795,847
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-847-16

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Query Match 99.8%; Score 3643; DB 9; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNQKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNQKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCVLG 120

QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

QY 241 EADDDDEDDSDVEEFAEPEEATEETSTATTITTTTTFSEVEEYVRPTTAASTPDVA 300
DB 241 EADDDDEDDSDVEEFAEPEEATEETSTATTITTTTTFSEVEEYVRPTTAASTPDVA 300

QY 301 DKYLETPGSENEHAHFQKAKERLEAKHRMSQVWREWEAEAEQAKNLKPAKAVIQHF 360
DB 301 DKYLETPGSENEHAHFQKAKERLEAKHRMSQVWREWEAEAEQAKNLKPAKAVIQHF 360

QY 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITACAVPPRPRHFNMLK 420
DB 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITACAVPPRPRHFNMLK 420

QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERNMQSLSLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERNMQSLSLYNVPAVA 480

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DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVYERNMQSLSLYNVPAVA 480
QY 481 BEIODEVDELLQKEQNYSDDVLANMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
DB 481 BEIODEVDELLQKEQNYSDDVLANMISEPRISYNDALMPSLTETKTVELLPVNGEFSL 540
QY 541 LDLOPWHSEFGADSVPAANTENEPVDPADPADRLTTRPGSGLINIKTEETSEVNLDAEF 600
DB 541 DDLOPWHSEFGADSVPAANTENEPVDPADPADRLTTRPGSGLINIKTEELISEVKMPAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIIGIMVGGVVIATVITVLVMIKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIIGIMVGGVVIATVITVLVMIKKQYTSIHGV 660
QY 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPERHLSKMOONGYENPTYKFFEQMONKK 697

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RESULTS 11

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US-09-794-743-16
; Sequence 16, Application US/09794743
; Patent No. US20010021391A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, A
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280BC
; CURRENT APPLICATION NUMBER: US/09/794,743
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-16

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Query Match 99.8%; Score 3643; DB 9; Length 697;
Best Local Similarity 99.7%; Pred. No. 1.3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNQKWDSPSGTK 60
DB 1 MLPGLALLLAATAWTAARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVNQKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYRCVLG 120

QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPGIDKFR 180

QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

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QY 241 EADDEDEGDEVEEAEPEEATERTTISATTTTTTSSVEEVRVPTTAASTPDV 300
DB 241 EADDEDEGDEVEEAEPEEATERTTISATTTTTTSSVEEVRVPTTAASTPDV 300
QY 301 DKYLETPGDNENAHAFKAKERLEAKHREMSOVMEWEAEAEQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDNENAHAFKAKERLEAKHREMSOVMEWEAEAEQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMKL 420
DB 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
DB 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
QY 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTYVELLPVNGEFSL 540
DB 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTYVELLPVNGEFSL 540
QY 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTEEISEVNLDADF 600
DB 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTEEISEVNLDADF 600
QY 601 RHDGSEVHHQKLVFFAEADVGSNKGAIIGLMVGCVIATVITVILVLMKKQVTSIHGV 660
DB 601 RHDGSEVHHQKLVFFAEADVGSNKGAIIGLMVGCVIATVITVILVLMKKQVTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 12

US-09-794-748-16
; Sequence 16, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 2834./6280.21
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 05/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 99.8%; Score 3643; DB 9; Length 697;
Best Local Similarity 99.7%; Pred. No. 1,3e-227;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLJLAAMWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNGKWDSPSGTK 60
|||||

DB 1 MLPGLALLJLAAMWTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNGKWDSPSGTK 60
QY 61 TCIDTREGILQYCOEYVPELQITNVYEAQPVTIQNMCKRGRKCKCTHPHFVTPYRCLVG 120
DB 61 TCIDTREGILQYCOEYVPELQITNVYEAQPVTIQNMCKRGRKCKCTHPHFVTPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQBEMDVCETHLHWHTVAKETCSFKSTNLDHSGYGMLLPCGTDKFR 180
DB 121 EFVSDALLVPDKCKFLHQBEMDVCETHLHWHTVAKETCSFKSTNLDHSGYGMLLPCGTDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYAGSSEDKVVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYAGSSEDKVVEVAEEVEEVEE 240
QY 241 EADDEDEGDEVEEAEPEEATERTTISATTTTTTSSVEEVRVPTTAASTPDV 300
DB 241 EADDEDEGDEVEEAEPEEATERTTISATTTTTTSSVEEVRVPTTAASTPDV 300
QY 301 DKYLETPGDNENAHAFKAKERLEAKHREMSOVMEWEAEAEQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDNENAHAFKAKERLEAKHREMSOVMEWEAEAEQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMKL 420
DB 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
DB 421 KYVRAEQKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNYPAVA 480
QY 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTYVELLPVNGEFSL 540
DB 481 BEIQDEVELLOKEQNYSDOVLANMISEPRISYGNDAIMPSTETKTYVELLPVNGEFSL 540
QY 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTEEISEVNLDADF 600
DB 541 DLQOPWHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNKTEEISEVNLDADF 600
QY 601 RHDGSEVHHQKLVFFAEADVGSNKGAIIGLMVGCVIATVITVILVLMKKQVTSIHGV 660
DB 601 RHDGSEVHHQKLVFFAEADVGSNKGAIIGLMVGCVIATVITVILVLMKKQVTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 13

US-09-794-925-16
; Sequence 16, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match
Best Local Similarity 99.8% Score 3643; DB 9; Length 697;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MLPGALLLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRLNMHMVONGKWDSPSGIK 60
Db 1 MLPGALLLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRLNMHMVONGKWDSPSGIK 60
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Db 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONCKRGKCKKTHFHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHILHWHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCEHILHWHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVYVAEAEFEVAAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVYVAEAEFEVAAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
Db 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAFKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAFKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
Db 361 QEVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
Db 421 KYVRAEKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
QY 481 BEIQDEVDLQEQNSDDVLANNISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
Db 481 BEIQDEVDLQEQNSDDVLANNISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLQPMHSGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNDLAEF 600
Db 541 DDLQPMHSGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNDLAEF 600
QY 601 RHDGSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
Db 601 RHDGSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMQNKK 697
Db 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMQNKK 697

RESULT 14
US-09-681-442-16
; Sequence 16, Application US/09661442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
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; CURRENT APPLICATION NUMBER: US/09/681.442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16

Query Match
Best Local Similarity 99.8% Score 3643; DB 9; Length 697;
Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MLPGALLLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRLNMHMVONGKWDSPSGIK 60
Db 1 MLPGALLLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRLNMHMVONGKWDSPSGIK 60
QY 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONCKRGKCKKTHFHFVPIYRCVLG 120
Db 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONCKRGKCKKTHFHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHILHWHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCEHILHWHHTVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVYVAEAEFEVAAEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSDKVVYVAEAEFEVAAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
Db 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTTSVEEVVVRVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAFKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAFKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
Db 361 QEVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVFNMKL 420
QY 421 KYVRAEKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
Db 421 KYVRAEKDRQHTLKHFHVRVMDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
QY 481 BEIQDEVDLQEQNSDDVLANNISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
Db 481 BEIQDEVDLQEQNSDDVLANNISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLQPMHSGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNDLAEF 600
Db 541 DDLQPMHSGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEVNDLAEF 600
QY 601 RHDGSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
Db 601 RHDGSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMQNKK 697
Db 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFEQMQNKK 697
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RESULT 15
 US-09-869-414-16
 : Sequence 16, Application US/09869414
 : Publication No. US2003007226A:
 : GENERAL INFORMATION:
 : APPLICANT: Brinkowski et al.
 : TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
 : FILE REFERENCE: 28341/6280M
 : CURRENT APPLICATION NUMBER: US/09/869.414
 : CURRENT FILING DATE: 2001-06-27
 : PRIOR APPLICATION NUMBER: 09/416.901
 : PRIOR FILING DATE: 1999-10-13
 : PRIOR APPLICATION NUMBER: 60/155.493
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: 09/404.133
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: PCT/US99/20881
 : PRIOR FILING DATE: 1999-09-23
 : PRIOR APPLICATION NUMBER: 60/101.594
 : PRIOR FILING DATE: 1998-09-24
 : NUMBER OF SEQ ID NOS: 73
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 16
 : LENGTH: 697
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-869-414-16

Query Match 99.8%; Score 3643; DB 11; Length 697;
 Best Local Similarity 99.7%; Pred. No. 1.3e-227;
 Matches 695; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB	1	MLPGLALLLAAWTAARALEVPTDGNAGLLARPOIAMFCGRLLNMNMVONGKWDSPSC	60
QY	61	TCIDTKEGTLOVCOEYVPELOITNVVEANOPVTIONMCKGRKQCKTHPHFVPIYRC	120
DB	61	TCIDTKEGTLOVCOEYVPELOITNVVEANOPVTIONMCKGRKQCKTHPHFVPIYRC	120
QY	121	EFVSDALLVPDKCFLLHQERMDVCETHLHWHTVAKETSEKSTNLDYGNMLPGIDK	180
DB	121	EFVSDALLVPDKCFLLHQERMDVCETHLHWHTVAKETSEKSTNLDYGNMLPGIDK	180
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DB	181	GVEFVCCPLAESDNDVSADAEEDSDVWVGADTDFALGSDKVVVEAEERVAEVEE	240
QY	241	EADDDDEDDGDRVEEAEPEVEEATERITISITATITTTTSEVEEVRVPTTAAST	300
DB	241	EADDDDEDDGDRVEEAEPEVEEATERITISITATITTTTSEVEEVRVPTTAAST	300
QY	301	DKYLETPGDENEHAFKAKBLEAKHREMSOVNREWEAEERAKNLPKADKKAVIC	360
DB	301	DKYLETPGDENEHAFKAKBLEAKHREMSOVNREWEAEERAKNLPKADKKAVIC	360
QY	361	QEKVESLEQEAANERQOLVETHMARVEAMINDRRRLALENYITALCAVPPRPHV	420
DB	361	QEKVESLEQEAANERQOLVETHMARVEAMINDRRRLALENYITALCAVPPRPHV	420
QY	421	KYVRAEQKQKQHTLKHFEHVRMVDPKKAAQIRSONWTHRVITYERNQSSLLYN	480
DB	421	KYVRAEQKQKQHTLKHFEHVRMVDPKKAAQIRSONWTHRVITYERNQSSLLYN	480
QY	481	EEQDEVEDELQEQNYSDDLANMISEPRISVGNDALEPSLTETKTIVELLVNGE	540
DB	481	EEQDEVEDELQEQNYSDDLANMISEPRISVGNDALEPSLTETKTIVELLVNGE	540
QY	541	DLQPNHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEV	600
DB	541	DLQPNHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTNIKTEEISEV	600

QY 601 RHDSGVEVHHQKLVFFAEADVGSNKGAIIIGLMVGGVVIATVIVILVMIKKQYTSIHG 660
 DB 601 RHDSGVEVHHQKLVFFAEADVGSNKGAIIIGLMVGGVVIATVIVILVMIKKQYTSIHG 660
 QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
 DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

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 Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 2, 2003, 13:56:04 ; Search time 16.5667 Seconds
(without alignments)
4021.774 Million cell updates/sec
Title: US-09-806-194-18
Perfect score: 3651
Sequence: 1 MLPGLALLLAANTARALEV.....QNGYENPTTKFFCQXNKK 697
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 28330e seqs, 95168682 residues
Total number of hits satisfying chosen parameters: 28330e
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR,76:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3633	99.5	695	1 A49795	Alzheimer's disease
2	3582.5	98.1	770	1 QRRJ04	Alzheimer's disease
3	3536	96.9	695	2 S00550	Alzheimer's disease
4	3511	96.2	695	2 A27485	Alzheimer's disease
5	3095	84.8	747	2 JH0773	Alzheimer's disease
6	2105	57.7	484	4 A32761	hypothetical Alzhe
7	1725	47.2	763	2 A49321	amyloid beta (A4)
8	1709	46.8	765	2 S42880	amyloid precursor
9	1699	46.5	751	2 A49974	beta-amyloid prec
10	1183	32.4	653	2 A46362	amyloid precursor
11	1138	31.2	511	2 JG1404	CDer-box RNA-bind
12	815.5	22.3	686	2 T15795	hypothetical prote
13	746	20.4	886	2 A32758	beta-amyloid-like
14	706	19.3	246	2 S38344	CDer-binding prote
15	403	11.0	82	2 P00438	Alzheimer's disease
16	289.5	7.9	191	2 A35981	sperm membrane pro
17	275	7.5	57	2 E60045	Alzheimer's disease
18	275	7.5	57	2 E60045	Alzheimer's disease
19	275	7.5	57	2 G60045	Alzheimer's disease
20	275	7.5	57	2 D60045	Alzheimer's disease
21	275	7.5	57	2 A60045	Alzheimer's disease
22	275	7.5	57	2 B60045	Alzheimer's disease
23	217	5.9	42	2 P00512	beta-amyloid prote
24	192.5	5.3	110	2 I51116	NP-180 - sea lamp
25	186	5.1	5170	2 T15348	hypothetical prote
26	185.5	5.1	407	1 E0B0Q3	immediate-early pr
27	185.5	5.1	993	2 S49461	synaptonemal compl
28	182	5.0	522	2 T32444	hypothetical prote
29	175.5	4.8	802	1 S48529	NAB3 protein - yea

30 175.5 4.8 1188 2 T46608 zinc finger protei
31 174 4.8 579 2 JH0820 150K golgi antigen
32 174 4.8 1087 2 T30340 myosin-related p
33 172 4.7 675 2 T03744 mycD protein inhib
34 172 4.7 784 2 PK0009 neurofilament trip
35 172 4.7 1182 2 T30189 myelin transcripti
36 171.5 4.7 793 1 JH0628 caldesmon - human
37 171.5 4.7 884 2 T20405 hypothetical prote
38 171.5 4.7 885 2 G71608 ATP-dept. acy-CoA
39 171 4.7 1271 2 A45555 glutamate rich pro
40 170 4.7 464 2 H90279 microtubule bindin
41 170 4.7 1948 2 S00485 gene 11-1 protein
42 169.5 4.6 298 1 TP0UTC troponin T, cardia
43 169.5 4.6 1875 2 S38173 myosin-like protei
44 169 4.6 771 1 A34330 h-caldesmon - chic
45 169 4.6 1187 2 T46637 transcription fact

ALIGNMENTS

RESULT: 1
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human: suppo
A:Reference number: A49795; MUID:9:273117; PMID:1905108
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <P0D>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz type prote
C:Keywords: alternative splicing

Query Match 99.5%; Score 3633; DB 1; Length 695;
Best Local Similarity 99.7%; Pred. No. 1.4e-183;
Matches 693; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIATMFCGRLLNMHNVQNGKWDSDPSGTK 60
Dd 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIATMFCGRLLNMHNVQNGKWDSDPSGTK 60
Qy 61 TCIDTKEGILQYCEVYPELQITNVVEANOPVTIONCKRGKCKCTHPHEVYRCLVG 120
Dd 61 TCIDTKEGILQYCEVYPELQITNVVEANOPVTIONCKRGKCKCTHPHEVYRCLVG 120
Qy 121 EFVSDALLVPDKKFLHQERNDVCETHLHWHYVAKETCEKSTNLHDYGMLLPGIDPKFR 180
Dd 121 EFVSDALLVPDKKFLHQERNDVCETHLHWHYVAKETCEKSTNLHDYGMLLPGIDPKFR 180
Qy 181 GVEFVCCPLAESNVDSADAEEDSDVWGGADTDYADGSEDKVVEAEVEEVEE 240
Dd 181 GVEFVCCPLAESNVDSADAEEDSDVWGGADTDYADGSEDKVVEAEVEEVEE 240
Qy 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITFSVEVYRVTPTAASTPDV 300
Dd 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITFSVEVYRVTPTAASTPDV 300
Qy 301 DKYLETFGDENEHAHFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKAVIQHF 360
Dd 301 DKYLETFGDENEHAHFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKAVIQHF 360
Qy 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHFNWKL 420
Dd 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHFNWKL 420
Qy 421 KYVRAEQKDRQHTLKHFHEHVMVDPKAAQIRSOVMTHLRVIYERMQSLSLNVPAPA 480
Dd 421 KYVRAEQKDRQHTLKHFHEHVMVDPKAAQIRSOVMTHLRVIYERMQSLSLNVPAPA 480

Db 421 KYVRAEQKDRHTLKHFEHVRVMDPKKAQIRSQVMHLRVYIERMNCSSLDYKNPVA 480

QY 481 EETQDEVDLQKEQNSCDVLNMISEPRISXGNALMPSLTETKTIVELLVNGFESL 540

Db 481 EETQDEVDLQKEQNSCDVLNMISEPRISXGNALMPSLTETKTIVELLVNGFESL 540

QY 541 DQCPWHSFGADSPANTENEVEPVDARPAADRGILTTPGSGLTNIXTEEISEVNLDAEF 600

Db 541 DQCPWHSFGADSPANTENEVEPVDARPAADRGILTTPGSGLTNIXTEEISEVNLDAEF 600

QY 601 RHDSGYEVHOKLVFFAEDVGSXKGAIGLVGVVATVIVITLVLMKKKKQVTSIRHGV 660

Db 601 RHDSGYEVHOKLVFFAEDVGSXKGAIGLVGVVATVIVITLVLMKKKKQVTSIRHGV 660

QY 661 VEYDAAVTPEERHLKSKQCGNYENPTYKFFEQMGN 695

Db 661 VEYDAAVTPEERHLKSKQCGNYENPTYKFFEQMGN 695

RESULT 2

GRHUA4

Alzheimer's disease amyloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor

N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular

protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence,revision 28-Jul-1995 #text,change 15-Sep-2000

C:Accession: S05194; A32277; A33260; A35486; I39451; I39453; I59562; A44468; A28583; A29102; A60805; J10038; S06121; A60355; A38384; S29076; S38252; S38253

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayne, R.M.; Unterbeck, A.; Beyreuther, K.

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PresA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by two exons and shows similarity to the epsilon A4 amyloid precursor protein

A:Reference number: S02260; MUID:89128427; PMID:2783775

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <EMBL>

A:Cross-references: EMBL:X13466; NID:G35558; PIDN:CAA1340.1; PID:Q87360

A:Note: alternative splice form APP(695)

R:La Fauri, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-amyloid precursor protein gene

A:Reference number: A32277; MUID:8915870; PMID:2518123

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <EMBL>

A:Cross-references: GR:M24545; GR:M24547; NID:G341202; PIDN:AACT3654.1; PID:Q516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, P.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity to the epsilon A4 amyloid precursor protein

A:Reference number: A33260; MUID:89392030; PMID:2675637

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOL>

A:Cross-references: NID:G178663; PIDN:AAA51768.1; PID:G178865

R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of the brain

A:Reference number: A35486; MUID:90321244; PMID:2196873

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PREI>

A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients

R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 87, 257-263, 1990

A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318; PMID:2110105

A:Accession: I39452

A:Status: nucleic acid sequence not shown; translation not shown; translated from

A:Molecule type: DNA

A:Residues: 1-770 <YOS>

A:Cross-references: GR:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616

A:Accession: I39451

A:Status: nucleic acid sequence not shown; translation not shown; translated from

A:Molecule type: DNA

A:Residues: 1-530, OWLMPVLPAPWEAKVGR' <YOS>

A:Cross-references: GR:M34875; NID:G178608; PIDN:AAB59501.1; PID:G178615

R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.

Gene 102, 291-292, 1991

A:Reference number: A59020; MUID:91340168; PMID:1908403

A:Contents: annotation: erratum

A:Note: revised physical map for reference I39451

R:Levy, E.; Carman, M.B.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van

Science 248, 1124-1126, 1990

A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral F

A:Reference number: I39453; MUID:90260663; PMID:2111584

A:Accession: I39453

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 656-737 <JOL>

A:Cross-references: NID:G178618; PIDN:AAA51727.1; PID:G178620

A:Note: a mutation with 693-Gln is presented

R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.

Science 254, 97-99, 1991

A:Title: A mutation in the amyloid precursor protein associated with hereditary A1

A:Reference number: I59562; MUID:92022553; PMID:1925564

A:Accession: I59562

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 689-716, 'F', 718-737 <MUR>

A:Cross-references: GR:S57665; NID:G236720; PIDN:AAB19991.1; PID:G236721

R:Kamano, K.; Orr, H.T.; Payami, H.; Wijisman, R.M.; Alonso, M.E.; Pulst, S.M.; And

arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; M

Am. J. Hum. Genet. 51, 998-1014, 1992

A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds fo

A:Reference number: A44017; MUID:93035397; PMID:1415269

A:Accession: A44017

A:Molecule type: DNA

A:Residues: 687-692, 'G', 694-716 <KAM1>

A:Cross-references: NID:G257377; PIDN:AAR23645.1; PID:G257379

A:Experimental source: familial Alzheimer disease family SB

A:Note: sequence extracted from NCBI backbone (NCBIP:115374)

A:Accession: B44017

A:Molecule type: DNA

A:Residues: 687-718 <KAM2>

A:Cross-references: GR:S45136; NID:G257179; PIDN:AAB23646.1; PID:G257380

A:Experimental source: familial Alzheimer disease family LIT

A:Note: sequence extracted from NCBI backbone (NCBIP:115376)

A:Note: this sequence has a silent mutation

R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik,

Nature 325, 733-736, 1987

A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-

A:Reference number: A03134; MUID:87144572; PMID:2881207

A:Accession: A03134

A:Molecule type: mRNA

A:Residues: 1-288, 'V', 365-770 <KAN>

A:Cross-references: GR:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G28526

A:Note: alternative splice form APP(695)

R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.

Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987

A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovasc

A:Reference number: A29030; MUID:87231971; PMID:3035574

A:Accession: A29030

A:Molecule type: mRNA

A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>

A:Cross-references: GR:M16765; NID:G178539; PIDN:AAA51722.1; PID:G178540

A:Note: the authors translated the codon GAG for residue 647 as Asp

R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.

Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <30L>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: Brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke-
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
EMBO J. 7, 949-957, 1988
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN>
A:Cross-references: GB:M15533; NID:g177957; PIDN:AAA5564.1; PID:g177958
R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.J.; Muel-
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation, and biogenesis of the amyloid A4 pro-
A:Reference number: 502638; MUID:88296437; PMID:2903137
A:Accession: 502638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: 500707; MUID:88122640; PMID:2893290
A:Accession: 500707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g292612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewhitt, P.; Scilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi-
A:Reference number: 500925; MUID:88122639; PMID:2893289
A:Accession: 500925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PC2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g292611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Boer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1998
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A:Molecule type: mRNA
A:Status: not compared with conceptual translation
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, K.E.; Marc-Lia, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

A:Residues: 507-770 <2AI>

A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resic
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for resi
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R: Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuth

Query Match 98.1%; Score 3582.5; DB 1; Length 770;
Best Local Similarity 89.9%; Pred. No. 7.2e-181;
Matches 692; Conservative 2; Mismatches 1; Indels 75; Gaps 1;

QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEFOJAMFCORLNHNNHNVONGKWDSPSGTK 60

DB : MLPGLALLLLAAWTAARALEVPTDGNAGLLAEFOJAMFCORLNHNNHNVONGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQIINVVEANQPTIOWKCKGRKCKCTHFFHVFVPRCLVG 120

DB TCIDTKEGILQYCOEYVPELQIINVVEANQPTIOWKCKGRKCKCTHFFHVFVPRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQERMDVCEHLHHTVAKETSEKSTNLHLDYGMLLPCGIDKPR 180

DB EFVSDALLVPDKCKFLHQERMDVCEHLHHTVAKETSEKSTNLHLDYGMLLPCGIDKPR 180

QY 181 GVEFVCCPLAERSDNVDADAEEDSDVWGGADTDYADGSEDKVVEAEAEAEAEAE 240

DB GVEFVCCPLAERSDNVDADAEEDSDVWGGADTDYADGSEDKVVEAEAEAEAEAE 240

QY 241 EADDEDEDEGGDEBEAEPEEAEATERITTSIATITTTTTSVEEVEVR 288

DB EADDEDEDEGGDEBEAEPEEAEATERITTSIATITTTTTSVEEVEVR 288

QY 241 EADDEDEDEGGDEBEAEPEEAEATERITTSIATITTTTTSVEEVEVR 300

DB EADDEDEDEGGDEBEAEPEEAEATERITTSIATITTTTTSVEEVEVR 300

QY 289 ----- 288

DB ----- 288

QY 301 RAMISRWYFDVTGKCAPFFYGGCGGNRNFDTEYCAVCGSAMQSLLKTIQEPARD 360

DB RAMISRWYFDVTGKCAPFFYGGCGGNRNFDTEYCAVCGSAMQSLLKTIQEPARD 360

QY 289 ---VPTTAASTPDVAKYLETGDENEHAHFQKAKERLEAKHRERMSQVMEWEAEQA 345

DB ---VPTTAASTPDVAKYLETGDENEHAHFQKAKERLEAKHRERMSQVMEWEAEQA 345

QY 361 PVKLPTAASTPDVAKYLETGDENEHAHFQKAKERLEAKHRERMSQVMEWEAEQA 420

DB PVKLPTAASTPDVAKYLETGDENEHAHFQKAKERLEAKHRERMSQVMEWEAEQA 420

QY 346 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT 405

DB KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT 405

QY 421 KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT 480

DB KNLPRADKKAVIQHFOEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYIT 480

QY 406 QAVPPPRHVFNMKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTLKVIER 465

DB QAVPPPRHVFNMKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTLKVIER 465

QY 461 QAVPPPRHVFNMKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTLKVIER 540

DB QAVPPPRHVFNMKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTLKVIER 540

QY 466 MNGSLLYNVPAAVEEIODEVDELLOKQEQNSDQVLANMISEPRISYGNDAIMPSTET 525

DB MNGSLLYNVPAAVEEIODEVDELLOKQEQNSDQVLANMISEPRISYGNDAIMPSTET 525

QY 541 MNGSLLYNVPAAVEEIODEVDELLOKQEQNSDQVLANMISEPRISYGNDAIMPSTET 600

DB MNGSLLYNVPAAVEEIODEVDELLOKQEQNSDQVLANMISEPRISYGNDAIMPSTET 600

QY 526 KITVELLPVNGEFLDLOPWSFGADSVDPANTENEVEPVDARPAADRLITRPSGSLTN 585

DB KITVELLPVNGEFLDLOPWSFGADSVDPANTENEVEPVDARPAADRLITRPSGSLTN 585

QY 601 KITVELLPVNGEFLDLOPWSFGADSVDPANTENEVEPVDARPAADRLITRPSGSLTN 660

DB KITVELLPVNGEFLDLOPWSFGADSVDPANTENEVEPVDARPAADRLITRPSGSLTN 660

QY 586 IKTEEISEVNLDAEPRHDSGYEVHOKLVFFAEYDGSNKGAIIGLMVGQVVIATVITL 645

DB IKTEEISEVNLDAEPRHDSGYEVHOKLVFFAEYDGSNKGAIIGLMVGQVVIATVITL 645

QY 661 IKTEEISEVNLDAEPRHDSGYEVHOKLVFFAEYDGSNKGAIIGLMVGQVVIATVITL 720

DB IKTEEISEVNLDAEPRHDSGYEVHOKLVFFAEYDGSNKGAIIGLMVGQVVIATVITL 720

RESULT 3

S00550

Alzheimer's disease amyloid beta protein precursor - rat

N:Alternate names: beta-A4 amyloid protein

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: S00550; A41245; A39820; S46251

R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein; expression pattern in rat brain
A:Reference number: S00550; MUID:88312583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:q55616; P-DN:CAA3C488-1; P-ID:q55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88284430; PMID:2469652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCR>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Beher, D.; Masters, C.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein: binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation: copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potemaska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
P:625-648/Domain: transmembrane #status predicted <TM>

Query Match 96.98; Score 3536; DB 2; Length 695;
Best Local Similarity 97.08; Pred. No. 1.8e-178;
Matches 674; Conservative a; Mismatches 13; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHHMVQNGKMSDPSGK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHHMVQNGKMSDPSGK 60
QY 61 TCIDTREGILQYCOEYVPE:QITNVVEANOPVTIQNCKRGKCKCKTHPHFVYRCLVG 120
DB 61 TCIDTREGILQYCOEYVPE:QITNVVEANOPVTIQNCKRGKCKCKTHPHFVYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETGSEKSTNLHDYGMILPGCKDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETGSEKSTNLHDYGMILPGCKDKFR 180
QY 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADTDYADGSKKVVVEAEVEAEVVEE 240
DB 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADTDYADGSKKVVVEAEVEAEVVEE 240
QY 241 EADDEDEDEGDEVEEAEPEEETTSIATITTTTSTVESVEEVVPTTAASTPDV 300
DB 241 EADDEDEGDEVEEAEPEEETTSIATITTTTSTVESVEEVVPTTAASTPDV 300
QY 301 DKYLETPTGDENEHAHFQKAKERLEAKHRRMSQVNRWEAEAEQAKNLKAKKAYIQH 360
DB 301 DKYLETPTGDENEHAHFQKAKERLEAKHRRMSQVNRWEAEAEQAKNLKAKKAYIQH 360
QY 361 QEKVESLEQEAANRQQLVTHMARVAMLNRRRLALENYITALQAVPRPRHVNMLK 420
DB 361 QEKVESLEQEAANRQQLVTHMARVAMLNRRRLALENYITALQAVPRPRHVNMLK 420
QY 421 KYVRAEQDKRQHTLKHFEHVRMDPKAAQIRSQVTHLRVIYERNQSLSLLYNPVAV 480
DB 421 KYVRAEQDKRQHTLKHFEHVRMDPKAAQIRSQVTHLRVIYERNQSLSLLYNPVAV 480
QY 481 BEIQDEVDLLOKEQNTSDVLANMISEPRIISYGNALMPSLTETKITTELLPVNGEFS 540
DB 481 BEIQDEVDLLOKEQNTSDVLANMISEPRIISYGNALMPSLTETKITTELLPVNGEFS 540

QY 541 DDLQPHWSFGADSVYPANTENEVEVDARPAADRG:TPRGSGLTNKITEELSEVNLDAEF 600
DB 541 DDLQPHWSFGADSVYPANTENEVEVDARPAADRG:TPRGSGLTNKITEELSEVNLDAEF 600
QY 601 RHDSYEVHHQKLVFFADVDGSKNGAIGLMVGWGIATVITVLVLMKKKQYTSIHGV 660
DB 601 RHDSYEVHHQKLVFFADVDGSKNGAIGLMVGWGIATVITVLVLMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
X:Alternate names: proteinase nexin 1;
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sakaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A:Reference number: A27485; MUID:88106489; PMID:3322280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:q15158; PIDN:AAA37139.1; PID:q309085
A:Experimental source: brain
R:De Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Iizumi, R.; Yamada, T.; Yoshikai, S.; Sakaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Status: translated from: GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D0603; NID:q220328; PIDN:BAA01456.1; PID:q220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 96.2%; Score 3511; DB 2; Length 695;
Best Local Similarity 96.5%; Pred. No. 3.6e-177;
Matches 571; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHHMVQNGKMSDPSGK 60
DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHHMVQNGKMSDPSGK 60
QY 61 TCIDTREGILQYCOEYVPELOITNVVEANOPVTIQNCKRGKCKCKTHPHFVYRCLVG 120
DB 61 TCIDTREGILQYCOEYVPELOITNVVEANOPVTIQNCKRGKCKCKTHPHFVYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETGSEKSTNLHDYGMILPGCKDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLHWHIVAKETGSEKSTNLHDYGMILPGCKDKFR 180
QY 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADTDYADGSKKVVVEAEVEAEVVEE 240
DB 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADTDYADGSKKVVVEAEVEAEVVEE 240
QY 241 EADDEDEDEGDEVEEAEPEEETTSIATITTTTSTVESVEEVVPTTAASTPDV 300


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Db 241 EADDDDEDGDEVEEAEPEYFATERITSTATTITTTTSEVEEVRVPTAASTPDV 300
Qy 301 DKYLETPGDENEHAFQAKERLEAKHRERMSQVREWEAEERQAKNLPKADKAVIQEF 360
Db 301 DKYLETPGDENEHAFQAKERLEAKHRERMSQVREWEAEERQAKNLPKADKAVIQEF 360
Qy 361 QKVESLEQEAANROOQVETHMARVEAMLNDRRLALENYITALQAYPPRPRHVENMLK 420
Db 361 QKVESLEQEAANROOQVETHMARVEAMLNDRRLALENYITALQAYPPRPRHVENMLK 420
Qy 421 KYVRAFORDQHTLKHFEVRVMDPKKAQIRSCVMTHLKVYERMNLSLSLYNVPAVA 480
Db 421 KYVRAFORDQHTLKHFEVRVMDPKKAQIRSCVMTHLKVYERMNLSLSLYNVPAVA 480
Qy 481 REIQDEVDLLOKEQNSDYDLANNISPRISYGNALMPSLTERKTIVVELLPVNGEFSI 540
Db 481 REIQDEVDLLOKEQNSDYDLANNISPRISYGNALMPSLTERKTIVVELLPVNGEFSI 540
Qy 541 DLOQPHHPFGVDSVPANTENEVEPVDARPAADRGILTTPGSGLTNIKTEEISEVKMDAEF 600
Db 541 DLOQPHHPFGVDSVPANTENEVEPVDARPAADRGILTTPGSGLTNIKTEEISEVKMDAEF 600
Qy 601 RHDSGVEVHHOKLVFFAEDVGSNGKAITGLMVGGVVATVITVLMKKKQYTSIHIGV 660
Db 601 RHDSGVEVHHOKLVFFAEDVGSNGKAITGLMVGGVVATVITVLMKKKQYTSIHIGV 660
Qy 661 VEVDAAVTPERHLSKMOQNGYENPTYKFFEOMON 695
Db 661 VEVDAAVTPERHLSKMOQNGYENPTYKFFEOMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1993
C:Accession: JH0773
R:Okada, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OK>
A:Cross-references: GB:S52417; NID:q263150; PTDN:AAB24853.1; PID:q263152
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 84.8%; Score 3095; DB 2; Length 747;
Best Local Similarity 80.8%; Pred. No. 2,9e+55;
Matches 59%; Conservative 36; Mismatches 42; Indels 54; Gaps 5;
Qy 17 ALEVPTDGNAGLAEPIQANF-CGRNLNMNMVQNGKWDSDPSGTICIDTKGICIQYCOE 75
Db 15 ALEVLVDGNGGLAEPIQANFVARLNMNMVQNGKWDSDPSGTICIDTKGICIQYCOE 71
Qy 76 VYPELOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDALLVPDKCKF 135
Db 72 VYPELOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDALLVPDKCKF 131
Qy 136 LQERMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDN 195
Db 132 LQERMDICETHLHHHTVAKESKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDN 192
Qy 196 VDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 253
Db 192 FDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 249
Qy 254 VEEAEPEYFATERITSTATTITTTTSEVEEVRVPTAASTPDV 300
Db 254 VEEAEPEYFATERITSTATTITTTTSEVEEVRVPTAASTPDV 300
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Db 250 AESEPEPEYFATERITSTATTITTTTSEVEEVRVVCSEQAETGFCRAMISRKYDVT 309
Qy 289 -----VPTTAASTPDVADKYLETFGDENEHAFQ 317
Db 310 SKCAQFTYGGCGGNRNPFESDDYCMVCGSVIPATAASTPDVADKYLENPDENEHDFEL 369
Qy 318 KAKEHLEAKHREKMSQVREWEAEERQAKNLPKADKAVIQHFOEKVYESLEQEAANROO 377
Db 370 KAKERLEGKEREKMSQVREWEAEERQAKNLPKADKAVIQHFOEKVYESLEQEAANROO 429
Qy 378 LVETIMARVAMLNDRLALENYITALQAVPPRPRHVENMLKKYVRAEOKDQHTLKH 437
Db 430 LVETIMARVAMLNDRLALENYITALQADPPRPRHVENMLKKYVRAEOKDQHTLKH 489
Qy 438 EHVMDVDPKKAQIRSCVMTHLKVYERMNLSLSLYNVPAVAEIGDEYDELLOKEQNY 497
Db 490 EHVMDVDPKKAQIRSCVMTHLKVYERMNLSLSLYNVPAVAEIGDEYDELLOKEQNY 549
Qy 498 SDDVLANNISPRISYGNALMPSLTERKTIVVELLPVNGEFSIDLOPHMSFGADSVPA 557
Db 550 SDDVLANNISPRISYGNALMPSLTERKTIVVELLPVNGEFSIDLOPHMSFGADSVPA 609
Qy 558 TENEEVEPVDARPAADRGILTTPGSGLTNIKTEEISEVNLDAAEFHRSQYEVHHOKLV 617
Db 610 TENEEVEPVDARPAADRGILTTPGSGLTNIKTEEISEVNLDAAEFHRSQYEVHHOKLV 669
Qy 618 EDVGSNGKAITGLMVGGVVATVITVLMKKKQYTSIHIGVVEVDAAVTPERHLSKM 677
Db 670 EDVGSNGKAITGLMVGGVVATVITVLMKKKQYTSIHIGVVEVDAAVTPERHLSKM 729
Qy 678 QONGYENPTYKFFEOMON 695
Db 730 QONGYENPTYKFFEOMON 747

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - hum
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J. N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secr
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain
C:Keywords: cloning artifact

Query Match 57.7%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 1.7e+103;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;
Qy 80 LOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDALLVPDKCKFLHQE 139
Db 80 LOITNVVEANQPVTIQNNCKRGRKOCKTHPHFVYPRCLVGEFVSDALLVPDKCKFLHQE 60
Qy 140 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDNVDSA 199
Db 61 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKFRGVFVCCPLAESDNVDSA 120
Qy 200 DAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 259
Db 121 DAEEDSDVMWGGADTDYADGSEDKVVEAEVEEAEADDEDDEGDEVEEAE 180
Qy 260 EPEYFATERITSTATTITTTTSEVEEVRVPTAASTPDV 300
Db 181 EPEYFATERITSTATTITTTTSEVEEVRVVCSEQAETGFCRAMISRKYDVTGKCAPF 240
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QY 289 -----VPTTAASPDVADKYLE:PGENHRAHQKAKERL 423
UB 241 FYCGCGGNRNFDIEEYCMVACCSAIPTTAASPDVADKYLETPGDNHRAHQKAKERL 400
QY 324 EAKHREMSQVMREWEAEARQAKNLPAKAKKAVIQHFKKVES:EOEAEAKKQVETIKM 383
DB 301 EAKHREMSQVMREWEAEARQAKNLPAKAKKAVIQHFKKVES:EOEAEAKKQVETIKM 360
QY 384 ARVEAMLNDRRRLALENYITIALQAVPPRPHVFNMLKKYVRAQOKROHTLKHFEIVKAV 443
DB 361 ARVEAMLNDRRRLALENYITIALQAVPPRPHVFNMLKKYVRAQOKROHTLKHFEIVKAV 426
QY 444 DPKAAQIRSQVMTHLRV:YERMNQSLSLYNNPVAVAEEIQDEV 487
DB 421 DPKAAQIRSQVMTHLRV:YERMNQSLSLYNNPVAVAEEIQDEV 464

RESULT 7
A:Name: amyloid beta (A4) homolog 2 precursor - human
N:Alternate names: CDEI-binding protein
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A49321; S34644; S40519
R:Spencer, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ex
A:Reference number: A49321; MUID:93250009; PMID:8485127
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: GB:S60099; NID:g300168; PIDN:AAC60589.1; PID:g300169
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P131199)
R:von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A:Description: The human homologue of the murine CDEI binding protein is an amyloid pre
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <ON>
A:Cross-references: EMBL:225252; NID:g394763; PIDN:CAA80295.1; PID:g394764
R:Wasco, W.; Gurubagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of A2P2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94335131; PMID:8220425
A:Accession: S40519
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:g450391; PIDN:AAC4170.1; PID:g450392
C:Genetics:
A:Gene: GDB:APLP2; APPL2
A:Cross-references: GDB:139159; OMIM:104776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type proteinase
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <3x1>

Query Match 47.28; Score 1725; DB 2; Length 763;
Best Local Similarity 45.94; Pred. No. 2,9e-83;
Matches 369; Conservative 112; Mismatches 170; Indels 136; Gaps 19;

QY 5 LALLLLAAATATALEV:-----PTDGNAG---LLAEFQIAFMFCGRLANHNVONGKNDSDP 56
DB 15 LLLLLLGLTAPALALAGYLEALAAAGATGFAEFOIAFMFCGRLANHNVNTQGRKEPSP 74

QY 57 SGTKCTDITREGILOVCOEYPELQITNVYAEANQPTIQNWCKRGKQCKTHPEFVYPR 116
DB 75 TGKSCFEIKEEVLOYCOEYPELQITNVYAEANQPTIQNWCKRGKQCKTHPEFVYPR 132

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QY 117 CLVGEFSDALLVPCKFLQERMDVCETHLRHMHTVAKETCSSEKSTNLHLYGMLLPGI 176
DB 133 CLVGEFSDALLVPCKFLQERMDVCETHLRHMHTVAKETCSSEKSTNLHLYGMLLPGI 192
QY 177 DKFRGVFVCCPLABESUNVDSADAEEDSDVMWGAGDITDYADSGSDKKVVEVAEEVAE 236
DB 193 DQFHGFEVCCPQTKLIGSVSKEEEDDFE-----EEBEDDFEYDYVYKSEFPPTAD 245
QY 237 VEE--EEA--DDDEDDDDDEVSSEAEPEY-----EEATEKTSIATTTTTTES 282
DB 246 LEDFTEAAVDEDDDEDEEGEEVVDROYDYDTFKGDDYNEENPTEPGSDGTMSSKE:THD 305
QY 283 VEEV-----VRRVP 290
DB 356 VKAVCSQEMTGPCRAVMPRWYFDLSKGVRFYVGGCGGNRNFESEYCNVCKAMIP 365
QY 291 TTAASPDVADKYLETPGDNHRAHQKAKERLEAKHREMSQVMREWEAEARQAKNLPAK 350
DB 366 PTPLEPTND-VDVYPTTSADDNEHARFQAKKECLEIRHNRNMRDVKVKPWEAEALQAKNLPAK 424
QY 351 ADKKAIVIQHFOEKVESLEQFAANERQOLVETIMARVEAMLNDRRRLALENYITIALQAVPP 410
DB 425 AEROTLIQHFQAMWKALEKAAASEKQQLVETHLARVEAMLNDRRRLALENYITIALQAVPP 484
QY 411 RPRHVENM:KKYVRAEOKDROHTLKHFEHVRWVDPKAAQIRSQVMTHLRVYERMNQSL 470
DB 485 RPRHILQALRRYVRAENKRLHRIHYOHVLAVDEPKAAQKQSKQVMTHLHVIESRRNQSL 544
QY 471 SLLYNPVAVAEEIQDEVDELLOKEQNSDDVLANNISEPRISYGNDAIMPFLTEIKTIVE 530
DB 545 SLLYKVPYVAQEQIEEIDELLQEQR-----ADM-----DQFASISETPPDVR 587
QY 531 LLPVNGEESLDLQPMHSGFADSVDPANTENEVPEVDARPAADRGLTIRPG-----SGLIN 585
DB 588 ---VSSES-REIPPFHPF--HPPFALPENE-----DTPELYHPMKKSGVGEQDGGUG 637
QY 586 IKTEISEVN-LDAEFRHDSGYEVHHQKLVFAEDVGS-----NKGAI 627
DB 638 ABEKVINSKNKYNVDKMDIETLDV--KEMIFNAERVGGLEERESVGPLREDFSLSSAL 695
QY 628 IGLMYGGVVIATVIITVLMKKKQYTSIHGCVVEVDRAVTPFEERHLSKMOONGYENPTY 687
DB 696 IGLLVIAVAIATVIIVISLVMLKRYGTISHGIVEVDPMLTPEERHLLKMHNGYENPTY 755
QY 688 KFEQOMQ 694
DB 756 KYLEOMQ 762

RESULT 8
S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide and deduced amino acid sequence of rat amyloid p
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein:
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein: animal Kunitz-type protein

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anyoid precursor-like protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A46362
R:Masco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
Proc Natl Acad Sci U S A 89, 10758-10762, 1992
A:Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer's disease amyloid beta protein: animal kunitz-type proteinase 2
A:Reference number: A46362; MIM:930632; PMID:1279653
A:Accession: A46362
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-653 <MAS>
A:Experimental source: brain
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: Alzheimer's disease amyloid beta protein: animal kunitz-type proteinase 2
C:Keywords: transmembrane protein

Query Match 32.4%; Score 1183; DB 2; Length 653;
Best Local Similarity 39.08; Pred. No. 6.9e-55;
Matches 275; Conservative 121; Mismatches 221; Indels 88; Gaps 20;

QY 1 M PGLAALLLAAMTAKA-LEVTIDGNAGLLAEPOIAFMFGRLNMHMNVQNGKWSQPSCT 59
DB 22 L L P L L L L L A Q L A V G N L A V G S P A A E A P G S A Q V A G L C G R L T L H R L R T G R N E P D P Q R S 80
QY 60 K T C I D T K E G I L O Y C O E V Y P E L O I T N V F A N O P V T I O N M C K E G K Q C K T H R F V I P Y R C L 116
DB 81 R C L L D F O R V L E Y C R Q M P E L H A R V Q A A Q A I P M E R W C G T S G R C A P H H E V W F P H C L 140
QY 119 V G E V S D A L L V P D K L H O L M D V C T H L H W T V A K E T C S E K S T N L H Y G M L L P G S D K 178
DB 141 P G E V S E A L L V P E G R F H O E R M D C E S T R R H O E A F A C S Q G L I L H G S M L L P G S D R 200
QY 179 P R G V E F V C C P L A E S D N V S A D A E E D S D V M - W G G A D T D V A D G S E D K V E A E E E V A E V 237
DB 201 P R G V E Y C C P - P P A T P M S G M A G D P T R S W P L G G R - - - - A E G G D - - - - - E E E V S F 248
QY 238 E E E A D D E D D E D G D E V E E A E P E E A T E R T T S I A T I T T T T S E V E V R V P T T A A S T P 297
DB 245 P O P V D D I F V E P P O A E E E E E E R A P P S S H T P M V S R V T P T R - - - - - P I - - - - - 294
QY 298 D A V D K Y L E T P C D E N E H A F U K A K E R L E A K H R M S O V R H E A E R Q A K N L P K A D K K A V I 357
DB 295 D G D V Y F G M P G E I G E H E G F L A K M D L E R R M R O I N E V Y R E W A M A D S Q S K N L P K A D R O A L N 364
QY 358 Q H F Q K Y E S E L O A A N E R Q U I V E T H M A R V E A M L N D R R K L A L E N Y I T A L Q A V P P R P R E V E N 417
DB 355 E H F Q S I L Q T L E E Q V S G E R Q N L V E - H A T E V - A L I N D Q R P A A L E G F L A A L G C P P Q A E N V L K 414
QY 418 M L K Y V R A E Q K D R O H T L K H P E R V E W Y P K K A Q I K S Q V W T H L A V I V E R M N O S L L Y N V P 477
DB 415 A L R Y L R A S Q E Q R H T L R Y O H V A A V D P E K A Q M R F C V Q T H Q V I E R M N O S L G L L Q N P 474
QY 478 A V A E E I D E V S E L C K E Q N T S D D V L A N N I S E P R I S Y G N O A L M P - S C T E T K T I V E L L P V N G 536
DB 475 H L A Q E L R P O I C E L L - - - - - L A E H L G P S E L - - - - - D A S V R G S S E D K - - - - - 510
QY 517 E F S L D D I O P W H S F G A D S V P A N T E N E V E V D A R P A A D R G L T T R F C S G - - - - - T N I T E E T 591
DB 511 - - - - - G S L O P - - - - - P E S K D D P P V T L P - - - - - K G S T D Q E S S S G S G K E L T F L E Q Y E - 550
QY 592 S E V N L D A E F R H D S G V E V H - - - - - O K L V F F A E D V S N K G A I L C M G V G V I A T V I V I L M L 648
DB 551 Q K V N A S A - - - - - P R G F P H S S I O R D E - A P S G T G V S R H A L S G L I M G A G G S G A V L S E L I I 606
QY 649 - K K Q Y T S I H G V E V D A A V T P E E R H L S K M Q O N G Y E N P T Y K F E Q 692
DB 607 R A K K P Y G T I S H G V E V D P M L T L E E Q Q L R E L O R H G Y E N P T Y R F L E E 651

RESULT 11
JC1404.

CDEI-box DNA-binding protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C:Accession: JC1404
R:Vidal, F.; Blandy, A.; Rassoulzadegan, M.; Cuzic, F.
Biochem Biophys Res Commun 189, 1336-1341, 1992
A:Title: A marine sequence-specific DNA binding protein shows extensive local similarity: reference number: JC1404; MIM:93129193; PMID:1482349
A:Accession: JC1404
A:Molecule type: mRNA
A:Residues: 1-511 <VID>
C:Comment: This protein plays an important role in the early development of the mouse embryo.
C:Keywords: DNA binding; transmembrane protein

Query Match 31.24; Score 1138; DB 2; Length 511;
Best Local Similarity 45.48; Pred. No. 1.2e-52;
Matches 251; Conservative 93; Mismatches 129; Indels 80; Gaps 16;

QY 174 C G I D K F R G V E V C C P L A E - E S D N V D S A D A E E D S D V M W G G A D T D V A D G S E D K V V E A E - 230
DB 6 C G V D F H G T E V C C P Q I K T V D S D T M S K E E E E E - - - - - D E E D E E D D L D K S E F 56
QY 231 - E E V A E V E F E A D - D E D D D E D G D E V E E A E - - - - - E P Y E A T E R T T S I A T T T T 279
DB 57 P T E A D L E D F T E A A A D E E E E E E G E E V E D R V Y D P F K G D D Y N E - - E N P T E S S E G T I S 114
QY 280 T E S V E V V R V P T T A A S T P D A V D K Y L E T P G D E N H A F U K A K E R L E A K H R M S O V R E M E 339
DB 115 D R E I V H D V K V P T P L P N D - V D V Y F E T S A D C N E H A R F O K A K E L E I H R M R M O R V K K E W E 173
QY 340 E A E R Q A K N L P K A D K K A V I Q H F Q E K V E S L E Q E A A N E R Q O L Y E T H M A R V E A M L N D R R L A L E 399
DB 174 E A E L Q A K N L P K T E R Q T L I Q H F Q A M V K A L E K E A A S E K Q O L V E T H L A R V E A M L N D R R I A L E 233
QY 400 N Y I T A L Q A V P P R P R H V N M L K K Y V R A E Q K D R Q H T L K H P E R V M V D P K K A Q I S Q V W T H L 459
DB 234 N Y L A A L S D P P R H R I L Q A U R Y V R A E N K D R L H T I R Y H V L A V D P E K A A Q M S Q V W T H L 233
QY 460 R V I Y E R M N O S L L Y N V P A V A E T I Q D E V D E L L O K E Q N Y S D D V L A N N I S E P R I S Y G N D A L M 519
DB 294 H V I E E R R N O S L L Y K V P Y V A Q E I O E I D E L L O B O R - - - - - A D M - - - - - D Q F T 336
QY 520 P S L T E T K T I T V E L L P V N G R F S L D C L O P W H S F G A D S V P A N T E N E V E P V D A R P A A D R G L T T R P 579
DB 337 S S I S E N P D V D V S S E E S E - E I P P F P L H P F - - - - - P S L S E N E - - - - - G S G M A E Q D 380
QY 580 G S G L T N I K T E I S E V N - I D A E F R H D S G Y E V H Q K L V F F A E D V G S - - - - - 622
DB 351 G - G L I G A E K V I N S K N K M D E N M V I D E L D V - - K E M I F N A E R V G L E E E P E S V G F L R E D F S 437
QY 623 - N K G A I C L M G V G V V I A T V I V I V M L K K Q Y T S I H G V E V D A A V T P E E R H L S K M Q O N G 691
DB 438 I S S N A L I G L L V I A V A I A I V I S L V M L R K K O Y G T I S H G I V E V D P M L T P E E R H L N K M Q N H G 497
QY 632 Y E N P T Y K F E E Q M Q 694
DB 438 Y E N P T Y K Y L E Q M Q 510

RESULT 12
T15795
Hypothetical protein C42D8.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C:Accession: T15795; A49414
R:Halishworth, K.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C42D8.
A:Reference number: Z18405
A:Accession: T15795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <HAL>


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QY 520 -----PSLTETKTVITVLPNGEFLSDLLQPHWSEFGADSVFANTEVERFVDAFPAADRG 574
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 714 VTAAFWLETTKS-----EKDLSDF-----YGEAVSTTKVQTVPFVDDDAVQRA 760
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 575 LTRPSGGLNITKEEISEVNLDAEFRHDSGYEVHHQKLVF-----PAEDVGSNK---CA 626
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 761 VEDVNA-----VAHQEAEPQVQHEMTDLAGHRESSFLSRKEFAQHAAKAGRN 811
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 627 IIGLWGVGVIAIVITLVNKKKQYTSIH-HGVVEVDAAVTP-----EERHLSKMQQ 679
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 812 YFTLSFAGIALMAAFVGVAVAKWRITSRSPHAGFIEVDQNVTHHPPIVREEKIVPNMQI 871
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 680 NGYENPTYKFE 691
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 872 NGYENPTYKFE 883
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
S38344
CDEI-binding protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996
C:Accession: S38344
R:Hanes, J.; von der Kammer, H.; Kristjansson, G.L.; Scheit, K.H.
Biochim. Biophys. Acta 1216, 154-156, 1993
A:Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
A:Reference number: S38344; MUID:94032480; PMID:8218408
A:Accession: S38344
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-246 <HAN>
A:Cross-references: EMBL:222592
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

Query Match 19.3%; Score 706; DB 2; Length 246;
Best Local Similarity 51.5%; Pred. No. 2.4e-10;
Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

QY 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPOIAMFCGRLNMHMNVQCKWDSOP 56
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 15 LVLVLLGLTAPAAALAGYIEALANAGTGFVAEPQIAMLCCKLNMHVNIQTGKKEPDP 74
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 57 SGTKTCIDITKEGILQYQCEIYPELOITNVVEANOPVTIONCKRGRKCKIHPHFVPIYR 116
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 75 IGTKSCIGTKREEVLYQCEIYPELOITNVMEANOPVNIIDSMCRDRKQCKS--HIV:PEK 132
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 CLVGEFVSALLVPDKCFILQERMDVCETELHHTYAKETCSEKSNLHDYGNLLPCGI 176
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 CLVGEFVSALLVPDNCQFFHQERMEVCEXIQRWHTLVKEACJTEGILTSYGMGLPCGV 192
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 DKFGSVFVGCPLAFESDVLSADAEFDSDVWNGSAITCYADGSEDKVVEVAPEFEVAF 216
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 QPHGTRFVCCP---QTKVDS-----DSTMSKEEERH--- 222
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 VEEREADDEED-DRDGDVEEEDAE 259
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 -FEDEDEEDYDLDKSEFPTAD 245
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
P00436
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00436; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Marous, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: P00436; MUID:93075180; PMID:1445131
A:Accession: P00436
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
```

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R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide i
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 11.0%; Score 403; DB 2; Length 82;
Best Local Similarity 97.6%; Pred. No. 5e-15;
Matches 80; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 581 SGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIATV 640
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 SGLTNIKTEEISEVNLDAEFRHDSGYEVHHQKLVFFAEEDVGSNKGAIIGLMVGGVVIATV 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 641 IVITLVMLKKKQYTSIHGGVVE 662
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 IVITLVMLKKKQYTSIHGGVVE 82
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: October 2, 2003, 14:00:33
Job time : 18.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 10 Seconds

(without alignments)
3277.761 Million cell updates/sec

Title: us-09-806-194-18

Perfect score: 3651

Sequence: 1 MDPGLALLLAAMTAAAEV.....QNCYENPTYKFFEQKNK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3582.5	98.1	770	1 A4_HUMAN	P05067 h amyloid b
2	3582.5	98.1	770	1 A4_MACEA	P53501 m amyloid b
3	3576	97.9	753	1 A4_SALIC	Q95241 s amyloid b
4	3527.5	96.6	770	1 A4_PIG	P79357 s amyloid b
5	3514.5	96.3	770	1 A4_CAVPO	Q60495 c amyloid b
6	3485.5	95.5	770	1 A4_MOUSE	P12023 m amyloid b
7	3485.5	95.5	770	1 A4_RAT	P08592 r amyloid b
8	1730	47.4	695	1 APP2_MOUSE	Q06335 mus musculus
9	1725	47.2	763	1 APP2_HUMAN	Q06481 homo sapien
10	1709	46.8	765	1 APP2_RAT	P15943 rattus norv
11	1191	32.6	650	1 APP1_HUMAN	P51693 homo sapien
12	1183	32.4	653	1 APP1_MOUSE	Q03157 mus muscul
13	815.5	22.3	686	1 A4_CAEEL	Q10651 caenorhabdi
14	747.5	20.5	887	1 A4_DROME	P14599 drosophila
15	284	7.8	59	1 A4_BOVIN	Q28053 bos taurus
16	280	7.7	58	1 A4_RABIT	Q28748 oryctolagus
17	280	7.7	58	1 A4_SHEEP	Q28757 ovis aries
18	279	7.6	58	1 A4_CANFA	Q28280 canis famil
19	275	7.5	57	1 A4_URNSA	Q29149 ursus marit
20	185.5	5.1	407	1 IE68_HSVSA	Q01042 herpesvirus
21	185.5	5.1	993	1 SCPI_MOUSE	Q52209 mus musculu
22	176	4.8	2004	1 MOZ_HUMAN	Q92794 homo sapien
23	175.5	4.8	802	1 NAB3_YEAST	P88996 saccharomyc
24	174	4.8	579	1 G160_HUMAN	Q88378 homo sapien
25	172.5	4.7	793	1 CALD_HUMAN	Q05582 homo sapien
26	169.5	4.6	297	1 TRT2_HUMAN	P45379 homo sapien
27	169.5	4.6	1875	1 MIP1_YEAST	Q02455 saccharomyc
28	169	4.6	771	1 CALD_CHICK	P12957 gallus gall
29	168	4.6	721	1 YCF2_OENPT	P31558 oenothera p
30	167.5	4.6	816	1 G3A_YEAST	P53278 saccharomyc
31	167	4.6	1240	1 YN3A_YEAST	P53945 saccharomyc
32	166.5	4.6	681	1 MP10_HUMAN	Q00556 homo sapien
33	164	4.5	2017	1 MYSN_DROME	Q09323 drosophila

34	163.5	4.5	1376	1 MYHA_HUMAN	P35580 homo sapien
35	162.5	4.5	712	1 NUC1_RAT	P13383 rattus norv
36	162.5	4.5	1325	1 G160_MOUSE	P55937 mus musculu
37	162.5	4.5	1332	1 SPT7_YEAST	P55177 saccharomyc
38	161.5	4.4	1976	1 MYHA_RAT	Q9J100 rattus norv
39	160.5	4.4	1955	1 PUNA_PARUN	O61308 parascaris
40	158	4.3	301	1 TRT2_CHICK	P02642 gallus gall
41	157.5	4.3	1976	1 MYHA_BOVIN	Q27392 bos taurus
42	157	4.3	706	1 NUC1_HUMAN	P19338 homo sapien
43	156.5	4.3	5596	1 MDN1_HUMAN	Q9NU22 homo sapien
44	156	4.3	694	1 NUC1_CHICK	P15771 gallus gall
45	155.5	4.3	747	1 KF35_HUMAN	G15066 homo sapien

ALIGNMENTS

```

RESULT 1
A4_HUMAN
ID   A4_HUMAN          STANDARD;          PRT:   770 AA.
AC   P05067; P09000; P78438; Q13764; Q13778; Q13793; Q16011; Q9B136;
AC   Q9UCB6; Q9UQ58;
DI   13-JUG-1987 (Rel. 05, Created)
DI   13-JUG-1987 (Rel. 20, Last sequence update)
DI   01-NOV-1991 (Rel. 42, Last annotation update)
DI   15-SEP-2003 (Rel. 42, Last sequence update)
DE   Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE   amyloid protein) (Cerebral vascular amyloid peptide) (CVAP) (Protease
DE   nexin-1) (PN-1) (APP1) (PreA4) [Contains: Soluble APP-alpha (S-APP-
DE   alpha); Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42
DE   (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42);
DE   P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59)
DE   (Amyloid intracellular domain 59) (AID(59)); Gamma-CTF(57) (Gamma-
DE   secretase C-terminal fragment 57) (Amyloid intracellular domain 57)
DE   (AID(57)); Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50)
DE   (Amyloid intracellular domain 50) (AID(50)); C31].
OS   APP OR A4 OR AD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORM APP695).
TI   TISSUE-Brain;
MEDLINE-87144572; PubMed-2881207;
Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RA   "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RA   cell-surface receptor";
PL   Nature 325:733-736(1987).
[2]
SEQUENCE FROM N.A. (ISOFORM APP751).
TI   TISSUE-Brain;
MEDLINE-88122639; PubMed-2893289;
Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA   Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA   Cordell B.;
RA   "A new A4 amyloid mRNA contains a domain homologous to serine
RA   proteinase inhibitors";
PL   Nature 331:525-527(1988).
[3]
SEQUENCE FROM N.A. (ISOFORM APP695).
TI   MEDLINE-89128427; PubMed-2783775;
Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA   Unterbeck A., Beyreuther K., Mueller-Hill B.;
RA   "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RA   is encoded by 16 exons.";
PL   Nucleic Acids Res. 17:517-522(1989).
[4]
SEQUENCE FROM N.A. (ISOFORM APP770).
TI   MEDLINE-90236318; PubMed-2110105;
Yoshikai S.-I., Sakaki H., Boh-Ura K., Furuya H., Sakaki Y.;
RA   "Genomic organization of the human amyloid beta-protein precursor
RA   gene.";

```

RL Gene 87:257-263(1990).
 RN [5]
 RP ERRATUM, AND REVISIONS.
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RL Gene 102:291-292(1991).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RA TISSUE=Leukocyte;
 RC MEDLINE=92288136; PubMed=1597857;
 RX Koenig G., Moenning U., Czech C., Prior R., Banati R.,
 RA Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 RT splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 RT leukocytes and brain microglial cells.";
 RL J. Biol. Chem. 267:10804-10809(1992).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RA MEDLINE=97263807; PubMed=909164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
 RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RA TISSUE=Pancreas;
 RC MEDLINE=92389257; PubMed=12477932;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Schoetz T.E.,
 RA Brownstein M.J., Ustin I.B., Toshiyuki S., Carninci P., Kravetz S.,
 RA Raha S., Loquellano N.A., Peters K.J., Abramson R.D., Mellary S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.L., Skalska J., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RT encodes a 95-kDa polypeptide.";
 RL Nucleic Acids Res. 16:935-945(1988).
 RN [10]
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RN [11]
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE=89165670; PubMed=2538723;
 RA LaFauci G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RT "Characterization of the 5'-end region and the first two exons of the
 RT beta-protein precursor gene.";
 RL Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RN [12]
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87250452; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN [13]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE=89346754; PubMed=2569763;
 RA de Sauvage F., Octave J.N.;
 RT "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 RT secreted protein.";
 RL Science 245:651-653(1989).
 RN [14]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN [15]
 RP SEQUENCE OF 266-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,
 RA Gasella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1986).
 RN [16]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1986).
 RN [17]
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN [18]
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE=96139497; PubMed=8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RT "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1620(1996).
 RN [19]
 RP SEQUENCE OF 656-737 FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [20]
 RP SEQUENCE OF 672-681.
 RC TISSUE=Brain cortex;
 RX MEDLINE=88035004; PubMed=3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Teitelotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN [21]
 RP SEQUENCE OF 674-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 RT brain amyloid of Alzheimer's disease.";

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 or send an email to license@isb-sib.ch).

EMBL: S61024; AA014347.1; ..
 HSSP: P05067; 1AAP.
 InterPro: IPR001868; A4_APP.
 InterPro: IPR001255; Beta_APP.
 InterPro: IPR002223; Kunitz_BPTI.
 Pfam: PF02177; A4_EXTRA; 1.
 Pfam: PF03494; Beta_APP; 1.
 Pfam: PF00014; Kunitz_BPTI; 1.
 PRINTS: P00203; AMYLOIDA4.
 PRINTS: P00759; BASICPTASE.
 ProDom: P0000222; Kunitz_BPTI; 1.
 SMART: SM00006; A4_EXTRA; 1.
 SMART: SM00131; K0; 1.
 PROSITE: PS00319; A4_EXTRA; 1.
 PROSITE: PS00320; A4_INTRA; 1.
 PROSITE: PS06280; BPTI_KUNITZ_1; 1.
 PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 Coated pits; Neutrone; Heparin-binding; Metal-binding; Copper; Iron;
 Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 751
 FT CHAIN 18 568
 FT CHAIN 18 552
 FT CHAIN 553 751
 FT CHAIN 653 694
 FT CHAIN 653 692
 FT CHAIN 669 751
 FT CHAIN 669 694
 FT CHAIN 669 692
 FT CHAIN 653 751
 FT CHAIN 595 751
 FT CHAIN 702 751
 FT CHAIN 721 751
 FT DOMAIN 18 680
 FT TRANSMEM 681 704
 FT DOMAIN 705 751
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 251 341
 FT DOMAIN 316 344
 FT DOMAIN 363 428
 FT DOMAIN 504 521
 FT DOMAIN 713 732
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 544
 FT ACT_SITE 301 302
 FT SITE 652 653
 FT SITE 653 654
 FT SITE 666 669
 FT SITE 685 685
 FT SITE 687 687
 FT SITE 692 693
 FT SITE 694 695
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neutrone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 751
 FT CHAIN 18 568
 FT CHAIN 18 552
 FT CHAIN 553 751
 FT CHAIN 653 694
 FT CHAIN 653 692
 FT CHAIN 669 751
 FT CHAIN 669 694
 FT CHAIN 669 692
 FT CHAIN 653 751
 FT CHAIN 595 751
 FT CHAIN 702 751
 FT CHAIN 721 751
 FT DOMAIN 18 680
 FT TRANSMEM 681 704
 FT DOMAIN 705 751
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 251 341
 FT DOMAIN 316 344
 FT DOMAIN 363 428
 FT DOMAIN 504 521
 FT DOMAIN 713 732
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 544
 FT ACT_SITE 301 302
 FT SITE 652 653
 FT SITE 653 654
 FT SITE 666 669
 FT SITE 685 685
 FT SITE 687 687
 FT SITE 692 693
 FT SITE 694 695

FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT	SITE	705	715	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT	SITE	720	721	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9) (BY SIMILARITY).
FT	SITE	738	741	CLEAVAGE (BY CASPASES-3,-6,-8 OR -9) (BY SIMILARITY).
FT	SITE	740	743	ENDOCYTOSIS SIGNAL. NPXY MOTIF.
FT	METAL	137	137	COPPER (BY SIMILARITY).

Query Match 97.9%; Score 3576; DB 1; Length 751;
 Best Local Similarity 91.7%; Pred No. 8.5e-171;
 Matches 689; Conservative 3; Mismatches 3; Indels 56; Gaps 1;

QY	1	MLPGLAILLLAAWTARALEVPTIDGNAGLLAPQIAMFGRLNMHMNYONGKWDSDPSGTK	60
DB	1	MLPGLAILLLAAWTARALEVPTIDGNAGLLAPQIAMFGRLNMHMNYONGKWDSDPSGTK	60
QY	61	TCIDTKEGILQYCEVYPELQITNVNEANQVPTTOMCKKCKCKCKTHPHVTPYRCLVG	120
DB	61	TCIDTKEGILQYCEVYPELQITNVNEANQVPTTOMCKKCKCKCKTHPHVTPYRCLVG	120
QY	121	EFVSDALLVPQCKFLHQRMDVCEVTHLRHWTVAKETCSEKSTNLDHYGMLLPGIDKFR	180
DB	121	EFVSDALLVPQCKFLHQRMDVCEVTHLRHWTVAKETCSEKSTNLDHYGMLLPGIDKFR	180
QY	181	GVFVCCPLAESDNDVSDADAEEDSDVWGGAUTDYADGSEDKVVEVAEEVAEEVEE	240
DB	181	GVFVCCPLAESDNDVSDADAEEDSDVWGGAUTDYADGSEDKVVEVAEEVAEEVEE	240
QY	241	EADDEDEDGDEVEEAEAEPEATEITTSIATITTTTTTTSVEEVVVR-----	258
DB	241	EADDEDEDGDEVEEAEAEPEATEITTSIATITTTTTTTSVEEVVVR-----	258
QY	289	-----VPTAASITPAVDKYL 304	
DB	301	RAMISRWYFDVTGKCAPFFYGGCGGNRNFTDEYCNVAGCVIPTTAASITPAVDKYL	360
QY	305	ETPGDENEHAFQKAKERLEAKHRRMSQVMRENEAEERQAKNLPKADKKAVIOHFOEKV	364
DB	361	ETPGDENEHAFQKAKERLEAKHRRMSQVMRENEAEERQAKNLPKADKKAVIOHFOEKV	420
QY	365	ESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQVPPRPRHVNMLKKYVR	424
DB	421	ESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQVPPRPRHVNMLKKYVR	480
QY	425	AFQKQKQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVEIQ	484
DB	481	AFQKQKQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVEIQ	540
QY	485	DEVDELLOKEQNSDDVIANMISEPRIISYGNDAIMPSTFTKTTVELLPVNGEFSLDLQ	544
DB	541	DEVDELLOKEQNSDDVIANMISEPRIISYGNDAIMPSTFTKTTVELLPVNGEFSLDLQ	600
QY	545	PWHSFGADSVPAANTENEVSPVCARPAADRGTLTRPGSLTNIKTTEISEVNLDAEERHDS	604
DB	601	PWHSFGADSVPAANTENEVSPVCARPAADRGTLTRPGSLTNIKTTEISEVNLDAEERHDS	660
QY	605	GVEVHHQKLVFPAEDVGSNKGAIIGLMVGGVVVATVITVITLMKKKKQYISIHGHVWEVD	664
DB	661	GVEVHHQKLVFPAEDVGSNKGAIIGLMVGGVVVATVITVITLMKKKKQYISIHGHVWEVD	720
QY	665	AAVTPEERHLSKMQONGYENPTYKFFQMQON 695	
DB	721	AAVTPEERHLSKMQONGYENPTYKFFQMQON 751	

RESULT 4
 A4_PIG
 ID A4_PIG STANDARD; PR: 770 AA.
 AC P79307; Q29023; Q9TU0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (A2P) (A2PP) (Alzheimer's disease
 DE Amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(4C);
 DE Gamma-C1F(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RA Kimura A., Takahashi T.;
 RP "Amyloid precursor protein 770.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RC [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RC TISSUE=Small intestine;
 RA Winteroe A.K., Fredholm M.;
 RP "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RC [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RI "Conservation of the sequence of the Alzheimer's disease amyloid
 RI peptide in dog, polar bear and five other mammals by cross-species
 RI polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APPB1/Tp60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(i) and JIP (By
 CC similarity). Inhibits G(i) alpha Arpase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-reconstituted APP1-
 CC induces neuronal death directly or is potentiated through Cu(II)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPRIP1, and SHC1. Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPB1, IB1, KNS2
 CC (via its TPR domains) (By similarity), APPB2 (via BASS) and DBP1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of APP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and

lysosomes. Some APP accumulates in secretory transport vesicles
 leaving the late Golgi compartment and returns to the cell
 surface. GammaCTF(59) peptide is located to both the cytoplasm and
 nuclei of neurons (By similarity).
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
 CC similarity).
 CC -!- PM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PM: N- and O-linked glycosylated (By similarity).
 CC -!- PM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- PM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-156, and the formation
 CC of a disulfide bond (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB032550; BAA84580.1;
 CC EMBL: Z84022; CAB06313.1;
 CC EMBL: X56127; CAA39592.1;
 CC HSP: P05067; IAAIP.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta_APP.
 CC InterPro: IPR002223; Kunitz_BPT1.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC PRINTS: PR00759; BASICPTASE.
 CC ProDom: PD000222; Kunitz_BPT1; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1;
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1;
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Amyloid.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
 FT CHAIN 18 687 SOLUBLE APP-ALPHA (POTENTIAL).
 FT CHAIN 671 SOLUBLE APP-BETA (POTENTIAL).
 FT CHAIN 672 770 C99 (BY SIMILARITY).
 FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
 FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
 FT CHAIN 688 770 C83 (BY SIMILARITY).
 FT CHAIN 688 713 P3(42) (BY SIMILARITY).
 FT CHAIN 688 711 P3(40) (BY SIMILARITY).
 FT CHAIN 712 770 GAMMA-CTF(59).
 FT CHAIN 714 770 GAMMA-CTF(57).
 FT CHAIN 721 770 GAMMA-CTF(50) (BY SIMILARITY).
 FT CHAIN 740 770 C31 (DURING APOPTOSIS) (BY SIMILARITY).
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 110 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 135 155 COPPER-BINDING (BY SIMILARITY).
 FT DOMAIN 181 188 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 291 341 BPTI/KUNITZ INHIBITOR.
 FT DOMAIN 391 423 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 491 522 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 523 540 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 732 751 INTERACTION WITH G(C)-ALPHA (BY SIMILARITY).
 FT DOMAIN 230 260 ASP/GLU-RICH (ACTINIC).
 FT DOMAIN 274 280 POLY-THR.
 FT SITE 144 144 REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
 FT AC1_SITE 301 302 REACTIVE BOND (BY SIMILARITY).
 FT SITE 671 672 CLEAVAGE (BY BETA-SECRETASE) (BY SIMILARITY).
 FT SITE 672 673 CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
 FT SITE 687 688 CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
 FT SITE 704 704 IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
 FT SITE 706 706 INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
 FT SITE 711 712 CLEAVAGE (BY GAMMA-SECRETASE: SITE 1) (BY SIMILARITY).
 FT SITE 713 714 CLEAVAGE (BY GAMMA-SECRETASE: SITE 2) (BY SIMILARITY).
 Query Match 96.5%; Score 3527.5; DB 1; Length 770;
 Best Local Similarity 88.2%; Pred. No. 2,26-168;
 Matches 679; Conservative 9; Mismatches 7; Indels 75; Gaps 1;
 QY 1 MLPGLALLLAATARALEVPTDGNAGLLAEPOIAFMFCGRUNMNMVONGWQSDPSGSK 60
 DB 1 MLPGLALVLAATARALEVPTDGNAGLLAEPOVAMFCGRUNMNMVONGWQSDPSGSK 60
 QY 61 TCIDTKESILQYCOEYPELQITNVNEANQPVTIQNWKCKKCKKTHPHVPIPYCLWG 120
 DB 61 TCIGTKESILQYCOEYPELQITNVNEANQPVTIQNWKCKKCKKTHPHVPIPYCLWG 120
 QY 121 EFVSDALLVPDKCKFLQKQRMVOCETHLJHWHVYAKETSEKSTNLHDYGMILLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLQKQRMVOCETHLJHWHVYAKETSEKSTNLHDYGMILLPGIDKFR 180
 QY 181 GVEFVCCPLAESDNDVSDADSDSDVWVGADTDYAGSDGKDVVEVAEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNDVSDADSDSDVWVGADTDYAGSDGKDVVEVAEVEAEVEE 240
 QY 241 EMDCDDSDSDGDEVEAEPEYEATERTISATITTTTIESVEVYEVVCEQAETGPC 300
 DB 241 EMDCDDSDSDGDEVEAEPEYEATERTISATITTTTIESVEVYEVVCEQAETGPC 300

DB 241 EMDCDDSDSDGDEVEAEPEYEATERTISATITTTTIESVEVYEVVCEQAETGPC 300
 QY 289 -----
 DB 301 RANISRWYFDVTEGKCAPFFYGGCGGNNEFDTEYCHAVCGSYMSSQSLKTTTOEHLPGD 360
 QY 289 ---VPTIAASTPDVADKYLETGPDENEHAHFQKAKERLEAKHREHMSQVMEWEAEHQA 345
 DB 361 PVKLTIAASTPDVADKYLETGPDENEHAHFQKAKERLEAKHREHMSQVMEWEAEHQA 420
 QY 346 KNLKADKKAIVIOHFQEKVESLEQEAANERQOLVETHEMARVEAKLNDKRRRLALENYITAL 405
 DB 421 KNLKADKKAIVIOHFQEKVESLEQEAANERQOLVETHEMARVEAKLNDKRRRLALENYITAL 480
 QY 406 QAVPPRPVHFNMLKKYVRAQOKDRQHTLKHPHEVHYMDPKKAAQIRSQVWTHLRVIYER 465
 DB 481 QAVPPRPVHFNMLKKYVRAQOKDRQHTLKHPHEVHYMDPKKAAQIRSQVWTHLRVIYER 540
 QY 466 MNQSLSLYNVPAVAEEIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTET 525
 DB 541 MNQSLSLYNVPAVAEEIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTET 600
 QY 526 KTVVLLPVNGEFSLDDQPHRSFGADSVDPANTENEVEPVDARPAADRGITTRPGSGLN 585
 DB 601 KTVVLLPVNGEFSLDDQPHRSFGADSVDPANTENEVEPVDARPAADRGITTRPGSGLN 660
 QY 586 IKTEEISEYNLDAERHDSGVEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVITL 545
 DB 661 IKTEEISEYNLDAERHDSGVEVHHQKLVFAEDVGSNGKAIIGLMVGGVVIATVITL 720
 QY 646 VMLKKKQYTSIHGVSVDAAVTPPEERHLSKMQQNGYENPYKFFEQMON 695
 DB 721 VMLKKKQYTSIHGVSVDAAVTPPEERHLSKMQQNGYENPYKFFEQMON 770
 RESULT 5
 A4_CAVPO STANDARD; PRT: 770 AA.
 ID A4_CAVPO
 AC Q60495; Q60496;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); Ctf-alpha; Ctf-beta; Beta-amyloid
 DE protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);
 DE P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-
 DE CTF(57) (Gamma-secretase C-terminal fragment 57); C31].
 GN APP.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_TaxId:10141;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Liver;
 RX MEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller B., Bigl V.;
 RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
 RT alternative splicing.";
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 RN [2]
 RP INTERACTION OF BETA-APP40 WITH APOE.
 RX MEDLINE=98007700; PubMed=9349544;
 RA Martel C.L., Mack C.J.B., Matsubara E., Governale S., Miquel C.,
 RA Mac W., McComb J.G., Frangione B., Ghiso J., Zlokovic B.V.;
 RT "Isoform-specific effects of apolipoproteins E2, E3, and E4 on
 RT cerebral capillary sequestration and blood-brain barrier transport of
 RT circulating Alzheimer's amyloid beta.";
 RL J. Neurochem. 69:1995-2004(1997).
 RN [3]
 RP PROCESSING.
 RX MEDLINE=20084499; PubMed=10619481;

RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA Bigl V.;
RT "Guinea-pig primary cell cultures provide a model to study expression
RT and amyloidogenic processing of endogenous amyloid precursor
RT protein.";
RT Neuroscience 95:243-254(2000).
RN [4]

RP GAMMA-SECRETASE PROCESSING;
RX MEDLINE=20576391; PubMed=11035007;
RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.;
RI "A novel gamma-secretase assay based on detection of the putative
RT C-terminal fragment-gamma of amyloid beta protein precursor.";
RL J. Biol. Chem. 276:481-487(2001).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons and relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metalated APP
CC induces neuronal death directly or is potentiated through C(11)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC -!- FUNCTION: Appicaps elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APPA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein BPP, FPR1, APP3P1, IBL, KNS2
CC (via its TPR domains), APPBP2 (via HaSS) and DBL1 (By similarity).
CC Associates with microtubules in the presence of APP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC ApoE3 appears to be the preferred amyloid binding isoform, while
CC the apoE4 isoform-beta-APP40 complex is capable of being
CC transported across the blood-brain barrier.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N
CC glycosylated in the endoplasmic reticulum) moves to the Golgi
CC complex where complete maturation occurs (O-glycosylated and
CC sulfated (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative Splicing: Named isoforms-2;
CC Comment-Additional isoforms, missing exons 7,8 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC appicans;
CC Name=APP770;

CC IsoId=Q60495-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=Q60495-2; Sequence=VSP_007221, VSP_007222;
CC TISSUE SPECIFICITY: Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the BPTI domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC -!- INDUCTION: Increased levels during neuronal differentiation.
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPXY site is also involved in
CC clathrin-mediated endocytosis.
CC -!- PTM: Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC Ctf-alpha and Ctf-beta. Subsequent processing of Ctf-alpha by
CC gamma-secretase yields P3 peptides. This is the major secretory
CC pathway and is non-amyloidogenic. Alternatively,
CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC -!- PTM: Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC -!- PTM: N- and O-linked glycosylated. O-linkage of chondroitin
CC sulfate to the L-APP isoforms produces the APP proteoglycan core
CC proteins, the appicans (By similarity).
CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC -!- PTM: Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-156, and the formation
CC of a disulfide bond (By similarity).
CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X97631; CAA66230.1; -;
CC EMBL; X99198; CAA67589.1; -;
CC HSSP; P05067; IBA4.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR008154; A4_extra.
CC InterPro; IPR01255; Beta_APP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC PRINTS; PR00203; AMYLOIDA4.
CC PRODOM; PD000222; Kunitz_BPTI; 1.
CC SMART; SM00006; A4_EXTRA; 1.
CC SMART; SM00131; KU; 1.
CC PROSITE; PS00319; A4_EXTRA; 1.
CC PROSITE; PS00320; A4_INTRA; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neutrone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 770 AMYLOID BETA A4 PROTEIN.
FT CHAIN 18 687 SOLUBLE APP-ALPHA (BY SIMILARITY).
FT CHAIN 18 671 SOLUBLE APP-BETA (BY SIMILARITY).
FT CHAIN 672 770 CTF-ALPHA (BY SIMILARITY).
FT CHAIN 672 713 BETA-AMYLOID PROTEIN 42 (BY SIMILARITY).
FT CHAIN 672 711 BETA-AMYLOID PROTEIN 40 (BY SIMILARITY).
FT CHAIN 688 770 CTF-BETA (BY SIMILARITY).
FT CHAIN 688 713 P3(42) (BY SIMILARITY).
FT CHAIN 688 711 P3(44) (BY SIMILARITY).
FT CHAIN 712 770 GAMMA-CTF(59) (BY SIMILARITY).
FT CHAIN 714 770 GAMMA-CTF(57) (BY SIMILARITY).
FT CHAIN 740 770 C31 (BY SIMILARITY).
Query Match 96.3%; Score 3514.5; DB 1; Length 770;
Best Local Similarity 87.9%; Pred No. 9.9e-168;
Matches 677; Conservative 8; Mismatches 10; Indels 75; Gaps 1;
QY 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRINMNMVNGCKWSPSPSK 60
DB 1 MLPGLALLLAWTARALEVPTDGNAGLLAEPOIAMFCGRINMNMVNGCKWSPSPSK 60
QY 61 TCDLTKEGILQYCOEYVPELQIINVEANQPVTONCKRGKCKKTHFHVLEYRGLNG 120
DB 61 TCDLTKEGILQYCOEYVPELQIINVEANQPVTONCKRGKCKKTHFHVLEYRGLNG 120
QY 61 TCIGSREGILQYCOEYVPELQIINVEANQPVTONCKRGKCKKTHFHVLEYRGLNG 180
DB 61 TCIGSREGILQYCOEYVPELQIINVEANQPVTONCKRGKCKKTHFHVLEYRGLNG 180
QY 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHWITVAKETCSKSTNLHJYGMILPGSIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHWITVAKETCSKSTNLHJYGMILPGSIDKFR 180
QY 181 GVEFVCCPLAEISDNVSDADAEEDSDVWNGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAEISDNVSDADAEEDSDVWNGADTDYADGSEDKVVEAEVEAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEVEATEKTSTATTITTTTSTESVEVW- 288
DB 241 EADDDEDDGDEVEEAEPEVEATEKTSTATTITTTTSTESVEVW- 288
QY 241 EADDDEDDGDEVEEAEPEVEATEKTSTATTITTTTSTESVEVWSEQAETGCP 300
DB 241 EADDDEDDGDEVEEAEPEVEATEKTSTATTITTTTSTESVEVWSEQAETGCP 300
QY 289 - 288
DB 289 - 288
QY 301 RSMISRWYEDVTGKCAPFFYGGCGGNRNNEPTEEYCMVAGCSVMSONLLKTSGEVPSQ 360
DB 301 RSMISRWYEDVTGKCAPFFYGGCGGNRNNEPTEEYCMVAGCSVMSONLLKTSGEVPSQ 360
QY 289 ---VPTTAASTPDVADKYLETGDENEHAFKAKERLEAKHREMSQVMEKEFAGQA 345
DB 289 ---VPTTAASTPDVADKYLETGDENEHAFKAKERLEAKHREMSQVMEKEFAGQA 345
QY 361 PVKLPPTAASTPDVADKYLETGDENEHAFKAKERLEAKHREMSQVMEKEFAGQA 420
DB 361 PVKLPPTAASTPDVADKYLETGDENEHAFKAKERLEAKHREMSQVMEKEFAGQA 420
QY 346 KNLPRADKKAVTCHFOEKVESLEQBAANERQOLVETHMARVEMLNDRRLALENYITAL 400
DB 346 KNLPRADKKAVTCHFOEKVESLEQBAANERQOLVETHMARVEMLNDRRLALENYITAL 400
QY 421 KNLPRADKKAVTCHFOEKVESLEQBAANERQOLVETHMARVEMLNDRRLALENYITAL 460
DB 421 KNLPRADKKAVTCHFOEKVESLEQBAANERQOLVETHMARVEMLNDRRLALENYITAL 460
QY 406 QAVPPRPRVFNMLKYYVRAEOKDCHTLKPHHVRMVDKPKAAQIRSOVWTHRVIVYR 465
DB 406 QAVPPRPRVFNMLKYYVRAEOKDCHTLKPHHVRMVDKPKAAQIRSOVWTHRVIVYR 465
QY 481 QAVPPRPRVFNMLKYYVRAEOKDCHTLKPHHVRMVDKPKAAQIRSOVWTHRVIVYR 540
DB 481 QAVPPRPRVFNMLKYYVRAEOKDCHTLKPHHVRMVDKPKAAQIRSOVWTHRVIVYR 540
QY 466 MNOSLLLYNPAVAEIQDEYDELLOKEQNSDQVAMISEPRISYGNDAIMPSLET 525
DB 466 MNOSLLLYNPAVAEIQDEYDELLOKEQNSDQVAMISEPRISYGNDAIMPSLET 525
QY 541 MNOSLLLYNPAVAEIQDEYDELLOKEQNSDQVAMISEPRISYGNDAIMPSLET 600
DB 541 MNOSLLLYNPAVAEIQDEYDELLOKEQNSDQVAMISEPRISYGNDAIMPSLET 600
QY 526 KTTVELLPNGEFLSDDLQPHWISFGADSVPAENTEVEPVFARPAADRLITRIGSLTN 585
DB 526 KTTVELLPNGEFLSDDLQPHWISFGADSVPAENTEVEPVFARPAADRLITRIGSLTN 585
QY 601 KTTVELLPNGEFLSDDLQPHWISFGADSVPAENTEVEPVFARPAADRLITRIGSLTN 660
DB 601 KTTVELLPNGEFLSDDLQPHWISFGADSVPAENTEVEPVFARPAADRLITRIGSLTN 660
QY 586 IKTEEISEVNLKAEPRDSSYEVHVKCLVFAEDYGSNKGALICLWGVYATVIVITL 643
DB 586 IKTEEISEVNLKAEPRDSSYEVHVKCLVFAEDYGSNKGALICLWGVYATVIVITL 643
QY 661 IKTEEISEVNLKAEPRDSSYEVHVKCLVFAEDYGSNKGALICLWGVYATVIVITL 720
DB 661 IKTEEISEVNLKAEPRDSSYEVHVKCLVFAEDYGSNKGALICLWGVYATVIVITL 720
QY 646 VMLKKKQYTSIHGVEVDAVTPERHLKSKMQONGYENPTYKFFEQMN 695
DB 646 VMLKKKQYTSIHGVEVDAVTPERHLKSKMQONGYENPTYKFFEQMN 695

Db 721 VMLKKKQYTSIHGVEVDAVTPERHLKSKMQONGYENPTYKFFEQMN 770
RESULT 6
A4_MOUSE STANDARD: PRI: 770 AA.
AC P12023; P97497; P97942; Q99K32;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease)
DE Soluble APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99;
DE Soluble APP-beta (S-APP-beta); Soluble APP-beta (S-APP-beta); C99;
DE (APP-C99); Beta-amyloid protein 42 (Beta A4P42); Beta-amyloid protein
DE 40 (Beta-A4P40); C83; P3(42); P3(40); Gamma-Ctf(59) (Gamma-secretase
DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE (APP-C59); Gamma-Ctf(57) (Gamma-secretase C-terminal fragment 57)
DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-Ctf(50)
DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain
DE 50) (AID(50)); C31].
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE-Brain;
RC MEDLINE=88106489; PubMed=3322280;
FA Yamada T., Sasaki H., Furiya H., Miyata F., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [2]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE=92096458; PubMed=1756177;
FA de Strooper B., van Leeuwen F., van den Bergh H.;
RT "The amyloid beta protein precursor or proteinase nexin 1 from mouse
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN-SAMP8; TISSUE-Hippocampus;
RX PubMed=11235921;
FA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
A.varez J., Morley J.E.;
RT "Molecular cloning, expression, and regulation of hippocampal amyloid
RL Biochem. Cell Biol. 79:57-67(2001).
RN [5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
FA Izumi R., Yamada T., Yoshikawa S.I., Sasaki H., Hattori M.,
Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Gene 112:189-195(1992).
RN [6]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RC TISSUE-Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
FA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,


```

121 EFVSDALLVPCKFLHGRMDVCEETHLHHHTVAKETCEKSTNLHDYGMLLPGIDKFR 180
181 GVEFFCCPLAESDNDVSADAEEDSDVMWGGADFDYADGSEDAVVAEVEEVEE 240
182 GVEFFCCPLAESDNDVSADAEEDSDVMWGGADFDYADGSEDAVVAEVEEVEE 240
241 EADDEDGDDGDEVEEFAEPEYERATRTSLATTTTITTESVEEVN----- 288
241 EADDEDGDDGDEVEEFAEPEYERATRTSLATTTTITTESVEEVN----- 300
289 ----- 298
301 RAKISRWTFDVTESKCVPFYGGGGGNNRNFDTSEYCMVCGSVSTQSLKLTSEPFGQ 360
289 ----VPTTAASPDAVKYLETPTGDNENHAFKCKAKERLEAKHRMSQVMKREAEARQA 345
361 PDKLPTTAASPDAVKYLETPTGDNENHAFKCKAKERLEAKHRMSQVMKREAEARQA 420
346 KNLPRADKKAVYQHFEQKVESLEGEAANEKGLVETHHARVEAMLNDRRLAENYITAL 400
421 KNLPRADKKAVYQHFEQKVESLEGEAANEKGLVETHHARVEAMLNDRRLAENYITAL 480
406 QAVFPRPRHVFNLKKYVRAEKDKROHTLKFEHVMVDPKKAQIRSQVNIHLRYIER 465
481 QAVFPRPRHVFNLKKYVRAEKDKROHTLKFEHVMVDPKKAQIRSQVNIHLRYIER 540
466 MNOSSLNLYNPVPAVEETODEVDELLQEQNSYDVIANMTSEPRISYGNALMPS:TFET 525
541 MNOSSLNLYNPVPAVEETODEVDELLQEQNSYDVIANMTSEPRISYGNALMPS:TFET 600
526 KITVELLPVNGEFLDDCQPHSFCAQSVPAANTEVEPEVDARPAAGLTFRPGSLGN 585
601 KITVELLPVNGEFLDDCQPHSFCAQSVPAANTEVEPEVDARPAAGLTFRPGSLGN 660
586 IKTEELSEVNLDAFRHDSGVEVHHQKLVFTAEVDGSKNGAIGLIMGVGVYATVIVITL 645
661 IKTEELSEVNLDAFRHDSGVEVHHQKLVFTAEVDGSKNGAIGLIMGVGVYATVIVITL 720
646 VMLKKKQYTSIHGVVVEYDAVTPTEERHLSKMQNGYENPYKTFEOMON 695
721 VMLKKKQYTSIHGVVVEYDAVTPTEERHLSKMQNGYENPYKTFEOMON 770

RESULT 7
A4_RAT
A4_RAT STANDARD: PRT; 770 AA.
AC P08592;
DI 01-AUG-1988 (Rel. 08, Created)
DI 01-DEC-1992 (Rel. 24, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains: Soluble
DE App-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C99; Beta-
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-CTF(59) (Gamma-secretase C-terminal
DE fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-CTF(50) (Gamma-secretase C-terminal fragment 50); G31];
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312583; PubMed=2900758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RT in rat brain suggests a role in cell contact.";
RL EMBO J. 7:1365-1376(1988).
RX [2]
RP SEQUENCE OF 289-364 FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassiliacopoulos D.,
RA Mytilineou C., Marqolis R.U., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX PubMed=8996634;
RA Sandbrink R., Wanning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX PubMed=9930726;
RA Katanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.;
RA Suzuki T., Nairn A.C., Greenkard P.;
RT "A 127-kDa protein (UV-DBB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX PubMed=10024358;
RA Brouillet E., Trembleau A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Gq heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthymiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., Cua Jungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
```

RA Liu S.-J., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12].
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX PubMed-11959460;
 RA Kanski J., Varadarajan S., Aksanova M., Butterfield D.A.;
 RT "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13].
 RP PHOSPHORYLATION.
 RX PubMed-9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Gandy S.E.,
 RT Greenberg P., Suzuki T.;
 RT "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14].
 RP PHOSPHORYLATION ON SER-730.
 RX PubMed-10329382;
 RA Isohara T., Horiuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RT Greenberg P., Nairn A.C., Suzuki T.;
 RT "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15].
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE-9927474; PubMed-10341243;
 RA Ando K., Gishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greenberg P., Suzuki T.;
 RT "Role of phosphorylation of Alzheimer's amyloid precursor protein
 during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16].
 RP PHOSPHORYLATION ON THR-743.
 RX PubMed-10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Itohara S.,
 RA Greenberg P., Kirino Y., Nairn A.C., Suzuki T.;
 RT "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17].
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX PubMed-11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RT "Appican, the proteoglycan form of the amyloid precursor protein,
 contains chondroitin sulfate E in the repeating disaccharide region
 and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 physiological functions on the surface of neurons relevant to
 neurite growth, neuronal adhesion and axonogenesis. Involved in
 cell mobility and transcription regulation through protein-protein
 interactions (By similarity). Can promote transcription activation
 through binding to APBB1/Trip60 and inhibit Notch signaling through
 interaction with Numb (By similarity). Couples to apoptosis-
 inducing pathways such as those mediated by G0 and JIP. Inhibits
 G0 alpha ATPase activity. Acts as a kinesin I membrane receptor,
 mediating the axonal transport of beta-secretase and presenilin 1
 (By similarity). May be involved in copper homeostasis/oxidative
 stress through copper ion reduction. Can regulate neurite
 outgrowth through binding to components of the extracellular
 matrix such as heparin and collagen I and IV (By similarity). The
 splice isoforms that contain the Bp1 domain possess protease
 inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-APP42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPX II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8-PL1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPRL1, APPBP1, IBI, KNS2
 CC (via its TPR domains), APPBP2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC Query Match 95.5%; Score 3485.5; DB 1; Length 770;
 CC Best Local Similarity 87.4%; Pred. No. 2.7e-166;
 CC Matches 673; Conservative 9; Mismatches 13; Indels 75; Gaps 1;
 QY 1 MLPGLALLLLAATARALEVPTDGNAGLLAPQIATMFCGRLLMHNVONGKWDSPSGTK 60
 DQ 1 MLPGLALLLLAATARALEVPTDGNAGLLAPQIATMFCGRLLMHNVONGKWDSPSGTK 60
 QY 61 TCIDTKESILLOYCOEVYPELQITNVVEANOPVTITONCKRGCKOCKTHPIFVIVPGLVG 120
 DQ 61 TCIDTKESILLOYCOEVYPELQITNVVEANOPVTITONCKRGCKOCKTHPIVIVPGLVG 120
 QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
 DQ 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
 QY 181 GVEFVCCPLAESNVDSADAEFDDSDVWNGGADTDYADGSEDKVVEVAEEVEAFVFEF 240
 DQ 181 GVEFVCCPLAESNVDSADAEFDDSDVWNGGADTDYADGSEDKVVEVAEEVEAFVFEF 240
 QY 241 FADDDDEDEGDEVEEEAEFPYEATERTTSTIAITTTTITTESVEEVVR----- 288
 DQ 241 FADDDDEDEGDEVEEEAEFPYEATERTTSTIAITTTTITTESVEEVVR----- 288
 QY 289 ----- 288
 DQ 301 RAMISRMYFDVTECKCAPFFYGGCGGNRNFDTTEECYNAVCGSVSSOSLLKTTSELPQD 360
 QY 289 ---VPTTAASTPDADVKYLETTPGDENEHAHPKAKERLEAKHRMRSQVWREWEAEERQA 345
 DQ 361 PVKLPPTAASTPDADVKYLETTPGDENEHAHPKAKERLEAKHRMRSQVWREWEAEERQA 420
 QY 346 KNLPAUKKAVIOHFOEKVESLEGEAANERQOLVETHMARVEAMLDNRRLALENYITAL 405
 DQ 421 KNLPAUKKAVIOHFOEKVESLEGEAANERQOLVETHMARVEAMLDNRRLALENYITAL 480
 QY 406 QAVPPRRHVNMLKKYVRAPQKDRQHTLKHFEHVRVDPKAAQIRSQWTHLRVIYER 465
 DQ 481 QAVPPRRHVNMLKKYVRAPQKDRQHTLKHFEHVRVDPKAAQIRSQWTHLRVIYER 540
 QY 466 MNQSLSLLYNVPAAVEEIQDEVDDELLOKEQNYSDVLANMISEPRIISYGNDAIMPSTLET 525
 DQ 541 MNQSLSLLYNVPAAVEEIQDEVDDELLOKEQNYSDVLANMISEPRIISYGNDAIMPSTLET 600
 QY 526 KTVTELLPVNGEFSLLDLQPHWHSFGADSVSPANTENEVEPVDARPAADRGTLTTRPGSLTN 585


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DB      685 PTIKYLEQMQ 694
||||| ||||
RESULT 9
APP2_HUMAN
ID APP2_HUMAN STANDARD: PRT: 763 AA.
AC Q06481;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APP2)
DE (CDEI-box binding protein) (CDEBP).
DE APLP2 OR APLP2.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8495127;
RA Sprecher C.A., Grant F.J., Grimm C., O'Hara P.J., Norris F.,
RA Morris K., Foster D.C.;
RI "Molecular cloning of the cDNA for a human amyloid precursor protein:
RI homolog: evidence for a multigene family.";
RI Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Ranes J., Klaudiny J., Scheit K.H.;
RA "A human amyloid precursor-like protein: is highly homologous to a
RA mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035111; PubMed=8220435;
RA Wasec W., Gurubhavadatula S., Paralis M., Romano D.M., Sisodia S.S.,
RA Hyman B.I., Neve R.L., Tanzi R.E.;
RA "Isolation and characterization of APLP2 encoding a homologue of the
RI Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477632;
RA Strausberg R.J., Feingold E.A., Grouse L.H., Gerde J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zdobych B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prance C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTACATG-3' (CDEI BOX).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
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CC CC (POENTIAL).
CC CC -!- ALTERNATIVE PRODUCTS:
CC CC Event-Alternative splicing: Named isoforms=3;
CC CC Comment-Additional isoforms seem to exist;
CC CC Name=1;
CC CC IsoId=Q06481-1; Sequence=Displayed;
CC CC Name=2;
CC CC IsoId=Q06481-2; Sequence=VSP_000018;
CC CC Name=3;
CC CC IsoId=Q06481-3; Sequence=VSP_000019;
CC CC TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
CC CC AND ENDOTHELIAL TISSUES.
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC or send an email to licens@sib-sib.ch).
CC CC
CC CC EMBL: S60099; AAC60589.1; -
CC CC EMBL: L09209; ARA35526.1; -
CC CC EMBL: Z22572; CA80295.1; -
CC CC EMBL: L27631; AAC41701.1; -
CC CC EMBL: BC000373; AAH00373.1; -
CC CC PIR: A49321; A49321.
CC CC ISSP: P05067; LMWP.
CC CC Genew: HGNC:598; APLP2.
CC CC MIM: 104776; -
CC CC GO: GO:0016021; C: integral to membrane; NAS.
CC CC GO: GO:0005634; C: nucleus; IDA.
CC CC GO: GO:0003677; F: DNA binding activity; NAS.
CC CC GO: GO:0007186; P: G-protein coupled receptor protein signaling; NAS.
CC CC InterPro: IPR001868; A4_APP.
CC CC InterPro: IPR002223; Kunitz_BPTI.
CC CC Pfam: PF02177; A4_EXTRA; 1.
CC CC Pfam: PF00014; Kunitz_BPTI; 1.
CC CC PR: PR:00203; AMYCID4.
CC CC PR: PR:00759; BASICPTASE.
CC CC ProDom: PD000222; Kunitz_BPTI; 1.
CC CC SMART: SM00006; A4_EXTRA; 1.
CC CC SMART: SM00133; KC; 1.
CC CC PROSITE: PS00319; A4_EXTRA; 1.
CC CC PROSITE: PS00320; A4_INTRA; 1.
CC CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC CC PROSITE: PS0279; BPTI_KUNITZ_2; 1.
CC CC Transmembrane: Signal: Alternative splicing; DNA-binding;
CC CC Nuclear protein; Serine protease inhibitor;
CC CC SIGNAL: 1 29
CC CC CHAIN 30 763
CC CC AMYLOID-LIKE PROTEIN 2.
CC CC DOMAIN 30 692
CC CC EXTRACELLULAR (POTENTIAL).
CC CC TRANSMEM 693 716
CC CC POTENTIAL.
CC CC DOMAIN 717 763
CC CC CYTOPLASMIC (POTENTIAL).
CC CC DOMAIN 225 280
CC CC ASP/GLU-RICH (HIGHLY ACIDIC).
CC CC DOMAIN 306 364
CC CC BPTI/KUNITZ INHIBITOR.
CC CC DOMAIN 215 231
CC CC POLY-GLU.
CC CC ACT SITE 320 321
CC CC REACTIVE BOND (BY SIMILARITY).
CC CC DISULFID 310 360
CC CC BY SIMILARITY.
CC CC DISULFID 319 343
CC CC BY SIMILARITY.
CC CC DISULFID 335 356
CC CC BY SIMILARITY.
CC CC VARSPDIC 308 363
CC CC Missing (in isoform 2).
CC CC Missing (in isoform 3).
CC CC /FTid=VSP_000018.
CC CC /FTid=VSP_000019.
CC CC VARSPDIC 613 624
CC CC Missing (in isoform 1).
CC CC CONFLICT 543 543
CC CC S -> I (IN REF. 1).
CC CC SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;
CC CC QUERY MATCH 47.2%; Score 1725; DB 1; Length 763;
CC CC Best Local Similarity 46.9%; Pred. No. 8.4e-79;
CC CC Matches 369; Conservative 112; Mismatches 170; Indels 136; Gaps 19;
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QY 5 LALLLLAATWAKALEV-----PTDGNAS---LLAEPOIAIEFCGGRJAHMHVQMGKNSDP 56
DB 15 LLLLLLVGLTAPALALAGYTEALAAAGTGFVAFAEPOIAIEFCGGLNHHVNIQTQKWPDP 74
QY 57 SGTKTCIDTKEGILQYCEVPELOITNVVANGPVTIQWCKRGKQCKTHFEVILPPI 116
DB 75 TGTSCFETKEVQLQYCEVPELOITNVVANGPVTIQWCKRGKQCKTHFEVILPPI 132
QY 117 CLVGFVSDALLVDPKCFJHQRNMDVCEHWHVETVAKFTCTSEKSNJNDYDGLMLPCCI 176
DB 133 CLVGFVSDALLVDPKCFJHQRNMDVCEHWHVETVAKFTCTSEKSNJNDYDGLMLPCCI 192
QY 177 DKFRGVFVCCPLAESONVSDAEEDSDVWVGADDTYADGSEDKVVEVAEEESVAE 236
DB 193 DGFHGTGVCCPQTKITGYSKVEEEDSDVWVGADDTYADGSEDKVVEVAEEESVAE 245
QY 237 VEE--EEA--DDEDDGDDGVEEAEDEPY-----DEATERKTSIATITITTES 282
DB 245 LEDFTEAAVDEDEDEECEEVVEDROYVYDTFKGDYNEENPTEPGSDGTMSEKE-THD 305
QY 283 VEEV-----VRVP 290
DB 306 KVAVCSQEMTGPRAVMPRTYDLSKGCVRFTYSGCGGNENFSEDIYCMAYCKAMIP 365
QY 291 TTAASIPDAVQKYLETPGDENEPHAFCKAKERLEAKHREMSOVNREWEAEAKKLNPK 353
DB 356 TPPLPTND-VVYFETSADCHERARFQAKCELEIRNRNMDRVKKKEWEAEACAKNLPK 424
QY 351 ADKAVIOHFORKVESLECEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPP 410
DB 425 AERQTLIGHFOAKVKALEKAASEKQQLVE-HLARVEAMLNDRRLALENYITALQAVPP 484
QY 411 RPRHVFNLKKYVRAEOKDROHTLKHFEHVRWDPFKAAQIIRSQVMTHLRVIVERNQSL 470
DB 485 RPRHQLALRRVRAENKRLHTIRHYQVLAVDPEKAAQKQSQVMTHLRVIVERNQSL 544
QY 471 SLLVNPVAAEIQDEVDPELLOKEQNSDDVLANNMISEPR-SYGNDAIMPELSTETKIVE 530
DB 545 SLLVNPVAAEIQDEVDPELLOKEQNSDDVLANNMISEPR-SYGNDAIMPELSTETKIVE 587
QY 531 LLPVNGEFLDQWPHSEFGADSVAPANTENEVEPVDARPAADRLTNPQ-----SGLTN 585
DB 588 ---VSSEES-EDIPPHFPE--HPPALPENE----DIQPELYHPNKKGSGVGEODGGLIG 632
QY 586 IKTEISIEVN-LDAEFHDCSGVEVHHCKLVFEADVGS-----NKGAI 627
DB 638 AEKVINKNKVDENKMWIDETLDV--KEMIFNAERVGGEIIEERSVGLPREDFSLSSSAL 695
QY 628 IGLMVGGVVIATVIIVITLVMLKKQYTSIIHHGVVEVDAAVTPEERH-SKMQQNGYENPIY 697
DB 696 IGLLVIAVAIATVIVISLVMLKKQYGTISHGIVEVDPLTPPEERHKKMQNHGYNPIY 755
QY 688 KFEQMQ 694
DB 756 KYLEQMQ 762

RESULT 10
APP2_RAT
ID APP2_RAT STANDARD: PRT: 765 AA.
AC P15943;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid-like protein 2 precursor (Sperm membrane protein YWK-I.).
GN APLP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE OF 1-627 FROM N.A.
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RC STRAIN-Wistar; TISSUE=Brain, and Heart;
RX MEDLINE=94368849; PubMed=8086458;
RA Sandriak R., Masters C.L., Beyreuther K.;
RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
RT difference to human and murine homologues.";
RL Biochim. Biophys. Acta 1219:167-170(1994).
RN [2]
RP SEQUENCE OF 575-765 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=90207205; PubMed=1690887;
RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
RT "Characterization of cDNA encoding a human sperm membrane protein
RT related to A4 amyloid protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=A;
CC IsoId=P15943-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P15943-2; Sequence=VSP_000021;
CC Name=C;
CC IsoId=P15943-3; Sequence=VSP_00002C;
CC Name=D;
CC IsoId=P15943-4; Sequence=VSP_00002D, VSP_000021;
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
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CC
DR EMBL; X7934; CAAS4906.1; -
DR EMBL; M31322; AAA42352.1; -
DR PIR; A35981; A35981.
DR PIR; S42880; S42880.
DR HSP; P05067; IIMP.
DR InterPro; IPR01866; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0219; BPTI_KUNITZ_2; 1.
KW Transmembrane; Alternative splicing; Serine protease inhibitor;
KW Signal; Glycoprotein.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 765 AMYLOID-LIKE PROTEIN 2.
FT DOMAIN 30 695 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 696 718 POTENTIAL.
FT DOMAIN 719 765 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 282 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 308 366 BPTI/KUNITZ INHIBITOR.
FT ACT_SITE 322 323 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 312 362 BY SIMILARITY.
FT DISULFID 321 345 BY SIMILARITY.
FT DISULFID 337 358 BY SIMILARITY.
FT DOMAIN 218 229 POLY-GLU.
FT CARBOHYD 628 628 O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT VARSPIC 311 365 Missing (in isoform C and isoform D).
FT VARSPIC 616 627 Missing (in isoform B and isoform D).
```


APPL_MOUSE
 ID APPL_MOUSE STANDARD: PRT: 653 AA.
 AC Q03157; Q8VC38;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
 GN APLP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93066322; PubMed=1275693;
 RA Wasco W., Bupp K., Magendanz M., Guseilia J.F., Tanzi R.E.,
 RA Solomon F.,
 RA "Identification of a mouse brain cDNA that encodes a protein related
 RT to the Alzheimer disease-associated amyloid beta protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
 RA Stapleton M., Soares M.B., Tonaldi M.F., Casavant I.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gharatne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay E.J., Hallyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalits D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [3]
 RP COLLAGEN-BINDING.
 RX MEDLINE=9613497; PubMed=8576150;
 RA Behr D., Hesse L., Masters C.L., Malthaup G.,
 RA "Regulation of amyloid protein precursor (APP) binding to collagen and
 RT mapping of the binding sites on APP and collagen type I.";
 RL J. Biol. Chem. 271:1613-1626(1996).
 RN [4]
 RP INTERACTION WITH DAB1.
 RX MEDLINE=9938980C; PubMed=10460257;
 RA Homayouni R., Rice D.S., Sheidon M., Curran T.,
 RA "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
 RT protein 1.";
 RL J. Neurosci. 19:7507-7515(1999).
 RN [5]
 RP INTERACTION WITH MAPK8IP1.
 RX MEDLINE=21408156; PubMed=11517249;
 RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
 RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
 RA Kyriakis J.M., Nishimoto I.,
 RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
 RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
 RL J. Neurosci. 21:6597-6607(2001).
 RN [6]
 RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
 TYR-641.
 RX MEDLINE=22313598; PubMed=12228233;
 RA Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamo L.,
 RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
 RT secretase regulates transcription.";
 RL J. Biol. Chem. 277:44195-44201(2002).
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, APLP1, activates transcription
 CC activation through APBB1 (Fe65) binding. Couples to JIP signal
 CC transduction through C-terminal binding. May interact with
 CC cellular G-protein signaling pathways. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I.
 CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB and APBA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
 CC similarity).
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: O-glycosylated.
 CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 CC -----
 DR EMBL: L04538; AAA37247.1;
 DR EMBL: BC021877; AAH21877.1;
 DR PIR: A46362; A46362.
 DR HSP: P05067; iMWP.
 DR KGB: MGI:88046; Ap1.
 DR InterPro: IPR001858; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 37 POTENTIAL.
 FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
 FT DOMAIN 624 653 C30 (BY SIMILARITY).
 FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 584 606 POTENTIAL.
 FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 157 177 COPPER-BINDING.
 FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
 FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
 FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
 FT DOMAIN 263 271 POLY-GLU.
 FT DOMAIN 535 538 POLY-SER.
 FT DOMAIN 601 606 POLY-LEU.
 FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
 FT SIMILARITY).
 FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY


```

Db      6 LMIGLLIPILVA-IYVAEGSPAGSKHKHF:PMWAFSCUYRQYM:ILEGSKTKDHYA 63
QY      61 TCIDTKEGILQVCEWYPELOITNNVEANOPVLIQNMCKGRGKQCK:HPHFVIPRCVVG 120
Db      64 TCFSGKLDILKCRKAYPSMNITNIVEYSISDMCKREEGSPCK-WTHSVRPYHC:DG 122
QY      121 EFVSALLVPDKCKFLHQBMDVCEIHLHWHFVAKETCEKSTN:-----LHDYGMLLPC 174
Db      123 EFHSALQVPHDCQSHVNSRDOCHNDYQHWKDFAGKQCK:KSKGNKMKMIVRSFAVLEPC 182
QY      175 GIDKRGVEVFCPLAEESDNDYSADAEDSDVVMWGGADTDYAGSDEKVVVEAESEV 234
Db      183 ALDMFTGVFVCCP:-----NDQNTKTDVQTK:----- 209
QY      235 AEVEEEDADDDEDDGDEVEEAEPEEATERITSTATTITTSVEEVVRVPTTAA 294
Db      210 -----EDDDDDDDDAYEDDYSESEKDEE:----- 236
QY      295 STPDADVDKYLETPGDENEHAHFQAKERLEAKHHRMSQVMREKDEA:-----EROAKNLP 349
Db      237 -EPSSODPYFKTANWTHNEHDDFKKEMRMDKHKRKKVQVMKEWGDLETTRYNEQAKD-P 294
QY      350 KADKKAVIQ:--HFQEKVSELEQEAANEQOVLVETHMARVEAMLDRRLALENYITAL- 405
Db      295 KGAERFKSOMNARFQKTVSSLEEEHKRMRKEIEAVHEERVQAMLNKKKRDATHQYRQALA 354
QY      406 -QAVPRPRHVFNMKKKYVRAEQKDRHTLKHFHFVRMVDPKKAAQIRSQVWTH:SVIYE 464
Db      355 THVKNPKNUSVLOSUKAYIRAEKDRMHTLNRI:RLHLKADSKRAAAYKPTVTHIRURY:DL 414
QY      465 RMNQSLSLYNP:-----AVA:--EEIQDEVELLQKEQNSYSDVILANM:SEPR:SY 513
Db      415 RINGTLAMLRDPDLEKYYVPINAVTYWYKDYRDEVSFDSVE:--DSELPT:--HDDFSK 470
QY      514 GN--DALMFSLT:-----ETKITVELLPVNGEFSLDLQPHWHSFGASVPANT:--ENEVEP 564
Db      471 NAKLDVKAPTITTAQPKVETDNKAVLPTEASDEEADYEYEDDQVKKTKDMMKKVKV 530
QY      555 VNARP:-----NADRGLTTRPGSLTNIKTEE:-----TSWNLDA 598
Db      531 VDIKPKIKVITTEERKAKPKLVETSQVTDDEDDDESSSTSESDDEDKK:KELRVSI 590
QY      599 E:-----FRDSEGYEVEHOKLVFFAFQVGSNKGALLGLMVGWVIVATV:VITLVMIK 649
Db      591 EPIIDEPASFYRID:-----KLQSPVEVSASSVFPYVLASAMFITA:CIITAFAT 642
QY      650 KQOYTSIHGVEVVDAAVTPTEERHLKMKMOGNOYENFTYKFFE 691
Db      643 NARRRRAMRGFTVD-VYTPTEERHVAGMOVGNENFTYSFED 683
[1]
RESULT 14
A4_DROME: STANDARD: FRT: 867 AA.
AC P14599; Q9TW0; Q9U4H3; Q9W5F1;
CT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-amyloid-like protein precursor.
GN APPL OR VND OR BCNA:GH04413 OR EG:65F1.5 OR CG7727.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184650; PubMed=2494667;
RA Rosen D.R., Martin-Morris L., Luo L., White K.;
RT "A Drosophila gene encoding a protein resembling the human
RL beta-amyloid protein precursor."
RL Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minoda B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schaeffler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valentini P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster."
RL Science 287:2220-2222(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RX MEDLINE=20196069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Reiman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RL systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minoda B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schaeffler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valentini P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster."
RL Science 287:2220-2222(2000).
RN [5]
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ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053.
CT C1-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: beta amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT *Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE G12-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56124; CAA39589.1; -
DR EMBL: X56126; CAA39591.1; -
DR HSSP: PC5067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutrons; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59
SQ SEQUENCE 59 AA; 6414 MW; F43465D486A2H12D CRC64;

Query Match 7.88; Score 284; DB 1; Length 59;
Best Local Similarity 96.6%; Pred. No. 1.5e-06;
Matches 57; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 591 ISEVNLDAEFRHDSGYEVHHQKLVFPAEDVGSNGKALIGLVGGVVTATVITLVMLK 649
Db 1 ISEVKMDAEFRHDSGYEVHHQKLVFPAEDVGSNGKALIGLVGGVVTATVITLVMLK 59

Search completed: October 2, 2003, 13:59:39
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:24 ; Search time 39 seconds
(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-18

Perfect score: 3651

Sequence: 1 MLPGLALLLAANTARALEV.....QNGSYENPTYYKFEQMKNK 697

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DS seq length: 0

Maximum DS seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_23:

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.protist.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.virus.*
- 16: sp.bacteriaph.*
- 17: sp.archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3565	97.6	695	1	Q60496	Q60496 cavia sp. p
2	3532	96.7	695	11	P97487	P97487 mus musculus
3	3527.5	96.6	770	6	Q9TU10	Q9TU10 sus scrofa
4	3420	93.7	695	13	Q9DGJ8	Q9DGJ8 gallus gall
5	3379	92.5	751	13	Q9DGJ7	Q9DGJ7 gallus gall
6	3206	87.8	693	13	Q98SG0	Q98SG0 xenopus lae
7	3182	87.2	695	13	Q98SF9	Q98SF9 xenopus lae
8	3095	84.8	747	13	Q91963	Q91963 xenopus lae
9	2956.5	81.0	699	13	Q57394	Q57394 carpe japon
10	2759.5	75.6	569	13	Q9PVL1	Q9PVL1 gallus gall
11	2627.5	72.0	607	11	Q99K32	Q99K32 mus musculus
12	2605	71.4	534	13	Q93286	Q93286 gallus gall
13	2568	70.3	780	13	Q73683	Q73683 tetraodon l
14	2524	69.1	738	13	Q90W28	Q90W28 brachydanio
15	2487.5	68.1	694	13	Q8UUR9	Q8UUR9 brachydanio
16	2446.5	67.0	737	13	O93279	O93279 fugu rubrip

17	2334	63.3	612	13	O919E7	O919E7 brachydanio
18	1920	52.6	384	11	Q8BPC7	Q8BPC7 mus musculus
19	1762	48.3	695	4	Q13861	Q13861 homo sapien
20	1746.5	47.8	659	4	Q14662	Q14662 homo sapien
21	1735	47.5	695	11	Q64348	Q64348 mus musculus
22	1701	46.6	763	11	Q61482	Q61482 mus musculus
23	1699	46.5	751	11	Q60709	Q60709 mus musculus
24	1650	45.2	472	13	Q8UUS0	Q8UUS0 brachydanio
25	1345.5	36.9	357	13	Q8UUI8	Q8UUI8 brachydanio
26	1301.5	35.6	522	4	Q9BT36	Q9BT36 homo sapien
27	1082	29.6	218	11	Q8BPV5	Q8BPV5 mus musculus
28	1048.5	28.7	523	4	Q14594	Q14594 homo sapien
29	771	21.1	239	13	Q6UUI7	Q6UUI7 brachydanio
30	678	18.6	136	6	P79307	P79307 sus scrofa
31	569	15.6	113	13	Q6JH58	Q6JH58 chelydra se
32	561	15.4	182	11	Q9CYS4	Q9CYS4 mus musculus
33	478	13.1	97	6	Q28673	Q28673 oryctolagus
34	385.5	10.6	82	4	Q16019	Q16019 homo sapien
35	381.5	10.4	82	4	Q16014	Q16014 homo sapien
36	379.5	10.4	82	4	Q16020	Q16020 homo sapien
37	368	10.1	79	11	O35463	O35463 cricetus
38	358.5	9.8	160	11	O9QZ78	O9QZ78 cavia sp. p
39	328	9.0	208	11	Q8R0R7	Q8R0R7 mus musculus
40	239	6.5	49	6	O97917	O97917 bos taurus
41	196.5	5.4	727	5	O95TG7	O95TG7 drosophila
42	196.5	5.4	5303	5	Q9V628	Q9V628 drosophila
43	194	5.3	785	5	O9GQ82	O9GQ82 drosophila
44	192.5	5.3	556	5	O95S93	O95S93 drosophila
45	192.5	5.3	1110	13	O91255	O91255 petromyzon

ALIGNMENTS

RESULT 1

Q60496	PRELIMINARY;	PRT:	695 AA.
AC	O60496;		
DT	01-NOV-1996 (TREMBLrel. Cl. Created)		
ET	01-NOV-1996 (TREMBLrel. 01, last sequence update)		
ET	01-OCT-2002 (TREMBLrel. 22, last annotation update)		
DF	Putative amyloid precursor protein.		
OS	Cavia sp.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.		
OX	NCBI_TaxID=10143;		
SN	[1]		
RP	SEQUENCE FROM N.A.		
RC	ISSUE=Brain;		
RX	MEDLINE=97236426; PubMed=9116031;		
RA	Beck M., Mueller D., Bigl V.;		
RT	"Amyloid precursor protein in Guinea pigs - complete cDNA sequence and		
R:	alternative splicing.";		
R:	Biochim. Biophys. Acta 1351:17-21(1997).		
DR	EMBL; X97631; CAA66230.1; -;		
DR	RSSP; P05067; IBA4.		
DR	InterPro; IPR001868; A4_APP.		
DR	InterPro; IPR002255; Beta_APP.		
DR	Pfam; PF02177; A4_EXTRA; 1.		
DR	Pfam; PF03494; Beta_APP; 1.		
DR	PR-NTS; PR02037; AMYLOIDA4.		
DR	SMART; SM00006; A4_EXTRA; 1.		
DR	PROSITE; PS00319; A4_EXTRA; 1.		
DR	PROSITE; PS00320; A4_INTRA; 1.		
SQ	SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;		

Query Match 97.6%; Score 3565; DB 11; Length 695;

Best Local Similarity 97.6%; Pred. No. 2e-206;

Matches 678; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAANTARALEVPTDGNAGLAEPQIAFMFCGRLLNMHMYNQNGKWDSPGSK 60

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MLPGLALLLTWTARALEVPTDGNAGLAEPQIAFMFCGRLLNMHMYNQNGKWEFDPGSK 60

QY 61 TCIDTKEGILQYCOEVYPELQITNWVEANQPTVIONWCKGRKCKOCTHPHFVPIYRCVLG 120
 DB 61 TCICSGEGILQYCOEVYPELQITNWVEANQPTVIONWCKGRKCKOCTHPHFVPIYRCVLG 120
 QY 121 EFVSDALLVPDKCFLEHQRMDVCEHLLHWHVAKETCSKSTNLHDYGMLLPGCIDKFR 160
 DB 121 EFVSDALLVPDKCFLEHQRMDVCEHLLHWHVAKETCSKSTNLHDYGMLLPGCIDKFR 160
 QY 181 GVEFVCCPLAESDNDVSDADEDDSDVMWGGADTDYADGSEDKVVEVAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNDVSDADEDDSDVMWGGADTDYADGSEDKVVEVAEVEEVAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTSVEEVEVVTPTAASPTDAA 300
 DB 241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTSVEEVEVVTPTAASPTDAA 300
 QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
 QY 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
 DB 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
 QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLHRYVERMNSLSLLYNVPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLHRYVERMNSLSLLYNVPAVA 480
 QY 481 BEIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVVLLPVNGEFSL 540
 DB 481 BEIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVVLLPVNGEFSL 540
 QY 541 DDLOPHSPFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTEISEVNMKDAEF 600
 DB 541 DDLOPHSPFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTEISEVNMKDAEF 600
 QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVITLVMLKKQYTSIHSGV 660
 DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVITLVMLKKQYTSIHSGV 660
 QY 661 VEYDAANTPEERHLSKMQQNGYENPTYKFFEQMON 695
 DB 661 VEYDAANTPEERHLSKMQQNGYENPTYKFFEQMON 695

RESULT 2

P97487
 ID P97487 PRELIMINARY; PRG: 695 AA.
 AC P97487; P97942;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Hippocampal amyloid protein.
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SAMP8; TISSUE-Hippocampus;
 RA Floed J.F., Kumar V.B., Sasser T., Word I., Morley J.E.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 581-662 FROM N.A.
 RC STRAIN-129SV;
 RA Wragg M.A., Basfield F., Duff K., Korenblat K., Capocchi M.,
 RA Loring J.P., Goate A.M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U84012; AAB41502.1;
 DR EMBL; U82624; AAB40919.1;
 DR HSSP; P05067; 1MWP.

MD; MG:188059; App.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78416 MW; 5A5FBRE2ED261236E CRC64;
 Query Match 96.7%; Score 3532; DB 11; Length 695;
 Best Local Similarity 97.0%; Pred. No. 1-9e-204;
 Matches 674; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAATARAALAEVPTDGNAGLLAEPOIAFMFCGLNMHNMVQNGKNDSPSGTK 60
 DB 1 MLPGLALLLAATARAALAEVPTDGNAGLLAEPOIAFMFCGLNMHNMVQNGKNDSPSGTK 60
 QY 61 TCIDTKEGILQYCOEVYPELQITNWVEANQPTVIONWCKGRKCKOCTHPHFVPIYRCVLG 120
 DB 61 TCIGIKEGILQYCOEVYPELQITNWVEANQPTVIONWCKGRKCKOCTHPHFVPIYRCVLG 120
 QY 121 EFVSDALLVPDKCFLEHQRMDVCEHLLHWHVAKETCSKSTNLHDYGMLLPGCIDKFR 180
 DB 121 EFVSDALLVPDKCFLEHQRMDVCEHLLHWHVAKETCSKSTNLHDYGMLLPGCIDKFR 180
 QY 181 GVEFVCCPLAESDNDVSDADEDDSDVMWGGADTDYADGSEDKVVEVAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNDVSDADEDDSDVMWGGADTDYADGSEDKVVEVAEVEEVAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTSVEEVEVVTPTAASPTDAA 300
 DB 241 EADDDDEDDGDEVEEAEPEYEATERTISATITTTTTSVEEVEVVTPTAASPTDAA 300
 QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
 QY 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
 DB 361 QKVESLEQEAANERQOLVETHMARVEAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
 QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLHRYVERMNSLSLLYNVPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLHRYVERMNSLSLLYNVPAVA 480
 QY 481 BEIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVVLLPVNGEFSL 540
 DB 481 BEIQDEVDLLOKEQNYSDVLANMISEPRISYGNDAIMPSTETKTTVVLLPVNGEFSL 540
 QY 541 DDLOPHSPFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTEISEVNMKDAEF 600
 DB 541 DDLOPHSPFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTEISEVNMKDAEF 600
 QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVITLVMLKKQYTSIHSGV 660
 DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIVITLVMLKKQYTSIHSGV 660
 QY 661 VEYDAANTPEERHLSKMQQNGYENPTYKFFEQMON 695
 DB 661 VEYDAANTPEERHLSKMQQNGYENPTYKFFEQMON 695

RESULT 3

Q9TUI0
 ID Q9TUI0 PRELIMINARY; PRG: 770 AA.
 AC Q9TUI0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Amyloid precursor protein.
 OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suiua; Suidae; Sus;
 OX NCBI_TaxID=9823;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RC "Amyloid precursor protein 770,"
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AB03255C; BAA84580.1;
 DR HSP: P05067; 1AAP.
 DK InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR ProDom: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM0131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Protease inhibitor; Serine protease inhibitor.
 SQ SEQUENCE 770 AA; 86961 MW; 577A1DCB28CC583E CRC64;

Query Match 96.6%; Score 3527.5; DB 6; Length 770;
 Best Local Similarity 98.2%; Pred. No. 4.1e-204;
 Matches 679; Conservative 9; Mismatches 7; Indels 75; Gaps 1;
 QY 1 MLPLGALLLAAMTARALEVPTDGNAGLLAEPOJAMFCGRNLNMHNVQNGKWDSPSGTK 60
 DB 1 MLPLGALLLAAMTARALEVPTDGNAGLLAEPOJAMFCGRNLNMHNVQNGKWDSPSGTK 60
 QY 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIQNMCKRKCKOCKTHPIVPIYRCVLG 120
 DB 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIQNMCKRKCKOCKTHPIVPIYRCVLG 120
 QY 121 EFVSDALLVPCKKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPCKKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVSDAEDDSDVWGGADIDYADGSDKVEVAEEVAEVEE 240
 DB 181 GVEFVCCPLAESDNVSDAEDDSDVWGGADIDYADGSDKVEVAEEVAEVEE 240
 QY 241 EADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVEVVR----- 288
 DB 241 EADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVEVVR----- 288
 QY 289 ---VPTTAASTPDAVDKYLETPDGENEHAHFQKAKERLEAKHRMSQVMREWEAEHQ 345
 DB 361 PVKLPDTTAASTPDAVDKYLETPDGENEHAHFQKAKERLEAKHRMSQVMREWEAEHQ 420
 QY 346 KNLPKADKKAVTQHFQEKVESIEQEAANERQOLVETHMARVEAM:NDRRRLALENYITAL 405
 DB 421 KNLPKADKKAVTQHFQEKVESIEQEAANERQOLVETHMARVEAM:NDRRRLALENYITAL 480
 QY 406 QAVPPRPRHVNMLKKYVRAEQDKROHTLKHFHVRVMYDPKKAQIRSQVMTHLRVIER 465
 DB 481 QAVPPRPRHVNMLKKYVRAEQDKROHTLKHFHVRVMYDPKKAQIRSQVMTHLRVIER 540
 QY 466 MNQSLSLLYNPVAAEETQDEVELLQKEONYSDVLANMISEPRISYGNALMPSLTET 525
 DB 541 MNQSLSLLYNPVAAEETQDEVELLQKEONYSDVLANMISEPRISYGNALMPSLTET 600
 QY 526 KTTVELLPVNGEFLDLDLQPHISFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTN 585

DB 60: KTTVELLPVNGEFLDLDLQPHISFGADSVPAANTENEVEPVDARPAADRGLTTRPGSLTN 660
 QY 586 IKTEE:SEVNCDAEFRHDSQYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITL 645
 DB 661 IKTEE:SEVNCDAEFRHDSQYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVITL 720
 QY 646 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695
 DB 721 VMLKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770
 RESULT 4
 Q9UGJ8
 ID Q9UGJ8 PRELIMINARY; PRT: 695 AA.
 AC Q9UGJ8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Beta-amyloid precursor protein 695 isoform.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolosse A., Sorribas V.;
 RC "Cloning of full-length chicken beta-amyloid precursor protein
 isoforms,"
 RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF289218; AAS00593.1;
 DR HSP: P05067; 1BA4.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;
 Query Match 93.7%; Score 3420; DB 13; Length 695;
 Best Local Similarity 93.7%; Pred. No. 1e-197;
 Matches 653; Conservative 18; Mismatches 22; Indels 4; Gaps 3;
 QY 1 MLPLGALLLAAMTARALEVPTDGNAGLLAEPOJAMFCGRNLNMHNVQNGKWDSPSGTK 60
 DB 1 MLPLGALLLAAMTARALEVPTDGNAGLLAEPOJAMFCGRNLNMHNVQNGKWDSPSGTK 60
 QY 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIQNMCKRKCKOCKTHPIVPIYRCVLG 120
 DB 61 TCIDTKEGILQYCOEVPPELOITNVVEANQPVTIQNMCKRKCKOCKTHPIVPIYRCVLG 120
 QY 121 EFVSDALLVPCKKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVPCKKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNVSDAEDDSDVWGGADIDYADGSDKVEVAEEVAEVEE 238
 DB 181 GVEFVCCPLAESDNVSDAEDDSDVWGGADIDYADGSDKVEVAEEVAEVEE 240
 QY 239 EEEADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVEVVRPTTAASPTD 298
 DB 241 EEEADDEDDDEDGEVEEAEPEEATEERTTSIATTTTTSVEEVEVVRPTTAASPTD 298
 QY 299 AVDKYLETPDGENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKKAVIQ 358
 DB 299 AVDKYLETPDGENEHAHFQKAKERLEAKHRMSQVMREWEAEERQAKNLPKADKKAVIQ 358
 QY 359 HFQKVESLEQEAANERQOLVETHMARVEAM:NDRRRLALENYITALQAVPPRPRHVN 418
 DB 359 HFQKVESLEQEAANERQOLVETHMARVEAM:NDRRRLALENYITALQAVPPRPRHVN 418


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Db 359 HFQKVESLEQFAANERQOLVETHMARVEMLNDHRRIALENYITACCTVPPRPRKHVYNN 418
Qy 419 LKKYVRAEOKDRQHTLKHFHVRYVDPKKAQIRSQVMTLKVYIERMNSLSLYNVA 478
Db 419 LKKYVRAEOKDRQHTLKHFHVRYVDPKKAQIRSQVMTLKVYIERMNSLSLYNVA 478
Qy 479 VABEIODEVDELLOKQNYSDVLANMISEPRISYGNALMPSLTETKYTVELLVNGEF 538
Db 479 VABEIODEVDELLOKQNYSDVLANMISEPRISYGNALMPSLTETKYTVELLVNGEF 538
Qy 539 SLDDLOPMISFAGDSVPANTENEVEPVDARPAADRGILTRPGSGLTNKTKEISELVNLA 598
Db 539 SLDDLOPMISFAGDSVPANTENEVEPVDARPAADRGILTRPGSGLTNKTKEISELVNLA 598
Qy 599 EFRHDSGYEVHOKLVFFAEDVGSNKGALIGLWGVGVYATVITVLVKKKKQYTSIH 658
Db 599 EFRHDSGYEVHOKLVFFAEDVGSNKGALIGLWGVGVYATVITVLVKKKKQYTSIH 658
Qy 659 GVVEVDAAVTPERILSKHQQNGYENPTYKFFEQMON 695
Db 659 GVVEVDAAVTPERILSKHQQNGYENPTYKFFEQMON 695

RESULT 5
Q98GJ7
ID Q98GJ7 PRELIMINARY; PRT: 751 AA.
AC Q98GJ7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolasse A., Sorribas V.:
RT "Cloning of full-length chicken beta-amyloid precursor protein
isoforms."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC289219; AAC00594.1; -.
DR HSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Kunitz_BP11.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_Bp1; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPHASE.
DR ProDom: PD000222; Kunitz_BP11; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS02079; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 92.5%; Score 3379; DR 13; Length 751;
Best Local Similarity 86.6%; Pred. No. 3 4e-199;
Matches 652; Conservative 19; Mismatches 22; Indels 50; Gaps 4;

Qy 1 MLPCALLLLAAWTAIAEVPITDGNAGLAEPQIAIFCGRLNMHNVQNGKWDSPGSK 60
Db 1 MLPCALLLLAAGAAALEVPADGNAGLAEPQIAIFCGRLNMHNVQNGKWDSPGSK 60
Qy 61 TCIDTREGILQYCOEYPPYLQITNVVEANQPTIOWCKRGKQCKTPEHFVIFRCLVG 120
Db 61 TCIDTREGILQYCOEYPPYLQITNVVEANQPTIOWCKRGKQCKGPHFIVVYRCLVG 120

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Qy 121 EFVSALLVPDKCKFLHOERMDVCEIHLHWHIVAKETSCSTNLHDYGMILPGCIDKFR 180
Db 121 EFVSALLVPDKCKFLHOERMDVCEIHLHWHIVAKETSCSTNLHDYGMILPGCIDKFR 180
Qy 181 GYEFVCCPLAESDNDVSDADAEEDSDVWVGGAUTDYADGSEDKVVE--VAEEVEVAEVE 238
Db 181 GYEFVCCPLAESDNDVSDADAEEDSDVWVGGAUTDYADGSEDKVVE--VAEEVEVAEVE 238
Qy 239 EBEADDDDDDDGDEVEEAEPEEATERISATITITITITITITITITITITITITITIT 288
Db 241 DECADD--DDDDGDEI-BETHEEVEEATERISATITITITITITITITITITITITIT 298
Qy 289 -----VPTTAATPDPAVDK 302
Db 299 PCRAMISRMYPDVAEGKCAPFFYGGCGGNRNNEFDEEYCMVCGSVLPTTAATPDPAVDK 358
Qy 303 YLETPGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKAVIOHFQE 362
Db 359 YLETPGDENEHAHFOKAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKAVIOHFQE 418
Qy 363 KYESLEQSAANERQOLVETHMARVEMLNDHRRIALENYITALQAVPPRPHVFNMLKKY 422
Db 419 KYESLEQSAANERQOLVETHMARVEMLNDHRRIALENYITALQAVPPRPHVFNMLKKY 478
Qy 423 VRAEOKDRQHTLKHFHVRYVDPKKAQIRSQVMTLKVYIERMNSLSLYNVAEAE 482
Db 479 VRAEOKDRQHTLKHFHVRYVDPKKAQIRSQVMTLKVYIERMNSLSLYNVAEAE 538
Qy 483 IQHWDELQKQNYSDVLANMISEPRISYGNALMPSLTETKYTVELLVNGEFSLDD 542
Db 539 IQHWDELQKQNYSDVLANMISEPRISYGNALMPSLTETKYTVELLVNGEFSLDD 598
Qy 543 LQPMISFAGDSVPANTENEVEPVDARPAADRGILTRPGSGLTNKTKEISELVNLADEF 602
Db 599 LQPMISFAGDSVPANTENEVEPVDARPAADRGILTRPGSGLTNKTKEISELVNLADEF 658
Qy 603 DSGYEVHOKLVFFAEDVGSNKGALIGLWGVGVYATVITVLVKKKKQYTSIHGWE 662
Db 659 DSGYEVHOKLVFFAEDVGSNKGALIGLWGVGVYATVITVLVKKKKQYTSIHGWE 718
Qy 663 VDAAVTPERHLSKMQNGYENPTYKFFEQMON 695
Db 719 VDAAVTPERHLSKMQNGYENPTYKFFEQMON 751

RESULT 6
Q98SC0
ID Q98SC0 PRELIMINARY; PRT: 593 AA.
AC Q98SC0;
DI 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein A.
DE CN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hark W.H.:
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1; -.
DR HSP: P05067; IZH3.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.

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DR PROSITE: PS00319; A4_EXTRA: 1.
DR PROSITE: PS00320; A4_INTRA: 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF659C1AB653 CRC64;

Query Match 87.8%; Score 3206; DB 13; Length 693;
Best Local Similarity 87.5%; Pred. No. 7.9e-185;
Matches 610; Conservative 37; Mismatches 44; Indels 6; Gaps 4;

Qy 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRINMHMNYONGKWDSPDSGTX 60
Db 1 MLPHTLLVLTV-GALALEVPADGNGLLAEPOIAMFCGKLNMHMNYONGKWEIDVSGTX 59

Qy 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONMCKRCKOCKKTHPHFVPIYPCVLG 120
Db 60 CGICGTEGILQYCOEYVPELQITNVVEANQPVTIONMCKRCKOCKKSRTHVWPYRCLVG 119

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHYVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
Db 120 EFVSDALLVPDKCKFLHQERMDICETHLHWHYVAKESKSKMSLSHEYGMLLPGCIDKFR 179

Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWGGADTDYADGSEDKVVA--EEEFVAVAE 238
Db 180 GVEFVCCPSAESSEFSADSA-EDSDAWGGADYVDRSDDKRAVEAQPDEEEVEVE 238

Qy 239 EEEADDDDEDDGEVEEAEPEYEEATERTSTTATTTTIESVEEVVPTTAASPD 298
Db 239 EEEADDDDEDDGEVEEAEPEYEEATERTSTTATTTTIESVEEVVPTTAASPD 296

Qy 299 AVDKYLETPGDENEHAFQKAKERLEAKHRMSQVWREWEAEACQAKLPKADKAVIQ 358
Db 297 AVDKYLENPNDENEHDFLKAERLEKGRHEKMSVWKEWEAEAEQAKNEPKADKAVIQ 356

Qy 359 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFN 418
Db 357 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQADPPRPHVFN 416

Qy 419 LKKYVRAQOKRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVIVERNMOSLSLLYNVA 478
Db 417 LKKYVRAQOKRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVIVERNMOSLSLLYNVA 476

Qy 479 VAEETQCEVDELLOKEQNYSDVLANNMISEPRISYGNALAKPSLTKTTVELLPVNGEF 538
Db 477 VAEETQCEVDELLOKEQNYSDVMNMVSDHRVSYGNALAKPSLTKTTVELLPVNGEF 536

Qy 539 SLDDQLQPHSFAGDVPANTENEVEFVDARPAADRGLTTRPGSGLINIKTEEISEVNLD 598
Db 537 NIEDQLQPHSFAGDVPANTENEVEFVDARPAADRGLTTRPGSGLINIKTEEISEVKMS 596

Qy 599 EFRHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMGVGVVATVITVLMLKKKQYTSIH 658
Db 597 EYRHDTAVEVHHQKLVFFAEADVGSNKGAIIGLMGVGVVATVITVLMLKKKQYTTIH 656

Qy 659 GVEVDAAVTPPEERHLSKMQONGYENPTYKFEFQMQN 695
Db 657 GVEVDAAVTPPEERHLSKMQONGYENPTYKFEFQMQN 693

RESULT 7
Q98SF9 PRELIMINARY; PRT; 695 AA.
AC Q98SF9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
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[1]
KV SEQUENCE FROM N.A.
RA Va: den Hurk W.R.;
RI Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298151; CAC37194.1;
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PR-NTS: PR00203; AMYLOIDA4.
DR SMART: SM00066; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 695 AA; 78603 MW; DC14EB02AFB0204A CRC64;

Query Match 87.2%; Score 3182; DB 13; Length 695;
Best Local Similarity 87.0%; Pred. No. 2.2e-183;
Matches 607; Conservative 40; Mismatches 45; Indels 6; Gaps 5;

Qy 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRINMHMNYONGKWDSPDSGTX 60
Db 1 MLPHTLLVLTV-GALALEVPADGNGLLAEPOIAMFCGKLNMHMNYONGKWEIDVSGTX 59

Qy 61 TCIDTKESILQYCOEYVPELQITNVVEANQPVTIONMCKRCKOCKKTHPHFVPIYPCVLG 120
Db 60 CGICGTEGILQYCOEYVPELQITNVVEANQPVTIONMCKRCKOCKKSRTHVWPYRCLVG 119

Qy 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHYVAKETCSEKSTNLHDYGMLLPGCIDKFR 180
Db 120 EFVSDALLVPDKCKFLHQERMDICETHLHWHYVAKESKSKMSLSHEYGMLLPGCIDKFR 179

Qy 181 GVEFVCCPLAESDNVDSADAEEDSDVWGGADTDYADGSEDKVVE--AAEEVEAEVE 238
Db 180 GVEFVCCPSAESSEFSADSA-EDSDVWGGADYVDRSDDKRAVEAQPDEEEVEVE 238

Qy 239 EEEADDDDEDDGEVEEAEPEYEEATERTSTTATTTTIESVEEVV-VPPTAASPT 297
Db 239 EEEADDDDEDDGEVEEAEPEYEEATERTSTTATTTTIESVEEVVAVPATAVSP 297

Qy 298 AVDKYLETPGDENEHAFQKAKERLEAKHRMSQVWREWEAEAEQAKN-LPKADKAVI 357
Db 298 AVDKYLENPNDENEHDFLKAERLEKGRHEKMSVWKEWEAEAEQAKN-LPKADKAVI 357

Qy 358 HFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFN 417
Db 356 HFQEVESLEQEAANERQQLVETHMARVEATLNDRRRLALENYITALQADPPRPHVFN 417

Qy 418 MLKKYVRAQOKRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVIVERNMOSLSLLYNVP 477
Db 418 MLKKYVRAQOKRQHTLKHFEHVRWDPKKAQIRSQVMTHLRVIVERNMOSLSLLYNVP 477

Qy 478 AVAEETQCEVDELLOKEQNYSDVLANNMISEPRISYGNALAKPSLTKTTVELLPVNGE 537
Db 478 AVAEETQCEVDELLOKEQNYSDVMNMVSDHRVSYGNALAKPSLTKTTVELLPVNGE 537

Qy 538 FSLDDQLQPHSFAGDVPANTENEVEFVDARPAADRGLTTRPGSGLINIKTEEISEVNLD 597
Db 538 FVVEDQLQPHSFAGDVPANTENEVEFVDARPAADRGLTTRPGSGLINIKTEEISEVKMD 597

Qy 598 AEFHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMGVGVVATVITVLMLKKKQYTSIH 657
Db 598 SEYRHDAAYEVHHQKLVFFAEADVGSNKGAIIGLMGVGVVATVITVLMLKKKQYTTIH 657

Qy 658 HGVVEVDAAVTPPEERHLSKMQONGYENPTYKFEFQMQN 695
Db 658 HGVVEVDAAVTPPEERHLSKMQONGYENPTYKFEFQMQN 695

RESULT 8
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Q91963          PRELIMINARY;          PRT: 747 AA.
ID Q91963
AC 01-NOV-1996 (TREMREL.01, Created)
DT 01-NOV-1996 (TREMREL.01, Last sequence update)
DT 01-MAR-2003 (TREMREL.23, Last annotation update)
DE APP747.
GN APP747.
CS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1282805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1563(1992).
DR EMBL; S52417; AAB34853.1;
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Kunitz_BPT1.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_Bpt1; 1.
DR PRINTS; PR00263; AMYLOIDA4.
DR PRINTS; PR00759; SAS-CPTASE.
DR PRODOM; PD000222; Kunitz_BPT1; 1.
DR SMART; SM00331; K0; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00260; BPT1_KUNITZ_1; 1.
DR PROSITE; PS00279; BPT1_KUNITZ_2; 1.
DR PROSITE; PS00279; Serine protease inhibitor.
KW Protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E8188581D949 CRC64;

Query Match 84.8%; Score 3095; DB 13; Length 747;
Best Local Similarity 80.8%; Pred. No. 4, 2e-178;
Matches 596; Conservative 36; Mismatches 42; Indels 64; Gaps 5;

Qy 17 ALEVPDGNAGLLAEPOAMF-CGRLNHMHNVQNKWDSPSGTKCTIDFKEGLDYQCF 75
Db 15 ALEVLVDGNGLLAEPOAMFVARLNHMHNVQNKWDSPSGTKCTIDFKEGLDYQCF 71
Qy 76 VYPELOITNVVEANOPVTIONCKRCKOCTHPHFVLPYRCLVGFVSDALLVPDKCF 135
Db 72 VYPELOITNVVEANOPVTIONCKRCKOCTSRTHVVPYRCLVGFVSDALLVPDKCF 131
Qy 136 LHOERMDVCETHLHHTVAKETCSKSTNLHDYGMPLPGC-DKFRGVEFVCCPLAESDN 195
Db 132 LHOERMDICETHLHHTVAKESCKSEKSLREYGMPLPGCIDKFRGVEFVCCPSARSES 191
Qy 196 VDSAAEDDSVWCGADTDVADGSEDKVVEVA-EFEVEAEVEEADDEDEGDE 253
Db 192 FDSAAEDDDCVWCGADTDVDRSGCKVRAQAEQDEEEVEVEEEDDEGDE -DGDE 249
Qy 254 VEEAEPEPEEATERTISATITTTTTSVEEVEVR----- 288
Db 250 ABEPEPEPEEATERTISATITTTTTSVEEVEVEVCGSEQAETGPCRAMISRWYDYE 309
Qy 289 -----VPTTAASTPDVADYKLETPDGENEHAHQ 317
Db 310 SKCAQFIYGGCGGNRRNFESDQYCMVCGSVIPATAASTPDVADYKLEPNDEHDFL 369
Qy 318 KAKERLEAKHREMSVYMEWEAEERQAKNLPKACKKAVIQHFQCKVLSLEQAEANRQ 377
Db 370 KAKERLEGHREKMSVEMWEAEERQAKNLPKADKAVIQHFQCKVLSLEQAEAKORQQ 425
Qy 378 LVETHMARVEAMLNDRRRALSNYITALQAVPPRRHVFNMLKKYVRAEQDRQHTLKH 437
Db 378 LVETHMARVEAMLNDRRRALSNYITALQAVPPRRHVFNMLKKYVRAEQDRQHTLKH 437

430 LVETHMARVEAMLNDRRRALSNYITALQAVPPRRHVFNMLKKYVRAEQDRQHTLKH 489
Qy 438 EHVWMDPKAAQIRSQVMTLRLVYIYERMNQSLSLLYNVPVAAVEEIQDEVDELQKQNY 497
Db 490 EHVWMDPKAAQIRSQVMTLRLVYIYERMNQSFSLLYKVPVAAVEEIQDEVDELQKQNY 549
Qy 498 SDDVLANMLSEPRISYGNDAIMPSTETKTTVELLPVNGEFSLDLQPHWHSFGADSPAN 557
Db 550 SDDVSNMVSDDRVSYGNDAIMPSTETKTTVELLPVNGEFSLDLQPHWHSFGADSPAN 609
Qy 558 TENVEPEVDARPAADRGLTTRPGSLGTNIKTEEISEVNLDAEFRHDSGYEVHVKLVFFA 617
Db 610 TENVEPEVDARPAADRGLTTRPGSLGTNIKTEEISEVNMDSYRHDITAYEVHVKLVFFA 669
Qy 618 EDVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIIHGIVVEVDAVTPERHLSKM 677
Db 670 EEVGSNKGAIIGLMVGGVVIATVITVLMLKKQYTSIIHGIVVEVDAVTPERHLSKM 729
Qy 678 QONGYENPTYKFFEQMN 695
Db 730 QONGYENPTYKFFEQMN 747

RESULT 9
Q57394          PRELIMINARY;          PRT: 699 AA.
ID Q57394
AC 057394
DT 01-JUN-1998 (TREMREL.06, Created)
DT 01-JUN-1998 (TREMREL.06, Last sequence update)
DT 01-OCT-2002 (TREMREL.22, Last annotation update)
DE EL amyloid precursor protein 699.
GN EL APP699.
OS Narke japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualea; Pristiogaster; Batoidae;
OC Torpediniformes; Narcinoidae; Naridae; Narke.
OX NCBI_TaxID=62965;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=98129705; PubMed=9461486;
RA Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA Suzuki T.;
RT "cDNA isolation of Alzheimer's amyloid precursor protein from
RT cholinergic nerve terminals of the electric organ of the electric
RT ray.";
RL Biochem. J. 330:29-33(1998).
DR EMBL; AB005544; BAA24230.1;
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 81.0%; Score 2956.5; DB 13; Length 699;
Best Local Similarity 80.5%; Pred. No. 8, 3e-170;
Matches 567; Conservative 59; Mismatches 59; Indels 19; Gaps 8;

Qy 2 LPG-LALLLAWTA-----RALEVPDGNAGLL-ABEQIAMFCGRLNHMHNVQNKW 52
Db 5 LPRLGMLLAAALVLAFLCLALEVPTDGGAGLLAEPOAMFCGRLNHMHNVQNKW 64
Qy 53 DSPSGTKCTIDFKEGLDYQCFVPELOITNVVEANOPVTIONCKRCKOCTHPHFV 112
Db 65 VDSPSGTNTCTFKEGLDYQCFVPELOITNVVEANOPVTIONCKRCKOCTHPHFV 124
Qy 113 IPYRCLVGFVSDALLVPDKCKFLHQRMDVCETHLHHTVAKETCSKSTNLHDYGM 172
Db 113 IPYRCLVGFVSDALLVPDKCKFLHQRMDVCETHLHHTVAKETCSKSTNLHDYGM 172

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Db 125 VPKRCLVGFVSALLVDFKCKFLHREKMDTCESHLWHTVAKETICGDKIMNLHDYGMIL 184
QY 173 PCGIDKFRGVFFVCCPLAESONWDSADAFEDDSFVWNGSACTDYAFGSHKXVVEVAEE 232
Db 185 PCGIDFRGVFFVCCPIFENDKIDS-DMEEDSDYWGSGDADYAFGG-DKTV-----EE 238
QY 233 EVAEEVEEEDDEDDEDGEVEEE-AEEFYEEATEERTTSIATTTTTSVEEVEVAVPT 291
Db 239 KPIEEEEEEDSDIDUEUDDLDDEVVVEQYEUPTHEHTS---STTTTAELEVVAVPT 295
QY 292 TAASTPDVADKYLLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNPKA 351
Db 296 TAASTPDVADKYLLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNPKA 355
QY 352 DKAVTQHFQEKVESLEGEAANERQGVETHMARVEAMLNDRRLALENYITALQAVPPR 411
Db 356 DKAVTQHFQEKVESLEGEAANERQGVETHMARVEAMLNDRRLALENYITALQAVPPR 415
QY 412 PRHVFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLVIYERMNQSLS 471
Db 416 PRHVLNMLKKYSRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLVIYERMNQSLS 475
QY 472 LLYNVPVAAEIQDEVELLQKEQNSDDVLANNMISEPRISYGNALMPSLTETKTIVEL 531
Db 476 LLYKVPVAAEIQDEVELLQKEQNSDDVLANNMISEPRISYGNALMPSLTETKTIVEL 535
QY 532 LPVNGEESLDDLOPHWSFGADSPANTENEVEPVDARPAADRGTLTRPGSGLTNKTEEI 591
Db 536 LPDQGEFIDDDLOPHWSPFVIESIPANTENEVEPVDARPAADRGTLTRPGSGLTNKTEEI 595
QY 592 SEYNLDAEFERHDSGYEVHVKLVFFAEVDGSKNGAIIGLMVGGVVATVITVLMKKK 651
Db 596 AELKMETEQDQSGYEVHVKLVFFAEVDGSKNGAIIGLMVGGVVATVITVLMKKK 655
QY 652 QYTSIHGGVVEVDAVTPERHLSKMQNGYENPTYKFFEQMON 695
Db 656 QYTSIHGGVVEVDAVTPERHLSKMQNGYENPTYKFFEQMON 699

RESULT 10
Q9PVL1 PRELIMINARY; PRT: 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CX NCBI_TaxID:9031;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RA Coulson E.J., Palliga K., Beyreuther K., Masters C.L.:
RI "What the evolution of the amyloid protein precursor supergene family
RJ tells us about its function."
RC Neurochem. Int. 0:0-0(2005).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA: 6475 MW: 0AB8B851863A19D CRC64;

Query Match 75.6%; Score 2759.5; DB 13; Length 569;
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Best Local Similarity 93.2%; Pred. No. 4 6e-158;
Matches 533; Conservative 15; Mismatches 19; Indels 5; Gaps 4;
QY 126 ALLVDPKCKFLHREKMDVCETHLWHTVAKETICSEKSNLHDYGMILPCGIDKFRGVFF 185
Db 1 ALLVDPKCKLLHQRMDVCETHLWHTVAKESCESEKSNLHDYGMILSCGIDKFRGVFF 60
QY 186 CQPLAESDNVDSADAFEDDSVWNGGADTDYADSESDKVE--VAEEVEVAEVEEAD 243
Db 61 CQPLAESDNVDSADAFEDDSVWNGGADTDYADSGDDKVVVEEQEPDELTWSEDEDAD 120
QY 244 DDEDEDDEDGEVEEAEFPYEATEKTTSIATTTTTSVEEVEVAVPTTAASPDAVKY 303
Db 121 DD-DDCDGDEI-EETEEVEEATEKTTSIATTTTTSVEEVEVAVPTTAASPDAVKY 178
QY 304 LETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNPKADKKAVIQHFOEK 263
Db 179 LETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNPKADKKAVIQHFOEK 238
QY 364 VESLGEAANERQGVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYV 423
Db 239 VESLGEAANERQGVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLKKYV 296
QY 424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLVIYERMNQSLSLLYNVPVAAE 483
Db 299 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLVIYERMNQSLSFLYNVPVAAE 358
QY 484 QDEVDLLOKEQNSDDVLANNMISEPRISYGNALMPSLTETKTIVELLPVNGEESLDD 543
Db 359 QDEVDLLOKEQNSDDVLANNMISEPRISYGNALMPSLTETKTIVELLPVNGEESLDD 418
QY 544 QPHWSFGADSPANTENEVEPVDARPAADRGTLTRPGSGLTNKITEEISEVNLDAEFERH 603
Db 419 QPHWSFGADSPANTENEVEPVDARPAADRGTLTRPGSGLTNKITEEISEVNLDAEFERH 476
QY 604 SGYEVHVKLVFFAEVDGSKNGAIIGLMVGGVVATVITVLMKKKQYTSIHGGVVEV 663
Db 479 SGYEVHVKLVFFAEVDGSKNGAIIGLMVGGVVATVITVLMKKKQYTSIHGGVVEV 536

RESULT 11
Q99K32 PRELIMINARY; PRT: 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 68.4 kDa protein (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC Submitted (MAX-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005490; AAF05490.1; -.
DR HSSP: P05067; 1AAP.
DR MGD: MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
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DR SMARI: SM0013.; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNIT2.1; 1.
DR PROSITE: PS00279; BPTI_KUNIT2.2; 1.
DR Hypothetical protein; Protease inhibitor; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 8391 MW; BF802214CBA7C172 CRC64;

Query Match
Best Local Similarity 85.3%; Score 2627.5; DB 11; Length 607;
Matches 518; Conservative 5; Mismatches 9; Indels 75; Gaps 1;

QY 164 NLHDYGMLLPGCIDKFRGVFCVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSED 223
DB 1 NLHDYGMLLPGCIDKFRGVFCVCCPLAESDSVDSADAEEDSDVMWGGADIDYADGSED 60
QY 224 KVEVAEEVAEEVAEEADDEDEDEDEVEEAEAEPEEATERTTSIATITTTTTE 283
DB 61 KVEVAEEVAEEVAEEADDEDEDEVEEAEAEPEEATERTTSIATITTTTTE 120
QY 284 EFVVR----- 285
DB 121 EGVREVCSEAGETGCRAMISRWFVDTGKVPFFYGGCGGRNNPDTFEYGMVCGS 180
QY 289 -----VPTTAASTPDADVCKYLETPGSENEHAHFQAKERLEAKHR 328
DB 181 VSTOSLLAKTTSEPLPQDDPKLPTTAASTPDADVCKYLETPGSENEHAHFQAKERLEAKHR 240
QY 329 ERMSQVMEWEAEARQAKNLPKADKAVIQHFQEKVESLEQEAANEKQVETINARVEA 388
DB 241 ERMSQVMEWEAEARQAKNLPKADKAVIQHFQEKVESLEQEAANEKQVETINARVEA 300
QY 389 MLNDRRLALENYITALQAVPRPRSHVFNMLKKYVRAEQKDRQHTLKHFHVRVMDPKA 448
DB 301 MLNDRRLALENYITALQAVPRPRSHVFNMLKKYVRAEQKDRQHTLKHFHVRVMDPKA 360
QY 449 AQRISQVTHLRVIERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISE 508
DB 301 AQRISQVTHLRVIERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISE 420
QY 509 PRISVGNALMPSLTETKTVELLPVNGEFLSDLDLPWHSFGADSVPAANTEVEVPDAP 568
DB 421 PRISVGNALMPSLTETKTVELLPVNGEFLSDLDLPWHSFGADSVPAANTEVEVPDAP 480
QY 569 PAADRGLTRPGSLTNIKTTEISEVNLDAEFHDSGYEVHVKLVFFAEVDGSKNGAIL 628
DB 481 PAADRGLTRPGSLTNIKTTEISEVNLDAEFHDSGYEVHVKLVFFAEVDGSKNGAIL 540
QY 629 GLMVGGVVIATVITVLNMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYK 688
DB 541 GLMVGGVVIATVITVLNMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYK 600
QY 689 FFEOMQN 695
DB 601 FFEOMQN 607

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RESULT 12

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O93296 PRELIMINARY: PRT: 534 AA.
AC O93296;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M.; Oppenheim R.W.;
RA Milligan C.R.;
RI "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1; -.
DR #SSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match
Best Local Similarity 94.4%; Score 2605; DB 13; Length 534;
Matches 504; Conservative 14; Mismatches 12; Indels 4; Gaps 3;

QY 164 NLHDYGMLLPGCIDKFRGVFCVCCPLAESDNVDSADAEEDSDVMWGGADIDYADGSED 223
DB 3 NLHDYGMLLPGCIDKFRGVFCVCCPLAESDNLDSDAEEDSDVMWGGADADYADGSD 62
QY 224 KVEE--VAPEEVAEEVAEEADDEDEDEVEEAEAEPEEATERTTSIATITTTTTE 281
DB 63 KVEEESPEDEEETVVEDDDADD--DDGDEI--EETEEPEATERTTSIATITTTTTE 120
QY 282 SVEEVVRVPTTAASTPDADVCKYLETPGSENEHAHFQAKERLEAKHRMSQVMEWEAE 341
DB 121 SVEEVVRVPTTAASTPDADVCKYLETPGSENEHAHFQAKERLEAKHRMSQVMEWEAE 180
QY 342 ERKAKNLPKADKAVIQHFQEKVESLEQEAANEKQVETINARVEA 401
DB 181 ERKAKNLPKADKAVIQHFQEKVESLEQEAANEKQVETINARVEA 240
QY 402 ITALQAVPRPRSHVFNMLKKYVRAEQKDRQHTLKHFHVRVMDPKAAGLRISQVTHLRV 461
DB 241 ITALQVPRPRSHVFNMLKKYVRAEQKDRQHTLKHFHVRVMDPKAAGLRISQVTHLRV 300
QY 462 IYERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISEPRISVGNALMPS 521
DB 301 IYERMQSLSLLYNVPAVAEEIQDEVELLQKEQNSDDVLANMISEPRISVGNALMPS 360
QY 522 LLETKTVELLPVNGEFLSDLDLPWHSFGADSVPAANTEVEVPDAPADRLTRPGS 581
DB 361 LLETKTVELLPVNGEFLSDLDLPWHSFGADSVPAANTEVEVPDAPADRLTRPGS 420
QY 582 GLTNIKTTEISEVNLDAEFHDSGYEVHVKLVFFAEVDGSKNGAILGLMVGGVVIATVI 641
DB 421 GLTNVTEEVESEVKMDAEFRHDSGYEVHVKLVFFAEVDGSKNGAILGLMVGGVVIATVI 480
QY 642 VITVLMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYKFFEOMQN 695
DB 481 VITVLMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYKFFEOMQN 534

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RESULT 13

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O73683 PRELIMINARY: PRT: 780 AA.
AC O73683;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE beta-amyloid protein (Beta-APP) (A-beta)].
CN App.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

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OC Tetradontolidae; Tetradontidae; Tetradont.
 OX NCBI_TaxID=47145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98252138; PubMed=959580;
 RA Villard L., Tassone F., Crogorac-Jurcevic I., Clancy K., Gardiner K.
 RT "Analysis of pufferfish homologues of the A1-rich human APP gene."
 RL Gene 210:17-24 (1998).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GIP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X1-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
 CC BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR EMBL: AF018165; AAC41275.1; .
 DR HSP: P05067; I183.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; FALSE_NEG.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Serine protease inhibitor.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 780 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT CHAIN 652 724 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 19 711 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 712 732 POTENTIAL.
 FT DOMAIN 733 780 CYTOPLASMIC (POTENTIAL).
 FT SITE 323 382 BPTI/KUNITZ INHIBITOR.
 FT SITE 769 772 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 327 378 BY SIMILARITY.
 FT DISULFID 336 361 BY SIMILARITY.
 FT CARBOHYD 560 560 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;
 Query Match 70.3%; Score 2568; DB 13; Length 780;
 Best Local Similarity 65.3%; Pred. No. 2.3e+146;
 Matches 512; Conservative 71; Mismatches 95; Indels 106; Gaps 10;
 QY 7 LLLAAWTAARALEVPTDGNAGLLAEPQIAMFCGRNLMHMYVQNGKWDSEPGTX:C:DTK 66
 DB 8 LLLVAAASTLAAREVPTDMSGLLAEPQVAMFCGRNLMHMYVQNGKWDSEPGTX:C:DTK 67
 QY 67 EGILQYCEVPELQITNVVEANQPTVTONKCKGRKCKTSPHFVTPYRCLVGEFVSDA 126
 DB 68 EGILQYCEVPELQITNVVEANQPTVTONKCKGRKCKTSPHFVTPYRCLVGEFVSDA 127
 QY 127 LLVPDKCKFLHQRMDVCEHLHWHYVAKETCEKSTNEHDYGMLLPGCIDKFRGVERVC 186
 DB 128 LLVPDKCKFLHQRMDVCEHLHWHYVAKETCEKSTNEHDYGMLLPGCIDKFRGVERVC 187
 QY 187 CPLAESDNVDSADAEEDSDVWGGAGTIDVADGS-----EDKVVVEVAHFE 232
 DB 188 CP-AEAERDMDSIEKDADDSDVWGGAGNDYSDNSKVRPEPAEQCEQETREPSVVEEEBEG 246

QY 233 EVAEVEEEE-----ADGDEDEDGDEVEEAEAEPEEATERTISIA 273
 DB 247 EVAEDDEFEHMYLDTQDQDQDGHEDHAEADDEFEEDVCKTIDAPGESDDVDADETTNWA 306
 QY 274 ---TTTITTTESVEFYVR-----
 DB 307 MTITTTITTTESVEEYVMEFCWAHADTGPCTASMSYFQAVDQRTMYELMYGCGGGMN 366
 QY 269 -----VPTIAASTPDVADVKYLETHGDNENHAHFOKAKERLPAKHRRMSQ 333
 DB 367 NFESEEXCLSVCSVVPVTPSPSPDAVDHYLETAPDENEHAHFOKAKESLEAKHRRMSQ 426
 QY 334 VMREWEAEAOAKNLPKADKKAVIQHFOEKVESLEGEAANEERQOLVETHMARVEAMLNDR 393
 DB 427 VMREWEAEAOAKNLPKADKKAVIQHFOEKVESLEGEAANEERQOLVETHMARVEAMLNDR 486
 QY 394 RRLALENYITALQAVPPRPRHVFHMLKKYVRAEOKDQHTLKHFEHVRMYVDPKKAQAIRS 453
 DB 487 RRLALENYITALQODPPRPRHVFHMLKKYVRAEOKDQHTLKHFEHVRMYVDPKKAQAIRP 546
 QY 454 QVTHLRVITYERMNQSIILLYNPVPAABETODEVDELLQKEQNYSDVLANMISEPRISY 513
 DB 547 QVTLHRLVIERMNQSLGLLYKVGVAADITQDQV-ELLQREQAEMAQOLANLOTDRVSY 605
 QY 514 GNDALMPSLTETKTITVELLPVNGEFSLDDLPWH--SFGADSVDPANTENEVEPVDARPA 571
 DB 606 GNDALMPDQELGQADLLP--QEDTLGGVGFVHPESFN-----QLNTENQVEPVDSPTF 659
 QY 572 DRGLTTRPGSLTNIKTETISEVNLDAERHDSGYEVHHQKLVFAEDVGSNKGAIIGLM 631
 DB 660 ERGVPTRP---VIGKSMEAVALRMETEDRQSTEVYEVHHQKLVFAEDVGSNKGAIIGLM 716
 QY 632 VGVVIATVIVITLVMLKKQYTSIHGVVVEVDAVTPPEERHLSKMGQNGYENPIYKFFE 692
 DB 717 VGVVIATVIVITLVMLKKQYTSIHGHIEVDAVTPPEERHLSKMGQNGYENPIYKFFE 776
 QY 692 QMQN 695
 DB 777 QMQN 780
 RESULT 14
 Q90W28 PRELIMINARY; PRT: 738 AA.
 AC Q90W28
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Amyloid precursor protein.
 GN APPA OR APP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 SE SEQUENCE FROM N.A.
 RA Groth C., Lardelli M.;
 RT "Expression analysis of zebrafish app.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/ODJB databases.
 DR EMBL: AF389401; AAK64495.1; .
 DR ZFIN: ZDB-GENE-000616-13; appa.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta-APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta-APP; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD000222; Kunitz_BPTI; 1.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.

QY 653 YTSIHGVEVDAVTPERHLSKMQNGYENPTYKFEQMON 695
DB 652 YTSIHGVEVDAVTPERHLSKMQNGYENPTYKFEQMON 694

Search completed: October 2, 2003, 14:02:16
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:55:09 ; Search time 38.3333 seconds
(without alignments)
2886.063 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653

Sequence: 1 MLPGLALLLAAWTAALV.....QQNGYENPTYKFEQMKNK 697

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3653	100.0	697	21	AA198430 Human APP695-VF-KK
2	3653	100.0	697	22	AAE10637 Human amyloid prot
3	3653	100.0	697	22	AAE06867 Human amyloid prec
4	3653	100.0	697	22	AAU06611 Human amyloid prec
5	3653	100.0	697	22	AAU07210 Human beta-amyloid
6	3653	100.0	697	22	AAE02589 Human amyloid prec
7	3653	100.0	697	23	ABB78598 Human APP695-VF-KK
8	3646	99.8	697	21	AA198428 Human APP695-KK am
9	3646	99.8	697	22	AAE10635 Human amyloid prot

10	3646	99.8	697	22	AAE05865 Human amyloid prec
11	3646	99.8	697	22	AAU06609 Human amyloid prec
12	3646	99.8	697	22	AAU07208 Human beta-amyloid
13	3646	99.8	697	22	AAE02587 Human amyloid prec
14	3646	99.8	697	23	ABB78596 APP695 mutant A-be
15	3643	99.7	695	18	AAW19498 APP695 mutant A-be
16	3643	99.7	695	18	AAW19484 Human APP695-VF am
17	3643	99.7	695	21	AA198436 Human amyloid prot
18	3643	99.7	695	22	AAE10634 Human amyloid prec
19	3643	99.7	695	22	AAE08864 Human amyloid prec
20	3643	99.7	695	22	AAU05608 Human amyloid prec
21	3643	99.7	695	22	AAU07207 Human beta-amyloid
22	3643	99.7	695	22	AAE02586 Human amyloid prec
23	3643	99.7	695	23	ABB78595 Human APP695-VF pr
24	3638	99.6	697	21	AA198429 Human APP695-KK am
25	3638	99.6	697	22	AAE10636 Human amyloid prot
26	3638	99.6	697	22	AAE08866 Human amyloid prec
27	3638	99.6	697	22	AAU06610 Human amyloid prec
28	3638	99.6	697	22	AAU07209 Human beta-amyloid
29	3638	99.6	697	22	AAE02588 Human amyloid prec
30	3638	99.6	697	23	ABB78597 Human APP695-Sw-KK
31	3636	99.5	695	9	APP81892 Sequence of human APP695
32	3636	99.5	695	13	AAR26338 Homo sapi APP695 mutant A-be
33	3636	99.5	695	18	AAW19481 Human beta-amyloid
34	3636	99.5	695	19	AA198423 Amyloid precursor
35	3636	99.5	695	20	AA198421 Human APP695 amino
36	3636	99.5	695	21	AA198434 Human beta amyloid
37	3636	99.5	695	21	AA1984705 Human wild-type am
38	3636	99.5	695	22	AAE10632 Human wild-type am
39	3636	99.5	695	22	AAE06862 Human amyloid prec
40	3636	99.5	695	22	AAU06606 Human amyloid prec
41	3636	99.5	695	22	AAE02584 Human amyloid prec
42	3636	99.5	695	23	ABG32721 Human amyloid prec
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44	3636	99.5	695	23	AAE068315 Human amyloid prec
45	3636	99.5	695	24	ABB99604 Amino acid sequenc

ALIGNMENTS

RESULT 1
AA198430
ID AA198430 standard; Protein; 697 AA.

XX AA198430;

AC AA198430;

XX 03-AUG-2000 (first entry)

DT Human APP695-VF-KK amino acid sequence.

DE Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;

DE Alzheimer's disease; beta secretase site; APP695-VF-KK.

XX Homo sapiens.

XX W0200017369-A2.

XX 30-MAR-2000.

XX 23-SEP-1999; 99WQ-US20881.

XX 24-SEP-1998; 98US-0101594.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Gurney ME, Bienkowski MJ, Heinrichson RL, Parodi LA, Yan R;

XX WPL: 2000-303209/26.

XX N-PSDB; AAA15667.

XX New enzyme designated human aspartase useful in research into

PT Alzheimer's Disease is capable of cleaving amyloid protein precursor at

PT the beta secretase site to produce amyloid beta peptide -
 XX Claim 133; Page 148-153; 187pp; English.
 XX This sequence represents a modified version of the human amyloid
 CC precursor protein (APP) amino acid sequence. The sequence is used in an
 CC example of the method of the invention, to show that modification of APP
 CC increases beta amyloid protein processing. The invention relates to a
 CC protease (e.g. Asp2) capable of cleaving the beta secretase site of
 CC amyloid precursor protein (APP). The protease contains a sequence
 CC encoding the amino acid sequence DTG and a sequence encoding EDC or DTG
 CC separated by 100-1000 amino acids. When mutated the APP gene causes an
 CC autosomal dominant form of Alzheimer's disease. APP localises to the cell
 CC surface membrane and have a single C-terminal transmembrane domain.
 CC Proteolytic processing of APP produces the amyloid beta protein, which is
 CC possibly very important in Alzheimer's disease. The invention includes a
 CC nucleotide sequence encoding the protease, a vector containing the
 CC nucleotide sequence, and a cell line comprising the vector. Methods for
 CC screening for inhibitors of beta secretase activity are also given in the
 CC invention. The human aspartase protein and nucleotide sequences and the
 CC methods for identifying inhibitors of the protease, are useful in the
 CC treatment of and research in to Alzheimer's disease.
 XX
 SQ Sequence 697 AA:
 Query Match 100.0%; Score 3653; DB 21; Length 697;
 Best Local Similarity 100.0%; Pred. No. 8,30-257;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPGALLLAANTARALEVPTDGNAGLLAEPO:AMFGRLNMHMVQNGKWDSPGSK 60
 DB 1 MLPGALLLAANTARALEVPTDGNAGLLAEPO:AMFGRLNMHMVQNGKWDSPGSK 60
 QY 61 TCIDTKGILQYQEVYPELOITNVYFANQVPTIQNCKRGKQCKTHFHFVTPKCLG 120
 DB 61 TCIDTKGILQYQEVYPELOITNVYFANQVPTIQNCKRGKQCKTHFHFVTPKCLG 120
 QY 121 EFVSDALLVPDKCKLFHQESMDVCYETELHHTYAKETCSKSTNLHDYCMLEPQIDKPF 180
 DB 121 EFVSDALLVPDKCKLFHQESMDVCYETELHHTYAKETCSKSTNLHDYCMLEPQIDKPF 180
 QY 181 GVEFVCCPLAESDNDVSDAEEDSDVNGGAGTLYAGSEDKVVEAESEEAVALVEEL 240
 DB 181 GVEFVCCPLAESDNDVSDAEEDSDVNGGAGTLYAGSEDKVVEAESEEAVALVEEL 240
 QY 241 EADDEDEDGDEVEEAEPEYEATERTTS:ATTTTITTESVEYVVPVPTAASTPCAY 300
 DB 241 EADDEDEDGDEVEEAEPEYEATERTTS:ATTTTITTESVEYVVPVPTAASTPCAY 300
 QY 301 DKYLETGDENEHNFQAKERLEAKHREKRSQVMPREWEAEKQAKNLPKACKKAVIQHF 360
 DB 301 DKYLETGDENEHNFQAKERLEAKHREKRSQVMPREWEAEKQAKNLPKACKKAVIQHF 360
 QY 361 QEKVESLEQEAERQQLVETHARVEAMLNDRRLALENYITALQAVPPRPRIHVENMLK 420
 DB 361 QEKVESLEQEAERQQLVETHARVEAMLNDRRLALENYITALQAVPPRPRIHVENMLK 420
 QY 421 KYVRAEKDKQHTLUKHFHEHVMVDPKAAQIRSQVMTLHVYTERNQSLSLYNNPVA 480
 DB 421 KYVRAEKDKQHTLUKHFHEHVMVDPKAAQIRSQVMTLHVYTERNQSLSLYNNPVA 480
 QY 481 EEIOEVEDELLOKQNSDVLNMISEPRISYGNDAIMPSTETTTVELLPVNGEFSL 540
 DB 481 EEIOEVEDELLOKQNSDVLNMISEPRISYGNDAIMPSTETTTVELLPVNGEFSL 540
 QY 541 DDLOPWHSGADSPANTENEVEPVDAPPAADRGLTTRPGSGLTNKTETSEVKKDCAF 600
 DB 541 DDLOPWHSGADSPANTENEVEPVDAPPAADRGLTTRPGSGLTNKTETSEVKKDCAF 600
 QY 601 RHDGSEYVHHQKLVFFAEEDVGSNGKAIIGLWGWGVIATVIFITLVMLKKQVTSIHGGV 660
 DB 601 RHDGSEYVHHQKLVFFAEEDVGSNGKAIIGLWGWGVIATVIFITLVMLKKQVTSIHGGV 660

QY 661 VEYDAAVTPPERHLSKMQQNGVYENPTYKFEQMQNKK 697
 DB 661 VEYDAAVTPPERHLSKMQQNGVYENPTYKFEQMQNKK 697
 RESULT 2
 AAE10637
 ID AAE10637 standard; Protein: 697 AA.
 AC AAE10637:
 XX 10-DEC-2001 (first entry)
 DT Human amyloid protein precursor 695-VF-KK (APP695-VF-KK) isoform.
 DE Human; aspartyl protease 1; Aspl; amyloid precursor protein;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW Amyloid plaque; neuronal loss; proteolytic; neuroprotective;
 KW APP695-VF-KK; mutant; mutain.
 XX Homo sapiens.
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT Misc-difference 642 /note= "Wild-type Val substituted with Phe"
 PN GB2357767-A.
 XX 04-JUL-2001.
 PF 22-SEP-2000; 2000GB-0023315.
 XX 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99US-0404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX (PNA) PHARMACIA & UPJOHN CO.
 XX Bionkowksi M7, Gurney M.
 XX WPI: 2001-444208/48.
 CR N-PSDB: AAD17671.
 XX Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 XX Example 8; Page 120-122; 187pp; English.
 CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
 CC Aspl proteins which lack transmembrane domain or amino terminal
 CC domain or cytoplasmic domain and retains alpha-secretase activity
 CC and amyloid protein precursor (APP) processing activity. The proteins
 CC of the invention are useful for assaying hu-Aspl alpha-secretase
 CC activity, which in turn is useful for identifying modulators of
 CC hu-Aspl alpha-secretase activity, where modulators that increase
 CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
 CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Aspl proteolytic activity. The present sequence is human amyloid
 CC protein precursor 695-VF-KK (APP695-VF-KK) isoform. This sequence
 CC is obtained by the addition of two lysine residues (KK motif) at
 CC the C-terminus of APP695-VF isoform which is generated by the London
 CC mutation in APP695, where Val at position 642 is replaced with Phe.
 CC APP695-VF-KK isoform is useful for assaying the beta-secretase
 CC activity of human aspartyl protease 2a (hu-Asp2a) protein.

```
XX SQ Sequence 697 AA:
Query Match: 100.0%; Score 3653; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.3e-257;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPLGLALLLAATAWTALEVPIDGNAGLLAEPOIAMFCGRLNHNNHNVONGKWDSPSGTK 60
DB : MLPLGLALLLAATAWTALEVPIDGNAGLLAEPOIAMFCGRLNHNNHNVONGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKRGRKOCKTHPHFVYPRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKRGRKOCKTHPHFVYPRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQERMDVCFELHWHHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCFELHWHHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEFVCCPLAEESDNVDSACAEEDSDVWVGADTDYADGSEDKVVEVAEESEVAEVESE 240
DB 181 GVEFVCCPLAEESDNVDSACAEEDSDVWVGADTDYADGSEDKVVEVAEESEVAEVESE 240

QY 241 EADDDEDDGDEVESEAEPEEATERITTSIATITTTTESVEEVVYVPTTAASTPDVAV 300
DB 241 EADDDEDDGDEVESEAEPEEATERITTSIATITTTTESVEEVVYVPTTAASTPDVAV 300

QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSOVWREWEAEERQAKNLPKAKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSOVWREWEAEERQAKNLPKAKKAVIQHF 360

QY 361 QEKVESLEGEAANERQOLVETHHARVEAMLNDRKLALENYITALOAVPRPRHFVNMJK 420
DB 361 QEKVESLEGEAANERQOLVETHHARVEAMLNDRRRLALENYITALOAVPRPRHFVNMJK 420

QY 421 KYVRAEQKQROHTLKHFERVMYDPPKAAQIRSOVMTHLRVIYERNQSLSLLYNPAVA 480
DB 421 KYVRAEQKQROHTLKHFERVMYDPPKAAQIRSOVMTHLRVIYERNQSLSLLYNPAVA 480

QY 481 EETQDEVELLQEQNYSDVLANMISEPRISYGNDAKPSLTETKTYVELLPVNGEFSI 540
DB 481 EETQDEVELLQEQNYSDVLANMISEPRISYGNDAKPSLTETKTYVELLPVNGEFSI 540

QY 541 DLQPHSHSGADSVPAANTENEVEPDARPAADRLTRPGSGLTNKTETFEISEVKMDAEF 600
DB 541 DLQPHSHSGADSVPAANTENEVEPDARPAADRLTRPGSGLTNKTETFEISEVKMDAEF 600

QY 601 RHDSGYEVHRSQKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFILYMLKKKQYTSIHGCV 660
DB 601 RHDSGYEVHRSQKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFILYMLKKKQYTSIHGCV 660

QY 661 VEYDAAVTPFERHLSKMQONGYENPTYKTFEOMONKK 697
DB 661 VEYDAAVTPFERHLSKMQONGYENPTYKTFEOMONKK 697
```

RESULT 3

AAE06667

ID AAE06667 standard: Protein; 697 AA.

XX AC

AAE06667;

XX 23-OCT-2001 (first entry)

XX Human amyloid precursor protein 695-VF-KK (APP695-VF-KK) isoform.

XX Human; aspartyl protease; Asp; beta-amyloid precursor protein 695-VF-KK;
KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotropic;
KW neuroprotective; antisense therapy; gene therapy; APP695-VF-KK; mutant;
KW mutagen.

XX Homo sapiens.

```
OS Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 642
XX /note= "Wild type Val substituted with Phe"
XX WO200150829-A2.
XX 19-JUL-2001.
XX 09-MAY-2001; 2001WO-IB00799.
XX 03-MAY-2001; 2001WO-IB00799.
XX (SIEN/) BLENKOWSKI M J.
XX (GURN/) GURNEY M E.
XX (HEIN/) HEINRIKSON R L.
XX (PARC/) PARODI L A.
XX (YANE/) YAN R.
XX Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX WP1; 2001-483072/52.
XX N-PSDB; AAD13029.
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
XX protease 2, lacking Asp2 transmembrane domain and retaining beta
XX secretase activity of Asp2 useful for identifying inhibitors of Asp2
XX activity -
XX Example 8; Page 150-152; 185pp; English.
XX The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
XX precursor protein (APP) isoforms and their corresponding DNA molecules.
XX Human aspartyl proteases can act as beta-secretase proteases useful for
XX treating Alzheimer's disease. APP isoforms are useful for identifying
XX modulators of amyloid-beta peptide production, for use in designing
XX therapeutics for the treatment and prevention of Alzheimer's disease,
XX dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
XX and neuronal loss. APP isoforms are also used in methods for identifying
XX inhibitors and modulators of human Asp2 activity. The invention relates
XX to a method for identifying agents that modulate the activity of human
XX aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
XX as a means to screen in cellular assays for the inhibitors of beta- and
XX gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
XX polymerase chain reactions (PCR). The probes are useful for detecting
XX Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
XX blots. The present sequence is modified human: amyloid precursor
XX protein 695-VF-KK (APP695-VF-KK) isoform. APP695-VF-KK isoform is
XX obtained by addition of two Lys residues (KK motif) at the C-terminal
XX end of APP695-VF isoform. APP695-VF isoform is obtained by London V-F
XX mutation in APP695 isoform, where Val at position 642 is replaced with
XX Phe. APP695-VF-KK isoform is useful for assaying the beta-secretase
XX activity of human aspartyl protease 2a (Hu-Asp2a) protein.
XX Sequence 697 AA:
```

Query Match 100.0%; Score 3653; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.3e-257;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPLGLALLLAATAWTALEVPIDGNAGLLAEPOIAMFCGRLNHNNHNVONGKWDSPSGTK 60
DB 1 MLPLGLALLLAATAWTALEVPIDGNAGLLAEPOIAMFCGRLNHNNHNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKRGRKOCKTHPHFVYPRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKRGRKOCKTHPHFVYPRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCFELHWHHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCFELHWHHTVAKETSEKSTNLHDYGMLLPCGIDKFR 180

DB 361 QEKVESLEQEAANERQQLVETHMARVCAMLNDRRLALENYITLQAVPPRPFRHVFNNLK 420
QY 421 KYVRAEQKDRQHTLKHFEEHVRVMDPKKAAQIRSQVMTFLRVIVYERMNQSLSLAYNPFAVA 480
DB 422 KYVRAEQKDRQHTLKHFEEHVRVMDPKKAAQIRSQVMTFLRVIVYERMNQSLSLAYNPFAVA 480
QY 481 EEIQDEVDLLOKQNYSDQVCAAMISEPRISYNDALMPSLTETKTVVLLPVGESFL 540
DB 481 EEIQDEVDLLOKQNYSDQVCAAMISEPRISYNDALMPSLTETKTVVLLPVGESFL 540
QY 541 DDLOPWHSGADSVPAANTENEVEPVDARPAADRGLTTPGSGSLTNIKTEEISEVKMDAEF 600
DB 541 DDLOPWHSGADSVPAANTENEVEPVDARPAADRGLTTPGSGSLTNIKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGGVVIATVIFITLMLKKQYVSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGGVVIATVIFITLMLKKQYVSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 697
DB 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 697

RESULT 5

AAU07210 standard: Protein.: 697 AA.

AAU07210;
24-OCT-2001 (first entry)

Human beta-amyloid protein precursor, APP695-VF-KK.

Human: aspartyl protease 1; Asp-1; nootropic; neuroprotective;
aspartyl protease 2; Asp2; amyloid protein precursor; APP;
beta-secretase; Alzheimer's disease; APP695-VF-KK.

OS Homo sapiens.

Key Location/Qualifiers
Misc-difference 642

/note= "Wild type Val substituted by Phe"

WO200149097-A2.

12-JUL-2001.

09-MAY-2001: 2001WO-IB00797.

09-MAY-2001: 2001WO-IB00797.

(BIEN/) BIENKOWSKI M J.

(GURN/) GURNEY M E.

(HEIN/) HEINRIKSON R L.

(PARO/) PARODI L A.

(YANR/) YAN R.

Bienskowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

WPI: 2001-502548/55.

N-PSDB; AAS11710.

Novel purified polypeptide comprising fragment of mammalian aspartyl
protease 2, lacking Asp2 transmembrane domain and retaining beta

secretase activity of Asp2 useful for identifying inhibitors of Asp2
activity

Example 8: Page 150-152; 185pp; English.

The invention relates to a novel purified polypeptide comprising a
fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
and the fragment retain the beta-secretase activity of the mammalian Asp2

protein. Also included is an isoform of amyloid protein precursor (APP)
comprising the amino acid sequence of a APP or its fragment containing
an APP cleavage site recognisable by a mammalian beta-secretase, and
further comprising two lysine residues at the carboxyl terminus of the
amino acid sequence of the mammalian APP or APP fragment. The
polypeptides are used for assaying for modulators of beta-secretase
activity; identifying agents that inhibit the APP processing activity
of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
modulate the activity of Asp2; and for reducing cellular production of
amyloid beta (A β) from APP. Agents identified by the above methods
are useful for treating Alzheimer's disease; and for identifying
modulators of amyloid-beta (A β) peptide production, for use in
designing therapeutics for the treatment or prevention of Alzheimer's
disease. Probes and primers derived from Asp nucleic acid sequences
are useful for detecting Hu-Asp nucleic acids in vitro assays and in
Northern and Southern blots. The present sequence represents the
amino acid sequence of human amyloid protein precursor, APP695-VF-KK,
used in the method of the invention.

XX Sequence 697 AA:

Query Match 100.0%; Score 3653; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 8.3e-257;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLFGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNHNQNKWDSFGSK 60

DB 1 MLFGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNHNQNKWDSFGSK 60

QY 61 TCIDTKREGILQYCOEYVPELQITNVVEANOPVTIONNCKRQCKQTHPHFVPIYRCLVG 120

DB 61 TCIDTKREGILQYCOEYVPELQITNVVEANOPVTIONNCKRQCKQTHPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVFEVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

DB 181 GVFEVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVVRVPTTAASFPDAV 300

DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTTSVEEVVVRVPTTAASFPDAV 300

QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEAKNLPKADKKAVIQHF 360

DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEAKNLPKADKKAVIQHF 360

QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPFRHVFNNLK 420

DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPFRHVFNNLK 420

QY 421 KYVRAEQKDRQHTLKHFEEHVRVMDPKKAAQIRSQVMTFLRVIVYERMNQSLSLAYNPFAVA 480

DB 421 KYVRAEQKDRQHTLKHFEEHVRVMDPKKAAQIRSQVMTFLRVIVYERMNQSLSLAYNPFAVA 480

QY 481 EEIQDEVDLLOKQNYSDQVCAAMISEPRISYNDALMPSLTETKTVVLLPVGESFL 540

DB 481 EEIQDEVDLLOKQNYSDQVCAAMISEPRISYNDALMPSLTETKTVVLLPVGESFL 540

QY 541 DDLOPWHSGADSVPAANTENEVEPVDARPAADRGLTTPGSGSLTNIKTEEISEVKMDAEF 600

DB 541 DDLOPWHSGADSVPAANTENEVEPVDARPAADRGLTTPGSGSLTNIKTEEISEVKMDAEF 600

QY 601 RHDSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGGVVIATVIFITLMLKKQYVSIHGV 660

DB 601 RHDSGYEVHHOKLVFFAEADVGSNGKGAIGLMVGGVVIATVIFITLMLKKQYVSIHGV 660

QY 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 697

DB 661 VEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQMKNK 697

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RESULT 6
AAE02589
ID AAE02589 standard; Protein: 697 AA.
XX
AC AAE02589;
D- 10-AUG-2001 (first entry)
XX
DE Human amyloid precursor protein 695-VF-KK (APP695-VF-KK).
XX
KW Human; alpha-secretase; therapy: amyloid precursor protein 695-VF-KK;
KW APP695-VF-KK; Alzheimer's disease; Alzheimer's.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN W0200123533-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26080.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-0169232.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Gurney M, Bienkowski MJ;
XX
DR WPI: 2001-290516/30.
DR N-PSDB; AAD06747.
XX
PI Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
PS Example 8; Page 143-151; 189pp; English.
XX
CC The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human APP695-VF-KK. This
CC sequence is characterised by a V to P alteration at position 642
CC and contains two carboxy-terminal lysine residues.
XX
SQ Sequence 697 AA;
Query Match 100.0%; Score 3653; DB 22; Length 697;
Best Local Similarity 100.0%; Pred. No. 8,30-257;
Matches 697; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLEGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRGNHMHVQNGKWDSPGSK 60
DB 1 MLEGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGRGNHMHVQNGKWDSPGSK 60
QY 61 TCIDTREGILYCOEVYPE-QITNVVEANOPVTIQNMCKGRKCKTHPHFVTPYSCVAG 120
DB 61 TCIDTREGILYCOEVYPE-QITNVVEANOPVTIQNMCKGRKCKTHPHFVTPYSCVAG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTYAKETCSKSTNLHDYGMGLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCETHLHWHTYAKETCSKSTNLHDYGMGLPCGIDKFR 180
QY 182 GVEFVCCPLAESNDVSDAEDDDSDVMWGGADTDYADGSDKVEVEAEVEAEVEE 240
DB 182 GVEFVCCPLAESNDVSDAEDDDSDVMWGGADTDYADGSDKVEVEAEVEAEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVVPPTTAAAS:PDVA 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVVPPTTAAAS:PDVA 300

```

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DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTITTESVEEVVVPPTTAAAS:PDVA 300
QY 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERLEAKHREMSQVWREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 OEKVESLEQEAANEROQLVETHMARVEAMLNDRRLALENITALQAVPPRPHVFNMLK 420
DB 361 OEKVESLEQEAANEROQLVETHMARVEAMLNDRRLALENITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYIERMNGSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVYIERMNGSLLYNVPAVA 480
QY 481 PEIQDEVDELLOKEONYSDDLANKMISPPRISYNDALMPSLTETKTIVELLVNGEFSL 540
DB 481 PEIQDEVDELLOKEONYSDDLANKMISPPRISYNDALMPSLTETKTIVELLVNGEFSL 540
QY 541 DDLQPHSHFGADSVFANTENEVEPVDPADPAADRGLTTRPGSLTNIKTEEISEYKMDAEF 600
DB 541 DDLQPHSHFGADSVFANTENEVEPVDPADPAADRGLTTRPGSLTNIKTEEISEYKMDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNGKAIIGLMVGGVVIATVIFITLMLKKQYTSIIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEADVGSNGKAIIGLMVGGVVIATVIFITLMLKKQYTSIIHGV 660
QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQMONKK 697
RESULT 7
ABB78598
ID ABB78598 standard; Protein: 697 AA.
XX
AC ABB78598;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human APP695-VF-KK protein sequence SEQ ID NO:20.
XX
KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
KW proteolytic; amyloid precursor protein; APP.
XX
OS Homo sapiens.
XX
PN G52367050-A.
XX
PC 27-MAR-2002.
XX
PF 29-OCT-2001; 2001GB-C025934.
XX
PR 23-SEP-1999; 99US-155493P.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-US20881.
PR 13-OCT-1999; 99US-0416901.
PR 06-DEC-1999; 99US-169232P.
PR 22-SEP-2000; 2000GB-C023315.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Bienkowski MJ, Gurney M;
XX
DR WPI: 2002-396337/43.
DR N-PSDB; ABL52465.
XX
PT Human aspartyl protease 1 substrates useful in assays to detect
PT aspartyl protease activity, e.g. for the diagnosis of Alzheimer's
XX disease.
PS Example 8; Page 120-122; 182pp; English.
XX
CC The present invention describes a human aspartyl protease 1 (hu-Asp1)

```

CC substrate (I) which comprises a peptide of no more than 50 amino acids,
 CC and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-
 CC G-u-Pro. Also described are: (1) a method (II) for assaying hu-Asp1
 CC proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with
 CC (1) under acidic conditions; and (b) determining the level of hu-Asp1
 CC proteolytic activity; (2) a purified polynucleotide (III) comprising a
 CC nucleotide sequence that hybridises under stringent conditions to the
 CC non-coding strand complementary to a defined 1804 nucleotide sequence
 CC (see ABL52456) where the nucleotide sequence encodes a polypeptide having
 CC Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane
 CC domain; (3) a purified polynucleotide (IV) comprising a sequence that
 CC hybridises under stringent conditions to (III) (the nucleotide sequence
 CC encodes a polypeptide further lacking a pro-peptide domain corresponding
 CC to amino acids 23-62 of hu-Asp1 (see ABB76589)); (4) a vector (IV)
 CC comprising (III) or (III') and (5) a host cell (V) transformed or
 CC transcribed with (III), (III') and/or (IV). The hu-Asp1 protease
 CC substrate (I) may be used as an enzyme substrate in assays to detect
 CC aspartyl protease activity, (II) and therefore diagnose diseases
 CC associated with aberrant hu-Asp1 expression and activity such as
 CC Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while
 CC hu-Asp2 has been localised to chromosome 11q23.3-24.1. The present
 CC sequence represents human amyloid precursor protein APP695-VF-KK, which
 CC is given in an example from the present invention.

XX Sequence 697 AA;
 SQ Query Match 100.0%; Score 3653; DB 23; Length 697;
 Best Local Similarity 100.0%; Pred. No. 8.3e-257;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAFCGRNLNMHMYQNGKWDSPSGTK 60
 DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAFCGRNLNMHMYQNGKWDSPSGTK 60
 QY 61 TCIDTKESILYCOEYVPELQITNVVEANQPVTIQNMCKGRKCKOCTHPHFVIPPYCLVG 120
 DB 61 TCIDTKESILYCOEYVPELQITNVVEANQPVTIQNMCKGRKCKOCTHPHFVIPPYCLVG 120
 QY 121 EFVSDALLVPDKCFELHQRMDVCETHLHWHYVAKETCSKSTNLHDYGMGLPGIDKFR 180
 DB 121 EFVSDALLVPDKCFELHQRMDVCETHLHWHYVAKETCSKSTNLHDYGMGLPGIDKFR 180
 QY 181 GVEFVCCPLAESNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAESNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
 QY 241 EADDEDEDEGDEVEEAEPEEATERTTSIAITTTTTSVEEVVRVPTTAASTPDV 300
 DB 241 EADDEDEDEGDEVEEAEPEEATERTTSIAITTTTTSVEEVVRVPTTAASTPDV 300
 QY 301 DKYLETCDENEHAHFQAKERLEAKHRRMSQVWRWEAEERQAKNLPKADKKAVIQHF 360
 DB 301 DKYLETCDENEHAHFQAKERLEAKHRRMSQVWRWEAEERQAKNLPKADKKAVIQHF 360
 QY 361 QEKVESLEQEAERQOLVTHMARVZAMLNDRRLALENYITLQAVPPAPRUVENKJK 420
 DB 361 QEKVESLEQEAERQOLVTHMARVZAMLNDRRLALENYITLQAVPPAPRUVENKJK 420
 QY 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTFLRVYERMNQSLSLYNYPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTFLRVYERMNQSLSLYNYPAVA 480
 QY 481 EEIQDEVELLQKQNYSDVLANMISEPRISYNGDALMPSLTETKTVELLPVNGEFSL 540
 DB 481 EEIQDEVELLQKQNYSDVLANMISEPRISYNGDALMPSLTETKTVELLPVNGEFSL 540
 QY 541 DDLQPMHSFGADSPANTENEVEVDPAADRGLTTPGSGSLTNKTEFEISEYKMDAEF 600
 DB 541 DDLQPMHSFGADSPANTENEVEVDPAADRGLTTPGSGSLTNKTEFEISEYKMDAEF 600
 QY 601 RDSGYEVHHOKLVFFAEEDVGSNGKAIIGLMVGWGIATVFTFLVLMKKKQYTSIHGV 660
 DB 601 RDSGYEVHHOKLVFFAEEDVGSNGKAIIGLMVGWGIATVFTFLVLMKKKQYTSIHGV 660

QY 661 VEVDAAVPEERHLSKMQNGYENPTYKFFEQMNKK 697
 DB 661 VEVDAAVPEERHLSKMQNGYENPTYKFFEQMNKK 697
 RESULT 2
 AAY8428
 ID AAY8428 standard; Protein: 697 AA.
 XX AAY8428;
 AC AAY8428;
 DT 03-AUG-2000 (first entry)
 XX Human APP696-KK amino acid sequence.
 LE Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 2;
 KW Alzheimer's disease; beta secretase site; APP696-KK.
 XX Homo sapiens.
 OS Homo sapiens.
 XX W0200017369-A2.
 XX 30-MAR-2000.
 XX 23-SEP-1999; 59WK0-US20881.
 XX 24-SEP-1998; 98US-0101594.
 XX (PHAA) PHARMACIA & UPJOHN CO.
 XX Gurney ME, Bienkowski MJ, Heinrikson RJ, Parodi LA, Yan R;
 XX WPI: 2000-303209/26.
 DR N-PSDB; AAA15665.
 XX
 PI New enzyme designated human aspartase useful in research into
 PI Alzheimer's disease is capable of cleaving amyloid protein precursor at
 PI the beta secretase site to produce amyloid beta peptide -
 XX Claim 132: Page 137-141; 183pp; English.
 XX This sequence represents a modified version of the human amyloid
 XX precursor protein (APP) amino acid sequence. The sequence is used in an
 XX example of the method of the invention, to show that modification of APP
 XX increases beta amyloid protein processing. The invention relates to a
 XX protease (e.g. Asp2) capable of cleaving the beta secretase site of
 XX amyloid precursor protein (APP). The protease contains a sequence
 XX encoding the amino acid sequence DTG and a sequence encoding DSG or DTG
 XX separated by 100-300 amino acids. When mutated the APP gene causes an
 XX autosomal dominant form of Alzheimer's disease. APP localises to the cell
 XX surface membrane and have a single C-terminal transmembrane domain.
 XX Proteolytic processing of APP produces the amyloid beta protein, which is
 XX possibly very important in Alzheimer's disease. The invention includes a
 XX nucleotide sequence encoding the protease, a vector containing the
 XX screening for inhibitors of beta secretase activity are also given in the
 XX invention. The human aspartase protein and nucleotide sequences and the
 XX methods for identifying inhibitors of the protease, are useful in the
 XX treatment of and research in to Alzheimer's disease.
 SQ Sequence 697 AA;
 Query Match 99.8%; Score 3646; DB 21; Length 697;
 Best Local Similarity 99.9%; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAFCGRNLNMHMYQNGKWDSPSGTK 60
 DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAFCGRNLNMHMYQNGKWDSPSGTK 60
 QY 61 TCIDTKESILYCOEYVPELQITNVVEANQPVTIQNMCKGRKCKOCTHPHFVIPPYCLVG 120
 DB 61 TCIDTKESILYCOEYVPELQITNVVEANQPVTIQNMCKGRKCKOCTHPHFVIPPYCLVG 120

Db 61 TCIDTKEGILQYCEVYPPELQITNVVEANQPV:IQNWCKRGRKQCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSNLHGYGMLLPCGICKER 280
DB 122 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSNLHGYGMLLPCGICKER 280
QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKYVEVAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKYVEVAEVEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPPEYEAETRTSTATTITTTTSTTTTSTTTTSTTTTSTTTT 300
DB 241 EADDDDEDDGDEVEEAEPPEYEAETRTSTATTITTTTSTTTTSTTTTSTTTTSTTTT 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREFEAEERCAKMLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREFEAEERCAKMLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
QY 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
DB 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
QY 541 DDQLPHSFGADSVAPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEISVKNDAEF 600
DB 541 DDQLPHSFGADSVAPANTENEVEPVDARPAADRGLTTRPGSGLTNKTETSEISVKNDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGGVVIATVIFLVLVNLKKOYTSIHHGV 660
DB 601 RHDSGYEVHHQKLVFFAEDVGSNKGATIGLWGGVVIATVIFLVLVNLKKOYTSIHHGV 660
QY 661 VEYDAAVTPPEERHLSKMOQNGYENPTYKFFEOQNK 697
DB 661 VEYDAAVTPPEERHLSKMOQNGYENPTYKFFEOQNK 697

RESULT 9

AAE10635
ID AAE10635 standard; Protein: 697 AA.
AC AAE10635;
XX
DT 10-DEC-2001 (first entry)
DE Human amyloid protein precursor 695-KK (APP695-KK) isoform.
XX
KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP695-KK;
KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KW amyloid plaque; neuronal loss; proteolytic; neurotrophic; neuroprotective.
OS Homo sapiens.
OS Synthetic.
XX GB2357767-A.
XX
PD 04-JUL-2001.
XX
PF 22-SEP-2000; 2000GB-0023315.
XX
PR 23-SEP-1999; 99US-0155493.
PR 23-SEP-1999; 99US-0404133.
PR 23-SEP-1999; 99WO-0520881.
PR 13-OCT-1999; 99US-0416901.
XX 06-DEC-1999; 99US-0169232.
XX
PA (PHAA) PHARMACIA & UPJOHN CO.

XX FI Bienkowski MJ, Gurney M;
XX WPI; 2001-444208/46.
DR N-PSDB: AAD17871.
XX
PT Polypeptide comprising fragments of human aspartyl protease with
PT amyloid precursor protein processing activity and alpha-secretase
PT activity, for identifying modulators useful in treating Alzheimer's
PT disease -
XX
XX Example 6: Page 114-116; 187pp; English.
XX
CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified
CC Aspl proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Aspl alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Aspl alpha-secretase activity, where modulators that increase
CC hu-Aspl alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Aspl protease substrate is useful for assaying
CC hu-Aspl proteolytic activity, by contacting hu-Aspl protein with
CC the substrate under acidic conditions and determining the level of
CC hu-Aspl proteolytic activity. The present sequence is human amyloid
CC protein precursor 695-KK (APP695-KK) isoform which is obtained by
CC the addition of two Lys residues (KK motif) at the C-terminus of
CC APP695 protein.
XX
SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 22; Length 697;
Best local Similarity 99.9%; Pred. No. 2,7e-256;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAMFCGRLMHNMVQNGKWDSPSCTK 60
DB 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAMFCGRLMHNMVQNGKWDSPSCTK 60
QY 61 TCIDTKEGILQYCEVYPPELQITNVVEANQPV:IQNWCKRGRKQCKTHPHFVPIYRCVLG 120
DB 61 TCIDTKEGILQYCEVYPPELQITNVVEANQPV:IQNWCKRGRKQCKTHPHFVPIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSNLHGYGMLLPCGICKER 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSNLHGYGMLLPCGICKER 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKYVEVAEVEEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGGADTDYADGSEDKYVEVAEVEEVAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPPEYEAETRTSTATTITTTTSTTTTSTTTTSTTTTSTTTT 300
DB 241 EADDDDEDDGDEVEEAEPPEYEAETRTSTATTITTTTSTTTTSTTTTSTTTTSTTTT 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREFEAEERCAKMLPKADKAVIOHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREKRSQVWREFEAEERCAKMLPKADKAVIOHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVWTHLRVIYERNQSLSLYNYPAVA 480
QY 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540
DB 481 EEIQDEVELLQKEQNYSDOVLANNMISEPRISYGNDAIMPSTETKTVELLPVNGEFSL 540

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 696..697
 FT /note= "2 Extra Lys residues added compared to
 FT wild-type APP695".
 XX WC200149098-A2.
 XX 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-1B00798.
 XX 09-MAY-2001; 2001WO-1B00798.
 XX (BIEN/) BIENKOWSKI M J.
 XX (GURNEY/) GURNEY M E.
 XX (HEIN/) HEINRIKSON R L.
 XX (PARO/) PARODI L A.
 XX (YANR/) YAN R.
 XX Blenkowski MJ, Gurney MF, Heinrichson RL, Parodi LA, Yan R;
 DR MPI: 2001-502549/55.
 DR N-PSDB; AAS11523.
 XX Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity .
 XX Example 6: Page 144-146; 185pp; English.
 XX The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp2) protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp
 CC proteins and vectors expressing them, and a polypeptide (isoform of
 CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
 CC APP or its fragment containing an APP cleavage site recognizable by a
 CC mammalian beta-secretase, and further comprising two lysine residues at
 CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
 CC APP fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and
 CC amyloid/beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease.
 CC APP comprising the App-Sw-beta-secretase peptide sequence (N2A), which
 CC is associated with increased levels of Abeta processing is useful in
 CC assays relating the Alzheimer's research. The expression vector is useful
 CC for recombinantly expressing APP. Nucleic acids that hybridize to
 CC Asp oligonucleotides are useful as probes or primers. The probes are
 CC useful for detecting hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence is the human
 CC APP695 mutant, APP695-KK which has 2 extra Lys residues added at
 CC the C-terminus compared to the wild-type APP695. The mutation alters the
 CC specificity of the APP gamma-secretase activity and increases the rate
 CC of processing of the amyloid Abeta peptide.
 XX Sequence 697 AA:
 SQ
 Query Match 99.8%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLPGLALLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNHNMVQNGKWDSPSGTK 60
 Db 1 MLPGLALLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRLNHNMVQNGKWDSPSGTK 60
 QY 61 TCIDTKEGILQYCOEVYPELQIINVVEANOPVTIONWCKRCKRCKTHPHFVPIYRCLVG 120
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 61 TCIDTKEGILQYCOEVYPELQIINVVEANOPVTIONWCKRCKRCKTHPHFVPIYRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHHTYAKETCSEKSTKLHDYGMLLPGIDKFR 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHHTYAKETCSEKSTKLHDYGMLLPGIDKFR 180
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 GVEFVCCPLAESDNVDSAAAEEDSDVMWGGADTDYADGSEDPKVVVAEEFFVAEVEE 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GVEFVCCPLAESDNVDSAAAEEDSDVMWGGADTDYADGSEDPKVVVAEEFFVAEVEE 240
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 EADDEDEDEGDEVEEEAEPEEATERTTSIAITTTTTTIESVFEVVVVPITTAASTPIAV 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 EADDEDEDEGDEVEEEAEPEEATERTTSIAITTTTTTIESVFEVVVVPITTAASTPIAV 300
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 DKYLETGGDENEHAFQKAKERLEAKHPRMSQVMREWEAEARQAKNLPRADKKAVTOHF 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 DKYLETGGDENEHAFQKAKERLEAKHPRMSQVMREWEAEARQAKNLPRADKKAVTOHF 360
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMK 420
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMK 420
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 421 KYRAEQKDRQHTLKFHFHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNPVA 480
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 KYRAEQKDRQHTLKFHFHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYNPVA 480
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 481 EEIODEVDELQKQONYSDDVLANNISEPRISYNDALMPSLTETKTIVELLPVNGEFSL 540
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 EEIODEVDELQKQONYSDDVLANNISEPRISYNDALMPSLTETKTIVELLPVNGEFSL 540
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 541 DDLOPHWSFGADSVPAANTENEVEPVDARPAADRLTRPGSGLTNIKTEEISEVKMDAEF 600
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 DDLOPHWSFGADSVPAANTENEVEPVDARPAADRLTRPGSGLTNIKTEEISEVKMDAEF 600
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVIATVIFILVLMKKQYTSIHGV 660
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVIATVIFILVLMKKQYTSIHGV 660
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 661 VEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMONKK 697
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 661 VEVDAAVTPPEERHLSKMOQNGYENPTYKFFEQMONKK 697
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 12
 AAU07208
 ID AAU07208 standard; Protein: 697 AA.
 XX AAU07208;
 XX 24-OCT-2001 (first entry)
 XX Human beta-amyloid protein precursor, APP695-KK.
 DE Human; aspartyl protease.; Asp-1; neotropic; neuroprotective;
 KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KW beta-secretase; Alzheimer's disease; APP695-KK.
 XX Homo sapiens.
 XX WC200149097-A2.
 XX 12-JUL-2001.
 XX 09-MAY-2001; 2001WO-1B00797.
 XX 09-MAY-2001; 2001WO-1B00797.
 XX (BIEN/) BIENKOWSKI M J.
 XX (GURNEY/) GURNEY M E.
 XX (HEIN/) HEINRIKSON R L.
 XX (PARO/) PARODI L A.
 XX (YANR/) YAN R.

PI Bienenkowski MJ, Gurney ME, Heinrikson RL, Farodi LA, Yan R;
 XX WPI: 2001-502548/55.
 DR N-PSDB: AAS11708.
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX
 PS Example 6; Page 144-146; 185pp; English.
 XX
 CC The invention relates to a novel purified polypeptide comprising a
 CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
 CC Asp2 transmembrane domain and the Asp2 protease, and where the polypeptide
 CC and the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. Also included is an isoform of amyloid protein precursor (APP)
 CC comprising the amino acid sequence of a APP or its fragment containing
 CC an APP cleavage site recognisable by a mammalian beta-secretase, and
 CC further comprising two lysine residues at the carboxyl terminus of the
 CC amino acid sequence of the mammalian APP or APP fragment. The
 CC polypeptides are used for assaying for modulators of beta-secretase
 CC activity; identifying agents that inhibit the APP processing activity
 CC of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that
 CC modulate the activity of Asp2; and for reducing cellular production of
 CC amyloid beta (Abeta) from APP. Agents identified by the above methods
 CC are useful for treating Alzheimer's disease; and for identifying
 CC modulators of amyloid-beta (Abeta) peptide production, for use in
 CC designing therapeutics for the treatment or prevention of Alzheimer's
 CC disease. Probes and primers derived from Asp nucleic acid sequences
 CC are useful for detecting Hu-Asp nucleic acids in in vitro assays and in
 CC Northern and Southern blots. The present sequence represents the
 CC amino acid sequence of human amyloid protein precursor, Asp695-KK.
 XX used in the method of the invention.
 XX
 SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAFMFCGRNLNMHMVQNGKWSDFSGTK 60
 Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAFMFCGRNLNMHMVQNGKWSDFSGTK 60

Qy 61 TCIDTKGIIQYCOEYVPELQITNVVANOPIVQNKCKRCKOCTHPHFVPIPCLVG 120
 Db 61 TCIDTKGIIQYCOEYVPELQITNVVANOPIVQNKCKRCKOCTHPHFVPIPCLVG 120

Qy 121 EFVSDALLVPCKKFLHQRWDVCETHLHWHIVAKETCSFKSTN:HPDYGMLLPGLIDKFR 180
 Db 121 EFVSDALLVPCKKFLHQRWDVCETHLHWHIVAKETCSFKSTN:HPDYGMLLPGLIDKFR 180

Qy 181 GVEFVCCPLAESNDVSADAEEDSDVWNGGADTVYADGSEDKVVFVAEEVEAEVEE 240
 Db 181 GVEFVCCPLAESNDVSADAEEDSDVWNGGADTVYADGSEDKVVFVAEEVEAEVEE 240

Qy 241 EAUDDDEDEGDEVEEAEPEEATERTTSIATITTTTTSVEFVVRVPTIAASTPDVAV 300
 Db 241 EAUDDDEDEGDEVEEAEPEEATERTTSIATITTTTTSVEFVVRVPTIAASTPDVAV 300

Qy 301 DKYLETGDENEHAHFCKAKERLEAKRKMSQVNMREWEAEERAKNLPKADKAVIQHF 360
 Db 301 DKYLETGDENEHAHFCKAKERLEAKRKMSQVNMREWEAEERAKNLPKADKAVIQHF 360

Qy 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPFRHFNMLK 420
 Db 361 QEKVESLEGEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPFRHFNMLK 420

Qy 421 KYVRAEQKDRQHTLUKHEHVMWDPKKAQIRSOVNT:HLRVIYERMNQS:SLINYPAVA 480
 Db 421 KYVRAEQKDRQHTLUKHEHVMWDPKKAQIRSOVNT:HLRVIYERMNQS:SLINYPAVA 480

Qy 481 ERIQDEVDLLOKEQNSDDVLANKMISEPRIISYGNALMPSLTETKTTVELLPVNGEFL 540
 Db 481 ERIQDEVDLLOKEQNSDDVLANKMISEPRIISYGNALMPSLTETKTTVELLPVNGEFL 540

Qy 541 DDLQPHSFSGADSVDPANTENEVEPVDARPAADRGLTIRPGSLGTLNIKTEEISEVKMDAEF 600
 Db 541 DDLQPHSFSGADSVDPANTENEVEPVDARPAADRGLTIRPGSLGTLNIKTEEISEVKMDAEF 600

Qy 601 RHDSGYEVSHQKLVFPFAEDVGSNGKAGIIGLMVGGVVIATVITILVMLKKQYTSIHGGV 660
 Db 601 RHDSGYEVSHQKLVFPFAEDVGSNGKAGIIGLMVGGVVIATVITILVMLKKQYTSIHGGV 660

Qy 661 VEVDAAVTPEERHLSKMOQNGYENPIYKPFQOMONKK 697
 Db 661 VEVDAAVTPEERHLSKMOQNGYENPIYKPFQOMONKK 697

RESULT 13
 AAE02587
 ID AAE02587 standard; Protein; 697 AA.
 XX
 AC AAE02587;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human amyloid precursor protein 695-KK (APP695-KK).
 XX
 KW Human: alpha-secretase; amyloid precursor protein 695-KK; APP695-KK;
 KW therapy; Alzheimer's disease; antialzheimer's.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN W0200123533-A2.
 XX
 PC 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US26080.
 XX
 PR 23-SEP-1999; 99US-0155493.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Gurney M, Bienenkowski MJ;
 XX
 DR N-PSDB; AAD06745.
 XX
 XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
 XX protein, useful for the treatment of Alzheimer's disease -
 XX
 XX Example 6; Page 143-145; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human APP695-KK. This
 CC sequence contains two carboxy-terminal lysine residues.
 XX
 SQ Sequence 697 AA;

Query Match 99.8%; Score 3646; DB 22; Length 697;
 Best Local Similarity 99.9%; Pred. No. 2.7e-256;
 Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAFMFCGRNLNMHMVQNGKWSDFSGTK 60
 Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPQIAFMFCGRNLNMHMVQNGKWSDFSGTK 60

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QY 61 TCIDTKESILLOYCOEYVPELOITNNVEANOPVTIONMCKKGRKCKOCTHPPHVPYPCVLG 120
DB 61 TCIDTKESILLOYCOEYVPELOITNNVEANOPVTIONMCKKGRKCKOCTHPPHVPYPCVLG 120
QY 121 EFVSDALLVPCKCKFLHQEMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPGGDKFR 180
DB 121 EFVSDALLVPCKCKFLHQEMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPGGDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYAGSEKVKVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYAGSEKVKVEVAEEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVVPITTAASPDAY 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVVPITTAASPDAY 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSOVMEFEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSOVMEFEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHEHVRMVDPKKAAQIRSOVMTHLRVIYERNQSLSLYNNPVA 480
DB 421 KYVRAEQKDRQHTLKHEHVRMVDPKKAAQIRSOVMTHLRVIYERNQSLSLYNNPVA 480
QY 481 EEIODEVDELQEKQNSYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
DB 481 EEIODEVDELQEKQNSYSDVLANMISEPRISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLQPHSHFGADSVPAANTEVEPVDARPAADRGLTTRPGSLTNKIKTEHSEVKNDAEF 600
DB 541 DDLQPHSHFGADSVPAANTEVEPVDARPAADRGLTTRPGSLTNKIKTEHSEVKNDAEF 600
QY 601 RHDGSEVHHOKLVFFAEDYGSNKGATIGLMWGGVVIATVIFITLVMLKKKQYTSIHGGV 660
DB 601 RHDGSEVHHOKLVFFAEDYGSNKGATIGLMWGGVVIATVIFITLVMLKKKQYTSIHGGV 660
QY 661 VEYDAAVTPERHLKSNQNGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPERHLKSNQNGYENPTYKFFEQMNKK 697

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RESULT 14
 ID ABB78596
 XX ABB78596 standard; Protein: 597 AA.
 AC ABB78596;
 XX
 DT 16-JUN-2002 (first entry)
 XX
 DE Human APP695-KK protein sequence SEQ ID NO:16.
 XX
 KW Human; Asp-1; Asp-2; aspartyl protease; Alzheimer's disease;
 KW proteolytic; amyloid precursor protein; APP.
 XX
 OS Homo sapiens.
 XX
 PN GB2367060-A.
 XX
 XX GB2367060-A.
 PD
 XX
 XX 27-MAR-2002.
 PF
 XX
 XX 29-OCT-2001; 2001GB-0025934.
 PR
 XX
 PR 23-SEP-1999; 99US-155493P.
 PR 23-SEP-1999; 99US-6404133.
 PR 23-SEP-1999; 99WO-US20881.
 PR 13-OCT-1999; 99US-0416901.
 PR 06-DEC-1999; 99US-169232P.
 PR 22-SEP-2000; 2000GB-0023315.

```

XX (PHAA ) PHARMACIA & UPJOHN CO.  

XX Bienkowski MJ, Gurney M;  

XX WPI: 2002-396337/43.  

XX N-PSDB: ABL52463.  

XX  

XX Human aspartyl protease 1 substrates useful in assays to detect  

XX aspartyl protease activity, e.g. for the diagnosis of Alzheimer's  

XX disease.  

XX  

XX Example 6: Page 114-116; 182pp; English.  

XX  

XX The present invention describes a human aspartyl protease 1 (hu-Asp1)  

XX substrate (I) which comprises a peptide of no more than 50 amino acids,  

XX and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-  

XX Glu-Pro. Also described are: (1) a method (II) for assaying hu-Asp1  

XX proteolytic activity, comprising: (a) contacting a hu-Asp1 protein with  

XX (1) under acidic conditions; and (b) determining the level of hu-Asp1  

XX proteolytic activity; (2) a purified polynucleotide (III) comprising a  

XX nucleotide sequence that hybridises under stringent conditions to the  

XX non-coding strand complementary to a defined 1804 nucleotide sequence  

XX (see ABL52456) where the nucleotide sequence encodes a polypeptide having  

XX Asp1 proteolytic activity and lacks nucleotides encoding a transmembrane  

XX domain; (3) a purified polynucleotide (III') comprising a sequence that  

XX hybridises under stringent conditions to (III) (the nucleotide sequence  

XX encodes a polypeptide further lacking a pro-peptide domain corresponding  

XX to amino acids 23-62 of hu-Asp1 (see ABB78589)); (4) a vector (IV)  

XX comprising (III) or (III'); and (5) a host cell (V) transformed or  

XX transfected with (III), (III') and/or (IV). The hu-Asp1 protease  

XX substrate (I) may be used as an enzyme substrate in assays to detect  

XX aspartyl protease activity, (II) and therefore diagnose diseases  

XX associated with aberrant hu-Asp1 expression and activity such as  

XX Alzheimer's disease. Hu-Asp1 has been localised to chromosome 21, while  

XX hu-Asp2 has been localised to chromosome 11q23.3-24.1; the present  

XX sequence represents human amyloid precursor protein APP695-KK, which is  

XX given in an example from the present invention.

```

Sequence 697 AA:

```

Query Match 99.8% Score 3646; DB 23; Length 697;
Best Local Similarity 99.9% Pred. No. 2.7e-236;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAPQIAMFCGRLLNMHMVQNKQKWDSPGSK 60
DB 1 MLPGLALLLAAWTAARALEVPTDGNAGLLAPQIAMFCGRLLNMHMVQNKQKWDSPGSK 60
QY 61 TCIDTKESILLOYCOEYVPELOITNNVEANOPVTIONMCKKGRKCKOCTHPPHVPYPCVLG 120
DB 61 TCIDTKESILLOYCOEYVPELOITNNVEANOPVTIONMCKKGRKCKOCTHPPHVPYPCVLG 120
QY 121 EFVSDALLVPCKCKFLHQEMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPGGDKFR 180
DB 121 EFVSDALLVPCKCKFLHQEMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPGGDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYAGSEKVKVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWGGADIDYAGSEKVKVEVAEEVEEVEE 240
QY 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVVPITTAASPDAY 300
DB 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTTSSVEEVVVPITTAASPDAY 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSOVMEFEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSOVMEFEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420

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QY 421 KYVRAEQKDRQHTLKHFHVRWVDPKKAQOIRSOVMTHLRVIERMNSUSLLYNYPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVRWVDPKKAQOIRSOVMTHLRVIERMNSUSLLYNYPAVA 480
 QY 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
 DB 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
 QY 541 DDLOPHWSFGADSPVANTENEVEPVDARPAADRLTTRPGSGLTNKTEISEVKMDAEF 600
 DB 541 DDLOPHWSFGADSPVANTENEVEPVDARPAADRLTTRPGSGLTNKTEISEVKMDAEF 600
 QY 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 DB 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNK 697
 DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNK 697

RESULT 15
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 ID AAW19498 standard: protein; 695 AA.
 XX
 AC AAW19498;
 XX
 DT 08-SEP-1997 (first entry)
 XX
 DE APP695 mutant A-beta-containing protein.
 XX
 KW Alzheimer's disease; transgenic mammal; beta-amyloid precursor protein;
 KW APP.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 642
 FT /note= "wild-type Val is preferably substituted by Pro"
 XX
 PN W09640895-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09857.
 XX
 PR 07-JUN-1995; 95US-0480653.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 XX
 PI Games KD, McConlogue LC, Rydel RE, Schenk DB, Seubert PA;
 XX
 DR WPI: 1997-052309/05.
 XX
 PT Testing compounds for an effect on an Alzheimer's disease marker -
 PT uses non-human transgenic animals which can control expression of
 PT major forms of beta-amyloid precursor protein.
 XX
 PS Claim 23; Page -: 139pp; English.
 XX
 CC A novel method has been produced for testing compounds for an effect on
 CC an Alzheimer's disease (AD) marker. The method involves administering
 CC the compound to be tested to a non-human transgenic mammal, or mammalian
 CC cells derived from the transgenic mammal, where the transgenic mammal
 CC has a nucleic acid construct stably incorporated into the genome which
 CC comprises a promoter for expression of the construct in a mammalian cell;
 CC operably linked to a region encoding an A-beta-containing protein. The
 CC region is selected from DNA encoding the A-beta-containing protein
 CC consisting of all, or a contiguous portion of APP70, APP751 or APP695,
 CC or a mutant comprising a mutation in one or more of amino acids 649,
 CC 670, 671, 690, 692 and 717, which includes amino acids 672-714 of human
 CC beta-amyloid precursor protein (APP). The present sequence represents a
 CC mutant APP695 protein in which the codon encoding amino acid 717 is

CC mutated (see features table). The amino acid positions referred to in
 CC the specification are as they appear in APP770 (see AAW19497) i.e.
 CC position 717 represents position 642 in APP695, and 698 in APP751. The
 CC larger forms of APP (APP751, APP770) consist of APP695 plus one or two
 CC additional domains. The method also involves detecting or measuring the
 CC AD marker such that any difference between the marker in the transgenic
 CC animal, or mammalian cells derived from the transgenic mammal, to which
 CC the compound has not been administered, is observed, where an observed
 CC difference in the marker indicates that the compound has an effect on
 CC the marker. The transgenic animals, or cells are used to screen for
 CC compounds which alter the pathological course of AD as measured by their
 CC effect on the amount and/or histopathology of AD markers in animals as
 CC well as behavioural alterations.
 CC N.B. The present sequence is shown in the specification, but has
 CC been derived from SEQ ID NO:2 which is on pages 103-105.
 XX
 SQ Sequence 695 AA:
 Query Match: 99.7%; Score 3643; DB 18; Length 695;
 Best Local Similarity 100.0%; Pred No. 4.4e-256;
 Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLEGLALLLAAMTARALEVFTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
 DB 1 MLEGLALLLAAMTARALEVFTDGNAGLLAEPOIAMFCGRNLNMHNVQNGKWDSPSGTK 60
 QY 61 TCIDTRGILQYCCYVPELOITNVYEAQNPVITQNMCKGRKCKTHPHFVLPYRCLVG 120
 DB 61 TCIDTRGILQYCCYVPELOITNVYEAQNPVITQNMCKGRKCKTHPHFVLPYRCLVG 120
 QY 121 EFVSDALVDPCKELHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCKGDKFR 180
 DB 121 EFVSDALVDPCKELHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMLLPCKGDKFR 180
 QY 181 GFVFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEKVVVEAEVEEVEE 240
 DB 181 GFVFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEKVVVEAEVEEVEE 240
 QY 241 EADDEDEDDGDEVEEAEPEEATERTTISIATITTTTSTESVEEVVYVTTAASPDV 300
 DB 241 EADDEDEDDGDEVEEAEPEEATERTTISIATITTTTSTESVEEVVYVTTAASPDV 300
 QY 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMEWEAEQAKNLPKADKAVIQHF 360
 DB 301 DKYLETPGDENEHAHFOKAKERLEAKHRERMSQVMEWEAEQAKNLPKADKAVIQHF 360
 QY 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMKL 420
 DB 361 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLQAVPPRPRHVFNMKL 420
 QY 421 KYVRAEQKDRQHTLKHFHVRWVDPKKAQOIRSOVMTHLRVIERMNSUSLLYNYPAVA 480
 DB 421 KYVRAEQKDRQHTLKHFHVRWVDPKKAQOIRSOVMTHLRVIERMNSUSLLYNYPAVA 480
 QY 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
 DB 481 EEIQDEYDELLQKEQNSDDVLANMISEPRISYGNDAIMPSTIKITVTELLPVNGEFSL 540
 QY 541 DDLOPHWSFGADSPVANTENEVEPVDARPAADRLTTRPGSGLTNKTEISEVKMDAEF 600
 DB 541 DDLOPHWSFGADSPVANTENEVEPVDARPAADRLTTRPGSGLTNKTEISEVKMDAEF 600
 QY 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
 DB 601 RHDSGYEVHGHOKLVFFAEDEVGSKNGAIIGLMVGWVIATVFTLVMLKKKQYTSIHGV 660
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 DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMKNK 695

Search completed: October 2, 2003, 13:59:01
 Job time : 40.3333 secs

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OK protein: protein search, using sw model

Run on: October 2, 2003, 13:56:59 ; Search time 18 Seconds
(without alignments)
1638.370 Million cell updates/sw

Title: US-09-806-194-20

Perfect score: 3653

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents_AA.*

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- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3653	100.0	697	4	US-09-548-372D-20 Sequence 20, Appl
2	3653	100.0	697	4	US-09-548-367D-20 Sequence 20, Appl
3	3653	100.0	697	4	US-09-551-853D-20 Sequence 20, Appl
4	3646	99.8	697	4	US-09-548-372D-16 Sequence 16, Appl
5	3646	99.8	697	4	US-09-548-367D-16 Sequence 16, Appl
6	3646	99.8	697	4	US-09-551-853D-16 Sequence 16, Appl
7	3643	99.7	695	4	US-09-548-372D-14 Sequence 14, Appl
8	3643	99.7	695	4	US-09-548-367D-14 Sequence 14, Appl
9	3638	99.6	697	4	US-09-551-853D-14 Sequence 14, Appl
10	3638	99.6	697	4	US-09-548-372D-13 Sequence 13, Appl
11	3638	99.6	697	4	US-09-548-367D-13 Sequence 13, Appl
12	3638	99.6	697	4	US-09-551-853D-18 Sequence 18, Appl
13	3636	99.5	695	1	US-08-123-702-2 Sequence 2, Appl
14	3636	99.5	695	2	US-08-104-165-1 Sequence 1, Appl
15	3636	99.5	695	3	US-08-464-250-1 Sequence 1, Appl
16	3636	99.5	695	4	US-08-464-250-1 Sequence 7, Appl
17	3636	99.5	695	4	US-09-458-481B-7 Sequence 7, Appl
18	3636	99.5	695	4	US-09-458-481B-9 Sequence 8, Appl
19	3636	99.5	695	4	US-09-548-372D-10 Sequence 10, Appl
20	3636	99.5	695	4	US-09-548-367D-10 Sequence 10, Appl
21	3636	99.5	695	4	US-09-551-853D-10 Sequence 10, Appl
22	3636	99.5	695	6	5218100-2 Patent No. 5218100
23	3630	99.4	694	1	US-08-339-152A-18 Sequence 18, Appl
24	3630	99.4	694	2	US-08-007-999B-5 Sequence 5, Appl
25	3630	99.4	694	2	US-08-689-276A-5 Sequence 5, Appl
26	3628	99.3	695	4	US-09-548-372D-12 Sequence 12, Appl
27	3628	99.3	695	4	US-09-548-367D-12 Sequence 12, Appl

28	3628	99.3	695	4	US-09-551-853D-12 Sequence 12, Appl
29	3624	99.2	695	1	US-08-371-930-27 Sequence 27, Appl
30	3624	99.2	695	5	PCT-US94-01712-27 Sequence 27, Appl
31	3612	98.9	695	1	US-08-339-152A-30 Sequence 30, Appl
32	3607	98.7	753	4	US-09-548-372D-61 Sequence 61, Appl
33	3607	98.7	753	4	US-09-548-367D-61 Sequence 61, Appl
34	3607	98.7	753	4	US-09-551-853D-61 Sequence 61, Appl
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38	3597	98.5	751	2	US-08-422-333-21 Sequence 21, Appl
39	3597	98.5	751	3	US-08-464-250-2 Sequence 2, Appl
40	3597	98.5	751	4	US-08-464-250-2 Sequence 2, Appl
41	3597	98.5	751	4	US-08-832-667-5 Sequence 5, Appl
42	3597	98.5	751	4	US-09-548-372D-57 Sequence 57, Appl
43	3597	98.5	751	4	US-09-548-367D-57 Sequence 57, Appl
44	3597	98.5	751	4	US-09-551-853D-57 Sequence 57, Appl
45	3597	98.5	751	6	5187153-2 Patent No. 5187153

ALIGNMENTS

RESULT 1
US-09-548-372D-20
Sequence 20, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US95/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-20

Query Match	100.0%	Score 3653	DB 4	Length 697
Best Local Similarity	100.0%	Pred. No. 4.9e-265	Mismatches 0	Indels 0
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Qy	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLNMHVMVQNGKWDSPSGTK	60	
Db	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLNMHVMVQNGKWDSPSGTK	60	
Qy	61	TCIDTREGILQYCOEYVPELQITNVVEANOPVTIQNCKRGRKQCKTHPHFVTPYRCLVG	120	
Db	61	TCIDTREGILQYCOEYVPELQITNVVEANOPVTIQNCKRGRKQCKTHPHFVTPYRCLVG	120	
Qy	121	EFVSDALLVVDCKKFLHOERMDVCEHLHHHTYAKETCSEKSTNLDHYGMLLPCGTDKFR	180	
Db	121	EFVSDALLVVDCKKFLHOERMDVCEHLHHHTYAKETCSEKSTNLDHYGMLLPCGTDKFR	180	
Qy	181	GVFVCCPLAEESDNVDSADAEDDDSDVMWGGADTYADGSEDKVVEAEVEEVEE	240	
Db	181	GVFVCCPLAEESDNVDSADAEDDDSDVMWGGADTYADGSEDKVVEAEVEEVEE	240	
Qy	241	EADDDDEDDGDEVEEAEPYEATERTTSIATTTTTTESVEEYVRVPTTAASPDV	300	
Db	241	EADDDDEDDGDEVEEAEPYEATERTTSIATTTTTTESVEEYVRVPTTAASPDV	300	

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DB 301 DKYLETPGDNENHAHFQKAKERLEAKHRERMSQVMREWEAEAEQAQKLPKADKKAVIQHF 360
QY 361 GEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 GEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMNQSLSLLYNPVAVA 480
QY 481 EBIQDEVDELLQKEQNSDQVLANMISEPRISYGNDAIMPSTETTKTVELLPVNGEFSL 540
DB 481 EBIQDEVDELLQKEQNSDQVLANMISEPRISYGNDAIMPSTETTKTVELLPVNGEFSL 540
QY 541 DDLOPHHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGJTNIKTEEISEVKMDAEF 600
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DB 601 RHDSGYEVHQQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
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DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 2
US-09-548-367D-20
; Sequence 20, Application US/09548367D
; Patent No. 6440598
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 4.9e-265;
Matches 697; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLIAEPQIAMFCGRNLNMHNVONGKWDSPSGTK 60
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QY 481 EBIQDEVDELLQKEQNSDQVLANMISEPRISYGNDAIMPSTETTKTVELLPVNGEFSL 540
DB 481 EBIQDEVDELLQKEQNSDQVLANMISEPRISYGNDAIMPSTETTKTVELLPVNGEFSL 540
QY 541 DDLOPHHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGJTNIKTEEISEVKMDAEF 600
DB 541 DDLOPHHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGJTNIKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHQQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSGYEVHQQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMKKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 3
US-09-551-853D-20
; Sequence 20, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280C
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-20

Query Match 100.0%; Score 3653; DB 4; Length 697;
Best Local Similarity 100.0%; Pred. No. 4.9e-265;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLLAAWTARALEVPTDGNAGLIAEPQIAMFCGRNLNMHNVONGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTARALEVPTDGNAGLIAEPQIAMFCGRNLNMHNVONGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVYPELQITNVNEANQPTIQNWCKRGRKQCKTHPHEVIPYRCLVG 120
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; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-16

Query Match      99.88; Score 3646; DB 4; Length 697;
Best Local Similarity 99.94; Pred. No. 1.6e-264;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPTQIANFQGRINMHMNVQNGKWDSDPSGK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPTQIANFQGRINMHMNVQNGKWDSDPSGK 60

QY 61 TCIDTKGILQYCOEVYPELQITNVVEANQPTVIONCKKRGCKOCTHPHFVPIYRCLVG 120
DB 61 TCIDTKGILQYCOEVYPELQITNVVEANQPTVIONCKKRGCKOCTHPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCFELHOERMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCFELHOERMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVRPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVRPTTAASTPDV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERAKNLPKADKKAVIQHF 360

QY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENITVIALQAVPPRPRHVNMLK 420
DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENITVIALQAVPPRPRHVNMLK 420

QY 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIYERMNOSLSLLYNPVA 480
DB 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIYERMNOSLSLLYNPVA 480

QY 481 ESIQDEVDLLOKQNYSDOVLANNISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540
DB 481 ESIQDEVDLLOKQNYSDOVLANNISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540

QY 541 DDLQPHSFGADSVFANTENEVEPVDARPAADRGTLTTPGSLTNIKTEISEVKMDAEF 600
DB 541 DDLQPHSFGADSVFANTENEVEPVDARPAADRGTLTTPGSLTNIKTEISEVKMDAEF 600

QY 601 RHDSGYEVHHQKLVPFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVPFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYTSIHGV 660

QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 6
US-09-551-853D-16
; Sequence 16, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551.853D
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23

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; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentLi: version 3.1
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-551-853D-16

Query Match      99.84; Score 3646; DB 4; Length 697;
Best Local Similarity 99.94; Pred. No. 1.6e-264;
Matches 596; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPTQIANFQGRINMHMNVQNGKWDSDPSGK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPTQIANFQGRINMHMNVQNGKWDSDPSGK 60

QY 61 TCIDTKGILQYCOEVYPELQITNVVEANQPTVIONCKKRGCKOCTHPHFVPIYRCLVG 120
DB 61 TCIDTKGILQYCOEVYPELQITNVVEANQPTVIONCKKRGCKOCTHPHFVPIYRCLVG 120

QY 121 EFVSDALLVPDKCFELHOERMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCFELHOERMDVCETHLHWHITVAKETCSEKSTNLHDYGMLLPCGIDKFR 180

QY 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GVEVCCPLAESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVRPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVRPTTAASTPDV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERAKNLPKADKKAVIQHF 360

QY 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENITVIALQAVPPRPRHVNMLK 420
DB 361 QKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENITVIALQAVPPRPRHVNMLK 420

QY 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIYERMNOSLSLLYNPVA 480
DB 421 KYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIYERMNOSLSLLYNPVA 480

QY 481 ESIQDEVDLLOKQNYSDOVLANNISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540
DB 481 ESIQDEVDLLOKQNYSDOVLANNISSEPRISYGNDAIMPSTETKTVELLPVNGEESL 540

QY 541 DDLQPHSFGADSVFANTENEVEPVDARPAADRGTLTTPGSLTNIKTEISEVKMDAEF 600
DB 541 DDLQPHSFGADSVFANTENEVEPVDARPAADRGTLTTPGSLTNIKTEISEVKMDAEF 600

QY 601 RHDSGYEVHHQKLVPFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVPFAEDVGSNKGAIIGLMVGGVVIATVIFITLVMLKKQYTSIHGV 660

QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMNKK 697

RESULT 7
US-09-548-372D-14
; Sequence 14, Application US/09548372D
; Patent No. 6420534
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND I
; TITLE OF INVENTION: THEREOF

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; FILE REFERENCE: 29915/62801
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-14

Query Match          99.7%; Score 3643; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQAMFCGRINMNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQAMFCGRINMNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTTIONMCKRGKCKCTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTTIONMCKRGKCKCTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSTNLHDYGMILPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSTNLHDYGMILPGGIDKFR 180
QY 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAEANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QEKVESLEQEAEANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYIYERMNQSLSLYNNPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYIYERMNQSLSLYNNPVA 480
QY 481 EETODEVDELLOKEQNSDDVLANMISEPRIISYGNALMPSLTETKTITVELLPVNGEFSL 540
DB 481 EETODEVDELLOKEQNSDDVLANMISEPRIISYGNALMPSLTETKTITVELLPVNGEFSL 540
QY 541 DDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
DB 541 DDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
QY 601 RHDSCYEVHHOKLVFFAEADVGSNKGAIGLMVGWVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSCYEVHHOKLVFFAEADVGSNKGAIGLMVGWVIATVIFITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPERHLKSKQONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPERHLKSKQONGYENPTYKFFEQMON 695

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RESULT 8

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US-09-548-367D-14
; Sequence 14, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-14

Query Match          99.7%; Score 3643; DB 4; Length 695;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQAMFCGRINMNMHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAANTARALEVPTDGNAGLLAPQAMFCGRINMNMHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTTIONMCKRGKCKCTHPHFVPIYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTTIONMCKRGKCKCTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSTNLHDYGMILPGGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSSEKSTNLHDYGMILPGGIDKFR 180
QY 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAESNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPVPTTAASTPDV 300
DB 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEVEVVPVPTTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHREMSQVMEWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAEANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
DB 361 QEKVESLEQEAEANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVENMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYIYERMNQSLSLYNNPVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSOVMTHLRVYIYERMNQSLSLYNNPVA 480
QY 481 EETODEVDELLOKEQNSDDVLANMISEPRIISYGNALMPSLTETKTITVELLPVNGEFSL 540
DB 481 EETODEVDELLOKEQNSDDVLANMISEPRIISYGNALMPSLTETKTITVELLPVNGEFSL 540
QY 541 DDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
DB 541 DDLQPMHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNKTETEEISEVKMDAEF 600
QY 601 RHDSCYEVHHOKLVFFAEADVGSNKGAIGLMVGWVIATVIFITLVMKKKQYTSIHGV 660
DB 601 RHDSCYEVHHOKLVFFAEADVGSNKGAIGLMVGWVIATVIFITLVMKKKQYTSIHGV 660

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QY 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTSVEEVRVPTAASTPDAY 300
DB 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTSVEEVRVPTAASTPDAY 300
QY 301 DKYLETPGDNHRAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKKAVIQHP 360
DB 301 DKYLETPGDNHRAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKKAVIQHP 360
QY 361 QEVESLEQFAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPRPHRVENMLK 420
DB 361 QEVESLEQFAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPRPHRVENMLK 420
QY 421 KYVRAEOKDROHTLKHFHVRMVDPKKAAQIRSOVMTHLRVIVERNMQSLSLLYNYPAVA 480
DB 421 KYVRAEOKDROHTLKHFHVRMVDPKKAAQIRSOVMTHLRVIVERNMQSLSLLYNYPAVA 480
QY 481 BEIODEVDELQKQONYSDDVLANNISPRISYGNDAIMPSTETKTIVELPVNGEFSL 540
DB 481 BEIODEVDELQKQONYSDDVLANNISPRISYGNDAIMPSTETKTIVELPVNGEFSL 540
QY 541 DDLQPHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLQPHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVATVITLVMKKKQYTSIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVATVITLVMKKKQYTSIHGV 660

RESULT 13
US-08-123-702-2
; Sequence 2, Application US/08123702
; Patent No. 5604131
; GENERAL INFORMATION:
; APPLICANT: Wadsworth, Samuel
; APPLICANT: Snyder, Benjamin
; APPLICANT: Reddy, Vermur, B.
; APPLICANT: Wei, Chamer
; TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
; Patent No. 5604131
; TITLE OF INVENTION: Containing a Genomic DNA Insert of the K1 and CX-2 Regions
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123.702
; FILING DATE: 17-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,264
; REFERENCE/DOCKET NUMBER: TS1121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 695 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-702-2
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Query Match: 99.9%; Score 3636; DB 1: Length 695;
Best Local Similarity 99.9%; Pred. No. 9e-264;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEQAIQAFCCGLNNHMNVQNGKWDSPGSK 60
DB 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEQAIQAFCCGLNNHMNVQNGKWDSPGSK 60
QY 61 TCIDTKGEGICYOEYVPELOITNVYFANOPVITONCKRGRKQCKTHPIHFVPIYRCJVG 120
DB 61 TCIDTKGEGICYOEYVPELOITNVYFANOPVITONCKRGRKQCKTHPIHFVPIYRCJVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHHWHITVAKETCSKSTNLHDYGNMLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHHWHITVAKETCSKSTNLHDYGNMLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
DB 181 GVEFVCCPLAESDNVSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEE 240
QY 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTSVEEVRVPTAASTPDAY 300
DB 241 EADDDEDDGDEVEEAEPEEAEETRTTSIATITTTTSVEEVRVPTAASTPDAY 300
QY 301 DKYLETPGDNHRAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKKAVIQHP 360
DB 301 DKYLETPGDNHRAHFOKAKERLEAKHRERMSOVHKEWFEAEKQAKNPKADPKKAVIQHP 360
QY 361 QEVESLEQFAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPRPHRVENMLK 420
DB 361 QEVESLEQFAANERQOLVETHMARVEAMLNDRRLALENYTALQAVPPRPHRVENMLK 420
QY 421 KYVRAEOKDROHTLKHFHVRMVDPKKAAQIRSOVMTHLRVIVERNMQSLSLLYNYPAVA 480
DB 421 KYVRAEOKDROHTLKHFHVRMVDPKKAAQIRSOVMTHLRVIVERNMQSLSLLYNYPAVA 480
QY 481 BEIODEVDELQKQONYSDDVLANNISPRISYGNDAIMPSTETKTIVELPVNGEFSL 540
DB 481 BEIODEVDELQKQONYSDDVLANNISPRISYGNDAIMPSTETKTIVELPVNGEFSL 540
QY 541 DDLQPHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLQPHSFGADSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVATVITLVMKKKQYTSIHGV 660
DB 601 RHDGSEYVHHOKLVFFAEADVGSNKGAIIGLMVGGVVATVITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMON 695
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RESULT 14
US-08 104-165-1
; Sequence 1, Application US/08104165
; Patent No. 5877015
; GENERAL INFORMATION:
; APPLICANT: HARDY, John Anthony
; APPLICANT: GOATE, Alison Mary
; APPLICANT: MULLAN, Michael John
; APPLICANT: CHARTIER-HARLIN, Marie-Christine
; APPLICANT: OWEN, Michael John
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
```

```
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ OPERATING SYSTEM: IBM PC compatible
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/104.165
/ FILING DATE: 21-JAN-1992
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 910307.8
/ FILING DATE: 21-JAN-1992
/ APPLICATION NUMBER: 9118445.7
/ FILING DATE: 28-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Liebeschuetz, Joe
/ REGISTRATION NUMBER: 37,505
/ REFERENCE/DOCKET NUMBER: 16163-000100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 695 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-104-165-1

Query Match 99.5%; Score 3636; DB 3; Length 695;
Best Local Similarity 99.9%; Pred. No. 9e-264;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 181 GVEFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEERVAEVEE 240
DB 181 GVEFVCCPLAESNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEERVAEVEE 240
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DB 301 DKYLETPGDENFHAHQAKERLZAKHRRNSOVNREWEAEFRQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETIHARVEAMLDNRRLALENYITLQAVPFRPRVPSMLK 420
DB 361 QEKVESLEQEAANERQQLVETIHARVEAMLDNRRLALENYITLQAVPFRPRVPSMLK 420
QY 421 KYVRAEQDRGHTLKHFHEVRMDPKKAAQIRSOVMTHLRVIERMNSGLLYNVPAVA 480
DB 421 KYVRAEQDRGHTLKHFHEVRMDPKKAAQIRSOVMTHLRVIERMNSGLLYNVPAVA 480
QY 481 EEIODEVDELLOKEQNSYSLQVIANMISEPRIYSYNDALMPSLTETKTVELLPYNGEFS 540
DB 481 EEIODEVDELLOKEQNSYSLQVIANMISEPRIYSYNDALMPSLTETKTVELLPYNGEFS 540

/
/ STREET: 379 Lytton Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: US
/ ZIP: 94301
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ OPERATING SYSTEM: IBM PC compatible
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/104.165
/ FILING DATE: 21-JAN-1992
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 910307.8
/ FILING DATE: 21-JAN-1992
/ APPLICATION NUMBER: 9118445.7
/ FILING DATE: 28-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Liebeschuetz, Joe
/ REGISTRATION NUMBER: 37,505
/ REFERENCE/DOCKET NUMBER: 16163-000100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 326-2400
/ TELEFAX: (415) 326-2422
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 695 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-464-250-1

RESULT 15
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: Sequence 1, Application US/08/464250
: Patent No. 6:07542
: GENERAL INFORMATION:
: APPLICANT: HARDY, John Anthony
: APPLICANT: GOATE, Alison Mary
: APPLICANT: MULLEN, Michael John
: APPLICANT: CHARLIER-HARLIN, Marie-Christine
: APPLICANT: OWEN, Michael John
: TITLE OF INVENTION: Test and Model for Alzheimer's Disease
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Hourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy Disk
: OPERATING SYSTEM: IBM PC compatible
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: FILING DATE: 21-JAN-1992
: APPLICATION NUMBER: 910307.8
: FILING DATE: 21-JAN-1991
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: FILING DATE: 28-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Liebeschuetz, Joe
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 16163-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 695 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
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Query Match 99.5%; Score 3636; DB 3; Length 695;
Best Local Similarity 99.9%; Pred. No. 9e-264;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      EEOQDEVDLLOKQONYSDDVLANMISEPRISYCNALMPSLTETKTVEELPVNGEFSL 540
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Qy      VEVDAAVTPPERHLSKMOQNGYENPTYKFFEQMON 695
Db      VEVDAAVTPPERHLSKMOQNGYENPTYKFFEQMON 695

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Search completed: October 2, 2003, 14:03:38
 Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 14:00:39 ; Search time 39 Seconds
(without alignments);
2827.550 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 597654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 567654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	3653	100.0	697	9	US-09-794-925-20
6	3653	100.0	697	9	US-09-681-442-20
7	3653	100.0	697	11	US-09-548-366-20
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45	3628	99.3	695	9	US-09-794-927-12

ALIGNMENTS

RESULT 1

US-09-794-927-20
Sequence 20, Application US/09794927
Patent No. US20010016324A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heindrikson, Robert L.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AT
TITLE OF INVENTION: USES
FILE REFERENCE: 28341/5280FG
CURRENT APPLICATION NUMBER: US/09/794,927
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 20
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-927-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAFMCGHLNMHVQNGKWSQSPGSK 60
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RESULT 2
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: Sequence 20, Application: US/09795847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USFS
: FILE REFERENCE: 28341/62800E
: CURRENT APPLICATION NUMBER: US/09/795,847
: CURRENT FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
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: PRIOR FILING DATE: 1999-09-23
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: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-795-847-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang

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: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: US
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280BC
: CURRENT APPLICATION NUMBER: US/09/794,743
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCI/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PR1
: ORGANISM: Homo sapiens
US-09-794-743-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.le-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMMNVQNGKWDSPSGTK 60
Qy 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNMCKGRKCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNMCKGRKCKTHPHFVPIYRCLVG 120
Qy 121 EFVSDALLVPDKCKFLHQERMOVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKER 180
Db 121 EFVSDALLVPDKCKFLHQERMOVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKER 180
Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEE 240
Qy 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRPTTAASPPDAV 300
Db 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRPTTAASPPDAV 300
Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVREWEAEERQAKNLPKADKKAVIQHF 360
Qy 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRPHVFNMLK 420
Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQNSLSLLYNVPAVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQNSLSLLYNVPAVA 480
Qy 661 VEVDAAVTPEERLSKMQQNGYENPTYKFFEQMONKK 697

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: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
: TITLE OF INVENTION: US
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280JL
: CURRENT APPLICATION NUMBER: US/09/794,748
: PRIOR FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCI/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 697
: TYPE: PRI
: ORGANISM: Homo sapiens
US-09-794-748-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.le-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMMNVQNGKWDSPSGTK 60
Qy 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNMCKGRKCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNMCKGRKCKTHPHFVPIYRCLVG 120
Qy 121 EFVSDALLVPDKCKFLHQERMOVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKER 180
Db 121 EFVSDALLVPDKCKFLHQERMOVCETHLHWHTVAKETCSKSTNLHDYGMLLPCGIDKER 180
Qy 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEE 240
Db 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAEVEEVEE 240
Qy 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRPTTAASPPDAV 300
Db 241 EADDEDEDDGDEVEEAEPEEATERTTSIATTTTTSVEEYVVRPTTAASPPDAV 300
Qy 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVREWEAEERQAKNLPKADKKAVIQHF 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVREWEAEERQAKNLPKADKKAVIQHF 360
Qy 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRPHVFNMLK 420
Db 361 QEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRPHVFNMLK 420
Qy 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQNSLSLLYNVPAVA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRMVDPKAAQIRSQVMTHLRVIIYERMQNSLSLLYNVPAVA 480

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QY 481 EEIQEVEDELLQKQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
DB 481 EEIQEVEDELLQKQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
QY 541 DDLOPHSFGADSVPAANTEVEPVDPADPAADRGTLTRPGSGLTNKTETSEISVKMDAEF 600
DB 541 DDLOPHSFGADSVPAANTEVEPVDPADPAADRGTLTRPGSGLTNKTETSEISVKMDAEF 600
QY 601 RHDSSYEVHHOKLVFFAEDVGSNKGAIIGLMVGWVATVIFITLVMLKKQVYSIRHGV 660
DB 601 RHDSSYEVHHOKLVFFAEDVGSNKGAIIGLMVGWVATVIFITLVMLKKQVYSIRHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 5
US-09-794-925-20
; Sequence 20, Application US/09794925
; Patent No. US20020064819A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280H1
; CURRENT APPLICATION NUMBER: US/09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNVQNCWKSDPSGK 60
DB 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNVQNCWKSDPSGK 60
QY 61 TCIDTKEGILQYCOFVPELQITNNVVEANOPVTIQNMCKRGRKOCKTHPRV:PYKCLVG 120
DB 61 TCIDTKEGILQYCOFVPELQITNNVVEANOPVTIQNMCKRGRKOCKTHPRV:PYKCLVG 120
QY 121 EHVSDALLVPCKFLHQRMDVCEHLHNTVAKETCSKSNLHNDYGMJLJPCGGIDKFR 180
DB 121 EHVSDALLVPCKFLHQRMDVCEHLHNTVAKETCSKSNLHNDYGMJLJPCGGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEEDSDVMWCGADTVADGSEDKVWVVAEEVEVAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEEDSDVMWCGADTVADGSEDKVWVVAEEVEVAEVEE 240
QY 241 EADDDEDDGDEVEEAEPEEATEKTTSIATTTTTTIESVEEVVRVPTTAASTPDVAV 300
DB 241 EADDDEDDGDEVEEAEPEEATEKTTSIATTTTTTIESVEEVVRVPTTAASTPDVAV 300
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DB 241 EADDDEDDGDEVEEAEPEEATEKTTSIATTTTTTIESVEEVVRVPTTAASTPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRRMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQBAANRQOLVETHMARVPEAMUNDERRR-ALENYITAIQAVYPRPHVFNMLK 420
DB 361 QEKVESLEQBAANRQOLVETHMARVPEAMUNDERRR-ALENYITAIQAVYPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIERMNQSLSLLYNPVAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYIERMNQSLSLLYNPVAVA 480
QY 481 BEIQDEVDLLOKEQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
DB 481 BEIQDEVDLLOKEQNYSDVLANMISEPRISYGNLALMPSLTETKTITVELLVNGEFSL 540
QY 541 DDLOPHSFGADSVPAANTEVEPVDPADPAADRGTLTRPGSGLTNKTETSEISVKMDAEF 600
DB 541 DDLOPHSFGADSVPAANTEVEPVDPADPAADRGTLTRPGSGLTNKTETSEISVKMDAEF 600
QY 601 RHDSSYEVHHOKLVFFAEDVGSNKGAIIGLMVGWVATVIFITLVMLKKQVYSIRHGV 660
DB 601 RHDSSYEVHHOKLVFFAEDVGSNKGAIIGLMVGWVATVIFITLVMLKKQVYSIRHGV 660
QY 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697
DB 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMONKK 697

RESULT 6
US-09-681-442-20
; Sequence 20, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/681,442
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 1999-10-13
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1999-09-23
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-20

Query Match 100.0%; Score 3653; DB 9; Length 697;
Best Local Similarity 100.0%; Pred. No. 2,1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNVQNCWKSDPSGK 60
DB 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMEYGPLNKHNNVQNCWKSDPSGK 60
QY 61 TCIDTKEGILQYCOFVPELQITNNVVEANOPVTIQNMCKRGRKOCKTHPRV:PYKCLVG 120
DB 61 TCIDTKEGILQYCOFVPELQITNNVVEANOPVTIQNMCKRGRKOCKTHPRV:PYKCLVG 120
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; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-366-20

Query Match      100.0%; Score 3653; DB 11; Length 697;
Best Local Similarity 100.0%; Pred. No. 2.1e-226;
Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNMHNMVQNGKWDSPSGTK 60
DB 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNMHNMVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVIPYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVIPYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPCGIDKPR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPCGIDKPR 180
QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDDDEDDGDEVEEAEPYEEATERTTSIAITTTTIESVEEVVVRPTTAASPTDAV 300
DB 241 EADDDDEDDGDEVEEAEPYEEATERTTSIAITTTTIESVEEVVVRPTTAASPTDAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLK 420
DB 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNQSLSLYNYPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNQSLSLYNYPAVA 480
QY 481 FEIQDEVDELLQKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540
DB 481 FEIQDEVDELLQKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540
QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600
QY 601 RHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660
DB 601 RHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQNGYENPTYKFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMQNGYENPTYKFEQMNKK 697
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RESULT 9

US-09-794-927-16

; Sequence 16, Application US/09794927

; Patent No. US20010016324A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

```
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
; TITLE OF INVENTION: USES
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-16
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Query Match 99.8%; Score 3646; DB 9; Length 697;

Best Local Similarity 99.8%; Pred. No. 5.8e-226;

Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNMHNMVQNGKWDSPSGTK 60

DB 1 MLPGLALLLAATAARALEVPTDGNAGLLAEPOIAMFCGRLNMHNMVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVIPYRCLVG 120

DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANQPVTIQNWKGRKCKTHPHFVIPYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPCGIDKPR 180

DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCEKSTNLHDYGMLLPCGIDKPR 180

QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240

DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240

QY 241 EADDDDEDDGDEVEEAEPYEEATERTTSIAITTTTIESVEEVVVRPTTAASPTDAV 300

DB 241 EADDDDEDDGDEVEEAEPYEEATERTTSIAITTTTIESVEEVVVRPTTAASPTDAV 300

QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKKAVIQHF 360

QY 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLK 420

DB 361 QEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLK 420

QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNQSLSLYNYPAVA 480

DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTLRLVIYERMNQSLSLYNYPAVA 480

QY 481 FEIQDEVDELLQKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540

DB 481 FEIQDEVDELLQKEQNYSDVLANMISEPRIISYGNALMPSLTETKTVELLPVNGEFSL 540

QY 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

DB 541 DDLPQWHSFGADSVPAANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEF 600

QY 601 RHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660

DB 601 RHDGSEYVHHQKLVFAEDVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660

QY 661 VEYDAVTPERHLKSMQONGYENPTYKFFEQMONKK 657
Db 661 VEYDAVTPERHLKSMQONGYENPTYKFFEQMONKK 657

RESULT 10

US-09-795-847-16
: Sequence 16, Application US/09795847
: Patent No. US20010018208A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrikson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280DF
: CURRENT APPLICATION NUMBER: US/09795,847
: CURRENT FILING DATE: 2001-02-28
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-795-847-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSPSGTK 63
Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
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Db 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
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Db 241 EADDEDEDEDEVEEAESEYEATENTTSIATTTTIESVEEVKVPPTAASTPDV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVNRWEAEERAKNLPKADKKAIVQHF 360
Db 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVNRWEAEERAKNLPKADKKAIVQHF 360
QY 361 QEKVESLQEAANERQOQLVETHMARVEAMLNDRRLALENTITALQVPPRPFRVFNMLK 420
Db 361 QEKVESLQEAANERQOQLVETHMARVEAMLNDRRLALENTITALQVPPRPFRVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRLVIERMNQSLSLLYNPVAPA 480
Db 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRLVIERMNQSLSLLYNPVAPA 480

Db 421 KYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRLVIERMNQSLSLLYNPVAPA 480
QY 481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNDAJLMPSLIETKTITVELLPVNGEFSL 540
Db 481 BEIQDEVDLQKEQNYSDVLANMISEPRISYGNDAJLMPSLIETKTITVELLPVNGEFSL 540
QY 541 DLOPWHISFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNIIKITEEISEVKMDAEF 600
Db 541 DLOPWHISFGADSVPAANTENEVEPVDARPAADRGTLTRPGSGLTNIIKITEEISEVKMDAEF 600
QY 601 RHDGSGYEVHHQKLVFFPAEDVGSNKGAIIGLMVGGVVIAIVIFILVMLKKQYTSIHGV 660
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QY 661 VEYDAVTPERHLKSMQONGYENPTYKFFEQMONKK 697
Db 661 VEYDAVTPERHLKSMQONGYENPTYKFFEQMONKK 697

RESULT 11

US-09-794-743-16
: Sequence 16, Application US/09794743
: Patent No. US20010021391A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrikson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AN
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280BC
: CURRENT APPLICATION NUMBER: US/09794,743
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-743-16

Query Match 99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
Db 1 MLPGLALLLAANTARALEVPTDGNAGLLAEPQIAMFCGRLLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEVPELQITNVVEANQPVTIONMCKRGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
Db 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240

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QY 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRPTTAASIPDAV 300
DB 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRPTTAASIPDAV 300
QY 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQO:VTHMARVEAMLDNRK:ALENYITLQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQO:VTHMARVEAMLDNRK:ALENYITLQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
QY 481 BEIODEVDELLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLVNGEFSJ 540
DB 481 BEIODEVDELLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLVNGEFSJ 540
QY 541 DDLQPHWSFGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNIKIEBISVKMDAEF 600
DB 541 DDLQPHWSFGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNIKIEBISVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 12
US-09-794-748-16
: Sequence 16, Application US/09794748
: Patent No. US200200373:5A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280JL
: CURRENT APPLICATION NUMBER: US/09/794.748
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416.901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 06/155.493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404.133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101.594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-794-748-16

Query Match 99.88; Score 3646; DB 9; Length 697;
Best Local Similarity 99.98; Pred. No. 5, Be-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPGALLLLAATARALETPTDGNAGLLAEPOIATMFCGLNMHMNVQNGKWDSPSGTK 60

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DB 1 MLPGALLLLAATARALETPTDGNAGLLAEPOIATMFCGLNMHMNVQNGKWDSPSGTK 60
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DB 61 TCIDTKESILQYQCVYYPPELQITNNVEANQPVYTONMCKRGKCKOCTHPHFVPIYRCLVG 120
QY 121 EFVSALLVPKCKFLHQRMDVCETHLHWHVTAKETSEKSTNLHDYGMILLPGGIDKFR 180
DB 121 EFVSALLVPKCKFLHQRMDVCETHLHWHVTAKETSEKSTNLHDYGMILLPGGIDKFR 180
QY 181 GVEFVCCPLAEESUNVDSDAE:EDDSOVNMGADTDYADGSEDKVVEVAEEVEEVEE 240
DB 181 GVEFVCCPLAEESUNVDSDAE:EDDSOVNMGADTDYADGSEDKVVEVAEEVEEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRPTTAASIPDAV 300
DB 241 EADDEDEDEGDEVEEAEPEEATERTTSTIA:TTTTTTSVEEVVVRPTTAASIPDAV 300
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DB 301 DKYLETPGDENEHAHFQAKERLEAKHRERMSQVMREWEAEARQAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQO:VTHMARVEAMLDNRK:ALENYITLQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQO:VTHMARVEAMLDNRK:ALENYITLQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSLSLLYNVPAVA 480
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DB 481 BEIODEVDELLOKEQNSDDVLANNISEPRISYGNDAIMPSTETKTIVELLVNGEFSJ 540
QY 541 DDLQPHWSFGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNIKIEBISVKMDAEF 600
DB 541 DDLQPHWSFGADSPVANTENEVEPVDARPAADRGITTRPGSGLTNIKIEBISVKMDAEF 600
QY 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHQKLVFFAEADVGSNKGAIIGLMVGGVVIATVIFITLVLMLKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEVDAAVTPPEERHLSKMQONGYENPTYKFFEQMNKK 697

RESULT 13
US-09-794-925-16
: Sequence 16, Application US/09794925
: Patent No. US20020064819A1
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Bienkowski, Michael J.
: APPLICANT: Heinrichson, Robert L.
: APPLICANT: Parodi, Luis A.
: APPLICANT: Yan, Riqiang
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/6280HI
: CURRENT APPLICATION NUMBER: US/09/794.925
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 09/416.901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155.493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404.133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20881
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101.594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-925-16

Query Match          99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPCIAMFCGRLLNMHNVQNGKWDSDPSGK 60
DB 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPCIAMFCGRLLNMHNVQNGKWDSDPSGK 60
QY 61 TCIDTKEGIIQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYKCLVG 120
DB 61 TCIDTKEGIIQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYKCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHVYAKETCEKSTNLDHYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHVYAKETCEKSTNLDHYGMLLPCGIDKFR 180
QY 181 GYEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GYEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEYEATERTISATITTTTTSVEEVRVPTTAASPDVAV 300
DB 241 EADDEDEDGDEVEEAEPEYEATERTISATITTTTTSVEEVRVPTTAASPDVAV 300
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DB 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEAPKAKNLPKADKKAVIQHF 360
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DB 361 QEKVESLEQEAANERQQLVETHMARVEAAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
QY 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVTHLRYIYERMNOSLSLLYNVPAVA 480
DB 421 KYVRAEQKDRQHTLKHFEHVRVMDPKAAQIRSQVTHLRYIYERMNOSLSLLYNVPAVA 480
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QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
DB 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 14

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US-09-681-442-16
; Sequence 16, Application US/09681442
; Patent No. US20020081634A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrichson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; THEREOF
; FILE REFERENCE: 28341/6280FG
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; CURRENT APPLICATION NUMBER: US/09/681,442
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-16
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Query Match          99.8%; Score 3646; DB 9; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPCIAMFCGRLLNMHNVQNGKWDSDPSGK 60
DB 1 MLPLGALLLLAAWTARALEVPTDGNAGLLAEPCIAMFCGRLLNMHNVQNGKWDSDPSGK 60
QY 61 TCIDTKEGIIQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYKCLVG 120
DB 61 TCIDTKEGIIQYCOEYVPELOITNVVEANOPVTIONMCKRGKQCKTHPHFVPIYKCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHVYAKETCEKSTNLDHYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHVYAKETCEKSTNLDHYGMLLPCGIDKFR 180
QY 181 GYEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
DB 181 GYEFVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEE 240
QY 241 EADDEDEDGDEVEEAEPEYEATERTISATITTTTTSVEEVRVPTTAASPDVAV 300
DB 241 EADDEDEDGDEVEEAEPEYEATERTISATITTTTTSVEEVRVPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEAPKAKNLPKADKKAVIQHF 360
DB 301 DKYLETPGDENEHAFQKAKERLEAKHRMSOVMEWEAEAPKAKNLPKADKKAVIQHF 360
QY 361 QEKVESLEQEAANERQQLVETHMARVEAAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEQEAANERQQLVETHMARVEAAMLDNRRLALENYITALQAVPPRPHVFNMLK 420
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DB 541 DDLPQWHSFGADSVPAANTEVEPVDPADPAADRGLTTRPGSLTNKTEEISEVKMDAEF 600
QY 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
DB 601 RHDSGYEVHHOKLVFFAEADVGSNKGAIIGLMVGGVVIATVITILVMLKKQYTSIHGV 660
QY 661 VEYDAAVTPEERHLSKMQONGYENPTYKFFEQMNKK 697
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RESULT 15

US-09-869-414-16
: Sequence 16, Application US/09869414
: Publication No. US20030077226A1
: GENERAL INFORMATION:
: APPLICANT: Beinkowski et al.
: TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE. APP SUBSTRATES THEREFOR, AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 28341/62804
: CURRENT APPLICATION NUMBER: US/09/869,414
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: 09/416,901
: PRIOR FILING DATE: 1999-10-13
: PRIOR APPLICATION NUMBER: 60/155,493
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 09/404,133
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: PCT/US99/20891
: PRIOR FILING DATE: 1999-09-23
: PRIOR APPLICATION NUMBER: 60/101,594
: PRIOR FILING DATE: 1998-09-24
: NUMBER OF SEQ ID NOS: 73
: SOFTWARE: Patent; Ver. 2.0
: SEQ ID NO 16
: LENGTH: 697
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-869-414-16

Query Match 99.8%; Score 3646; DB 11; Length 697;
Best Local Similarity 99.9%; Pred. No. 5.8e-226;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MLPGLALLLAANTARALEVPTDGNAGLLAEQIAMFCGRLLNNHNVQNGKWDSPSGTK	60
DB	1	MLPGLALLLAANTARALEVPTDGNAGLLAEQIAMFCGRLLNNHNVQNGKWDSPSGTK	60
QY	61	TCIDTREG:LOYCOEYYPELOITNVYEAQPTIQNKCKGRKQCKTHPHFVPIPYRCLVG	120
DB	61	TCIDTREG:LOYCOEYYPELOITNVYEAQPTIQNKCKGRKQCKTHPHFVPIPYRCLVG	120
QY	121	EFVSDALLVPDKCKFLUQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKPR	180
DB	121	EFVSDALLVPDKCKFLUQERMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKPR	180
QY	181	GVFEVCCPLAEESDNDVSADAEEDSDVVMWGADTDYADGSEDKVVEVAEEVEEVEE	240
DB	181	GVFEVCCPLAEESDNDVSADAEEDSDVVMWGADTDYADGSEDKVVEVAEEVEEVEE	240
QY	241	EADDDDEDDGDEVEEAEPEYEATEERTTSIATTTTITTESVEEVVRYPTTAAS7PDAV	300
DB	241	EADDDDEDDGDEVEEAEPEYEATEERTTSIATTTTITTESVEEVVRYPTTAAS7PDAV	300
QY	301	DYLETIPGDENEHAHTQKAKERLEAKHRMSQVMREKEEAEQAQNLKPADKAVIQHF	360
DB	301	DYLETIPGDENEHAHTQKAKERLEAKHRMSQVMREKEEAEQAQNLKPADKAVIQHF	360
QY	361	QEKVESLEQAAEROGVETHMARVEAMLNDRRLALENYITALQAVPRPRHVFNMKLK	420
DB	361	QEKVESLEQAAEROGVETHMARVEAMLNDRRLALENYITALQAVPRPRHVFNMKLK	420
QY	421	KYVRAEQKDRQHTLKHFHVRMYDPKKAQIRSQVMTLRLVIYERMNQSLSLLYNPAVA	480
DB	421	KYVRAEQKDRQHTLKHFHVRMYDPKKAQIRSQVMTLRLVIYERMNQSLSLLYNPAVA	480
QY	481	RETQDEVELLQXSONYSDOVLANMISEPRISYGNALMPSLTETKTTHL:PVNCFSL	540
DB	481	RETQDEVELLQXSONYSDOVLANMISEPRISYGNALMPSLTETKTTHL:PVNCFSL	540
QY	541	DOZQPHSFCADSVPAANTENEVEVPDARPAADRGLTTRCGSLTNIKTBEISEVKMDAEP	600
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QY	601	RHDSGYEVHHOKLVFFFAEDVGSNKGAIIGLMVGQVIATVIFITLVMLKKKQXSIHHGV	660
DB	601	RHDSGYEVHHOKLVFFFAEDVGSNKGAIIGLMVGQVIATVIFITLVMLKKKQXSIHHGV	660
QY	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMONKK	697
DB	661	VEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMONKK	697

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Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 13:56:04 ; Search time 16.6667 Seconds
(without alignments)
4021.774 Million cell updates/sec

Title: US-09-806-194-20
Perfect score: 3653
Sequence: 1 MLPGLALLLAANTARALEV.....QQNCYENPTYKFFPEQMKNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3636	99.5	695	A49795	Alzheimer's disease
2	3583.5	98.2	770	QRR044	Alzheimer's disease
3	3539	96.9	695	S00550	Alzheimer's disease
4	3514	95.2	595	A27485	Alzheimer's disease
5	3098	84.8	747	JR0773	Alzheimer's disease
6	2105	57.6	484	A32761	hypothetical Alzhe
7	1723	47.2	763	A49321	amyloid beta (A β)
8	1711	46.8	765	S42880	amyloid precursor
9	1593	46.5	751	A49974	beta-amyloid precu
10	1180	32.3	653	A46362	amyloid precursor
11	1138	31.2	511	JG1404	CDEI-box DNA-bind
12	816.5	22.4	686	T15795	hypothetical prote
13	754	20.6	886	A32758	beta-amyloid-like
14	706	19.3	246	S38344	CDEI-binding prote
15	406	11.1	82	P00438	Alzheimer's disease
16	291.5	8.0	191	A35981	sperm membrane pro
17	278	7.6	57	E60045	Alzheimer's disease
18	278	7.6	57	F60045	Alzheimer's disease
19	278	7.6	57	G60045	Alzheimer's disease
20	278	7.6	57	D60045	Alzheimer's disease
21	278	7.6	57	A60045	Alzheimer's disease
22	278	7.6	57	B60045	Alzheimer's disease
23	217	5.9	42	P00512	beta-amyloid prote
24	192.5	5.3	1110	2	NP-180 - sea lamp
25	185.5	5.1	407	1	immediate-early pr
26	184	5.0	5170	2	hypothetical prote
27	182	5.0	522	2	hypothetical prote
28	180.5	4.9	993	2	synaptonemal compl
29	179.5	4.9	1188	2	zinc finger protei

30	175.5	4.8	802	1	S48529	NAB3 protein - yea
31	174.5	4.8	464	2	H90279	microtubule bindin
32	174.5	4.8	884	2	T20405	hypothetical prote
33	174	4.8	579	2	JH0820	160K golgi antigen
34	174	4.8	1087	2	T30330	gelatin-related p
35	174	4.8	1271	2	A45555	glutamate rich pro
36	173.5	4.7	793	1	JH0628	caldesmon - human
37	173	4.7	1187	2	T46637	transcription fact
38	172	4.7	771	1	A33430	h-caldesmon - chis
39	172	4.7	784	2	PN0009	neurofilament trip
40	172	4.7	1182	2	T30189	myelin transcripti
41	169.5	4.6	298	1	IPHUTC	troponin T, cardia
42	169.5	4.6	721	2	S29795	hypothetical prote
43	169	4.6	885	2	G71608	ATP-dept. acyl-CoA
44	168.5	4.6	675	2	T03744	myoD protein inhib
45	168.5	4.6	913	2	T52485	neurofilament prot

ALIGNMENTS

RESULT 1

A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (Crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlisny, M.B.; Tolan, D.R.; Seikoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human support
A:Reference number: A49795; MUID:91273117; PMID:1905108
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type prote.
C:Keywords: alternative splicing

Query Match 99.5%; Score 3636; DB 1; Length 695;

Best Local Similarity 99.9%; Pred. No. 3.7e-184;

Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSDPSGK	60
Db	1	MLPGLALLLAANTARALEVPTDGNAGLLAEPOIAMFCGRLLNMHNVQNGKWDSDPSGK	60
Qy	61	TCIDTKESILQYCOEVYPELQITNVVEANQPVTIQNMCKRGKCKTTPHFVYPRCLVG	120
Db	61	TCIDTKESILQYCOEVYPELQITNVVEANQPVTIQNMCKRGKCKTTPHFVYPRCLVG	120
Qy	121	EFVSDALLVPDKCFKHQERMDVCETHLHWHVTAKFTCSKSTNLDHYGMLLPGCIDKFR	180
Db	121	EFVSDALLVPDKCFKHQERMDVCETHLHWHVTAKFTCSKSTNLDHYGMLLPGCIDKFR	180
Qy	181	GVEFVCCPLAESDNVSADAEEDSDVWVGADTDVADGSEDKVVEAEVEEVEE	240
Db	181	GVEFVCCPLAESDNVSADAEEDSDVWVGADTDVADGSEDKVVEAEVEEVEE	240
Qy	241	EADDEDEDEDEVEEAEPEEATERTTSIATTTTTTSSVEEVVVRPTTAASTPDV	300
Db	241	EADDEDEDEDEVEEAEPEEATERTTSIATTTTTTSSVEEVVVRPTTAASTPDV	300
Qy	301	DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEWEAEAEAKNLPKADKAVIQHF	360
Db	301	DKYLETPGDENEHAHFOKAKERLEAKHREMSQVMEWEAEAEAKNLPKADKAVIQHF	360
Qy	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLALQAVPRPRHVFNMKL	420
Db	361	QEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYITLALQAVPRPRHVFNMKL	420
Qy	421	KYVRAEQKDKQHTLKHFEHVRVMDPKKAAQITRSQVMTHLRVIVERMNQSLLYNVPAVA	480
Db	421	KYVRAEQKDKQHTLKHFEHVRVMDPKKAAQITRSQVMTHLRVIVERMNQSLLYNVPAVA	480

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810159
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St. George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dykes, I.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kanq, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pro
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Ba
Nature 331, 525-527, 1986
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <P02>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g25720; PIDN:CAA30050.1; PID:g26721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibiti
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g529611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Boer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1998
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 506-770 <VT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA

A:Residues: 507-770 <ZA>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for resid
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for res;
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Master's, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuth
Query Match 98.2%; Score 3585.5; DB 1; Length 770;
Best Local Similarity 90.0%; Pred. No. 1.9e-181;
Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;
Cy 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGLNNHNMVQNGKWDSDSGTK 60
Db 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPOIAMFCGLNNHNMVQNGKWDSDSGTK 60
Oy 61 TCIDTKEGILQYCOEYPELQITNVYEAQPVITQNMCKRGRKQCKTHPHFVPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYPELQITNVYEAQPVITQNMCKRGRKQCKTHPHFVPIYRCLVG 120
Oy 121 EFVSDALLYPDKCKFLHQRMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLYPDKCKFLHQRMDVCETHLHWHVTAKETCSEKSTNLHDYGMLLPCGIDKFR 180
Oy 181 GVEFVCCPLAEESDNDVSDAEDDDSDVMWGGADTDYADGSDKVVEVEAEVEEVEE 240
Db 181 GVEFVCCPLAEESDNDVSDAEDDDSDVMWGGADTDYADGSDKVVEVEAEVEEVEE 240
Oy 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTITESTVEEVV 288
Db 241 EADDDDEDDGDEVEEAEPEYEATERTTSIATTTTITESTVEEVV 300
Oy 289 288
Db 301 RAMLSRWYFDVTGSKCAPFYGGCGNNRNFDEEYCMVCGSAMSGSLKTIQELARD 360
Oy 289 ---VPTTAASPDPAVKYLETGPDENEHAHFKAKERLEAKHRERMSQVMEAEERQA 345
Db 361 PVKLPTTAASPDPAVKYLETGPDENEHAHFKAKERLEAKHRERMSQVMEAEERQA 420
Oy 346 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAHLNDRRLALENYITAL 405
Db 421 KNLPKADKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAHLNDRRLALENYITAL 480
Oy 406 OAVPPRPRHVFNMKKYVRAEQDKRQHTLKFHEHVRWVDPKAAQJRSQVTHLRVIER 465
Db 481 OAVPPRPRHVFNMKKYVRAEQDKRQHTLKFHEHVRWVDPKAAQJRSQVTHLRVIER 540
Oy 466 MNGSLSLYNYVPAVAPEIQDEVDDELLOKEONYSDVLANNMISEPRIISYGNALMPSLTET 525
Db 541 MNGSLSLYNYVPAVAPEIQDEVDDELLOKEONYSDVLANNMISEPRIISYGNALMPSLTET 600
Oy 526 KTIIVELLPVNGEFTSLDLPQWHSFGADSVPAANTENEVEPYDADPAADRGLTTPGSGLTN 585
Db 601 KTIIVELLPVNGEFTSLDLPQWHSFGADSVPAANTENEVEPYDADPAADRGLTTPGSGLTN 660
Oy 586 IKTEEISEVKMDAEFRHDSGYEVHHOKLVHFAEDVGSNGKGAIIGLVMGVVIAVITFI 645
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVHFAEDVGSNGKGAIIGLVMGVVIAVITFI 720
Oy 646 VMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMON 695
Db 721 VMLKKQYTSIHGGVVEVDAAVTPPEERHLSKMQNGYENPTYKFFEQMON 770
RESULT 3
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, G.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg,
EMBO J. 7, 1365-1370, 1988

A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
A:Reference number: S00550; MUID:8832583; PMID:2900758
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:q55616; PIDN:CAA30488.1; P-D:q55617
Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88284430; PMID:2468652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behner, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein: binding to copper.
A:Reference number: S45251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potompska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:2673481
A:Accession: A39820
A:Molecule type: protein
A:Status: preliminary
A:Residues: 18-32 <PO>
A:Experimental source: brain
A:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane *status predicted <TM>
Query Match 96.9%; Score 3539; DB 2; Length 695;
Best Local Similarity 97.1%; Pred. No. 4.8e-179;
Matches 675; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAIFCGRLNHNHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAIFCGRLNHNHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVPIYRCLVG 120
DB 61 TCIGTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
DB 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
QY 241 EADDEDEDEGDEVEAEPEEATERTTSIAITTTTITESTVEEVVPTTAASPTDAV 300
DB 241 EADDEDEDEGDEVEAEPEEATERTTSIAITTTTITESTVEEVVPTTAASPTDAV 300
QY 301 DKYLETPGDENEHAHFOKAKERI, EAKHRRMSQVMREWEAEARQAKNPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFOKAKERI, EAKHRRMSQVMREWEAEARQAKNPKADKAVIQHF 360
QY 361 QEKVESLEQAAANERQOOLVETHHARVEAMLNDRRLALFNYITALQAVPPRPHVENMLK 420
DB 361 QEKVESLEQAAANERQOOLVETHHARVEAMLNDRRLALFNYITALQAVPPRPHVENMLK 420
QY 421 KYVRAEQKQRHTLKHFEHVRVMDPKAAQIRSQVMTLHVIVYERNQSLSLLYNYPVA 480
DB 421 KYVRAEQKQRHTLKHFEHVRVMDPKAAQIRSQVMTLHVIVYERNQSLSLLYNYPVA 480
QY 481 EETQDEVELLOKEGNYSDVLANMISEPRISYGNALMPSLETETKTVELLPVNGEESL 540
DB 481 EETQDEVELLOKEGNYSDVLANMISEPRISYGNALMPSLETETKTVELLPVNGEESL 540

QY 541 DDLQPHWSEFGADSVSPANTENEPVVDARPAADRGLTTRPGSLTNIKTEETSEVKMDAEF 600
DB 541 DDLQPHWSEFGADSVSPANTENEPVVDARPAADRGLTTRPGSLTNIKTEETSEVKMDAEF 600
QY 601 RHDSEYEVHOKLVFFAEDVGSNKCAITGLMVGVIATVITLVMKKKQYTSIHGV 660
DB 601 GHDSEYEVHOKLVFFAEDVGSNKCAITGLMVGVIATVITLVMKKKQYTSIHGV 660
QY 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMON 695
DB 661 VEVDAAVTPPEERHLSKMOONGYENPTYKFFEQMON 695
RESULT 4
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Ramada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein
A:Reference number: A27485; MUID:88106489; PMID:332280
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:q191568; PIDN:AAA37139.1; PID:q309085
A:Experimental source: brain
R:De Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is c
A:Reference number: S19727; MUID:92096458; PMID:1756177
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR
A:Cross-references: EMBL:X59379
R:Izumii, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzhe
A:Reference number: I49485; MUID:92209998; PMID:1555768
A:Accession: I49485
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:q220328; PIDN:BA001456.1; PID:q220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; amyloid; transmembrane protein
Query Match 96.2%; Score 3514; DB 2; Length 695;
Best Local Similarity 96.7%; Pred. No. 9.9e-178;
Matches 672; Conservative 5; Mismatches 18; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAIFCGRLNHNHNVQNGKWDSPSGTK 60
DB 1 MLPGLALLLLAANTARALEVPTDGNAGLLAEPQIAIFCGRLNHNHNVQNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVPIYRCLVG 120
DB 61 TCIGTKEGILQYCEVPELQITNVVEANQPVITQNCGRKGRKCKTHPHFVPIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQRMDVCEHLLHWHHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
DB 181 GVEFVCCPLAESDNDSDADAEEDSDVMWGGADIDYADGSDKVVVEAEVEEVARVEE 240
QY 241 EADDEDEDEGDEVEAEPEEATERTTSIAITTTTITESTVEEVVPTTAASPTDAV 300

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Db 241 EADDDEVEDGDEVEEAEPEYERATRTTATTTTTTTSVEEVVVFVTTTAASTPDV 300
Qy 301 DKYLETPGDENEHAHFQKAKERLEAKIRHRMSQVMREWEAEARQAKNLPKADKKAVIQRP 360
Db 301 DKYLETPGDENEHAHFQKAKERLEAKIRHRMSQVMREWEAEARQAKNLPKADKKAVIQRP 360
Qy 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVENMLK 420
Db 361 QEKVESLEQEAANEERQQLVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVENMLK 420
Qy 421 KYVRAEQKDRQHTLKHFEBHVMVDPKKAQATRSQVMTHLRVYERMNQSLSLLYNPAPA 480
Db 421 KYVRAEQKDRQHTLKHFEBHVMVDPKKAQATRSQVMTHLRVYERMNQSLSLLYNPAPA 480
Qy 481 BEIODEVELLQKEQNTSDOVLANMISEPRISYGNDAIMPSTLTETKTIVELLVNGEFS 540
Db 481 BEIODEVELLQKEQNTSDOVLANMISEPRISYGNDAIMPSTLTETKTIVELLVNGEFS 540
Qy 541 DDLOPHSFGADSVPAANTEVEVPDARPAADRGTLTRPGSLTNIKTEELSEVKMDAEF 600
Db 541 DDLOPHSFGADSVPAANTEVEVPDARPAADRGTLTRPGSLTNIKTEELSEVKMDAEF 600
Qy 601 RHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGWGIATVITFLVMLKKQYTSIHGV 660
Db 601 GHDSGFVRRHQLVFAEDVGSNKGAIIGLMVGWGIATVITFLVMLKKQYTSIHGV 660
Qy 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695
Db 661 VEVDAAVTPEERHLSKMQONGYENPTYKFFEQMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 *sequence_revision 10-Jun-1993 *text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1566, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1262805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein: animal kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 84.8%; Score 3098; DB 2; Length 747;
Best Local Similarity 80.9%; Pred. No. 8.7e-156;
Matches 597; Conservative 35; Mismatches 42; Indels 64; Gaps 5;

Qy 17 ALEYPTDGNAGLLAEPQIAMP-CGRLLNHNHNVQKWDSPSGTKTCTIDTKESILQYQCE 75
Db 15 ALEVLVDGNGLLAEPQ:AMF:SVARLNNHNNVQKWNEDVSG---CLGTKEG-LQYQCE 71
Qy 76 VYPELQITNVVEANQPVTIQNWCKRGKQCKTHPHFVIPYRCLYGEFVSQALLVPDKCKF 135
Db 72 VYPELQITNVVEANQPVTIQNWCKRGKQCKSRTEIIVVYRCLYGEFVSQALLVPDKCKF 131
Qy 136 LHOERMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKPRGVEFVCCPLAESDN 195
Db 132 LHOERMDICETHLHHHTVAKESKSKSLHEYGMLLPCGIDKPRGVEFVCCPLAESSES 191
Qy 196 VDSADAECDQVNMGGADTDYADGSEDKVVEVA-EEEEVAEEAEADDEDDDEDCDE 253
Db 192 FDSADAECDQVNMGGADTDYDRSDKVAEAPQDEEEVEVEEBEEDDDED--DGDE 249
Qy 254 VEERAEPEYERATRTTATTTTTTTSVEEVVVFVTTTAASTPDV 300
Db 254 VEERAEPEYERATRTTATTTTTTTSVEEVVVFVTTTAASTPDV 300
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Db 250 AESEPEPEYERATRTTATTTTTTTSVEEVVVFVCCSEQAETGPCRAMISRMYDYVTE 309
Qy 289 -----VPTTAASTPDVADVKILETPGDENEHAHFQ 317
Db 310 SKCAQFIYGGCGGNRRNFESDDYCHAVCGSVIPATAASTPDVADVKYLENPNDEHDEFL 369
Qy 318 KAKERLEAKIRHRMSQVMREWEAEARQAKNLPKADKKAVIQHFOEKVESLEQEAANEERQ 377
Db 370 KAKERLEAKIRHRMSQVMREWEAEARQAKNLPKADKKAVIQHFOEKVESLEQEAANEERQ 377
Qy 378 LVETHMARVEAMLNDRRRLALENYITALQAVPPRPRHVENMLKKYVRAEQKDRQHTLKHF 437
Db 430 LVETHMARVEAMLNDRRRLALENYITALQADPPRPRHVENMLKKYVRAEQKDRQHTLKHF 489
Qy 438 EHVRYMDPKKAAQIRSQVMTHLRVYERMNQSLSLLYNPAPAAEEIODEVELLQKEQNT 497
Db 490 EHVRYMDPKKAAQIRSQVMTHLRVYERMNQSLSLLYNPAPAAEEIODEVELLQKEQNT 549
Qy 498 SDOVLNMISEPRISYGNDAIMPSTLTETKTIVELLVNGEFSUDDLQPHWSFGADSVPA 557
Db 550 SDOVLNMISEPRISYGNDAIMPSTLTETKTIVELLVNGEFSUDDLQPHWSFGADSVPA 557
Qy 558 TENEPVDPARPAADRGTLTRPGSLTNIKTEELSEVKMDAEFRHDSGYEVHHQKLVFA 617
Db 610 TENEPVDPARPAADRGTLTRPGSLTNIKTEELSEVKMDAEFRHDSGYEVHHQKLVFA 669
Qy 618 EDVGSNKGAIIGLMVGWGIATVITFLVMLKKQYTSIHGVVEVDAAVTPEERHLSK 677
Db 670 EDVGSNKGAIIGLMVGWGIATVITFLVMLKKQYTSIHGVVEVDAAVTPEERHLSK 729
Qy 678 QONGYENPTYKFFEQMON 695
Db 730 QONGYENPTYKFFEQMON 747

RESULT 6
A32761
hypoetical Alzheimer's disease amyloid beta protein, Alu-containing clone - huma
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 *sequence_revision 10-Apr-1996 *text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secre
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DPS>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as leu
C:Comment: This is the hypothetical translation of a sequence believed to contain
C:Keywords: cloning artifact

Query Match 57.6%; Score 2105; DB 4; Length 484;
Best Local Similarity 87.7%; Pred. No. 9.9e-104;
Matches 407; Conservative 1; Mismatches 0; Indels 56; Gaps 1;

Qy 80 LQITNVVEANQPVTIQNWCKRGKQCKTHPHFVIPYRCLYGEFVSQALLVPDKCKELH 139
Db 1 LQITNVVEANQPVTIQNWCKRGKQCKTHPHFVIPYRCLYGEFVSQALLVPDKCKELH 60
Qy 140 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKPRGVEFVCCPLAESDNVDS 199
Db 61 RMDVCETHLHHHTVAKETCSKSTNLHDYGMLLPCGIDKPRGVEFVCCPLAESDNVDS 120
Qy 200 DAEEDSDQVNMGGADTDYADGSEDKVVEVAEEVEAEAEADDEDDDEGDEVEEEAE 259
Db 121 DAEEDSDQVNMGGADTDYADGSEDKVVEVAEEVEAEAEADDEDDDEGDEVEEEAE 180
Qy 260 EPEERATRTTATTTTTTTSVEEVVVFVTTTAASTPDV 300
Db 181 EPEERATRTTATTTTTTTSVEEVVVFVCCSEQAETGPCRAMISRMYDFVTEGKCAPF 240
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QY 289 -----VPTTAASTPDVADKYLETPTGDENEHAFQAKERL 323
Db 241 FYGCGGGRNNFTDEEYCMVACGSAITPTAASTPDVADKYLETPTGDENEHAFQAKERL 300
QY 324 EAKHRRMSQVMEWEAEARQAKNPKADKAVIQHFQKVESLEGEAEANERQQLVFETHM 363
Db 301 EAKHRRMSQVMEWEAEARQAKNPKADKAVIQHFQKVESLEGEAEANERQQLVFETHM 360
QY 384 ARVEMMLNDRRLALENYITALQAVPRPRHIVFMMLKKVYRAEQKQKHILKHFSIVRVV 443
Db 361 ARVEMMLNDRRLALENYITALQAVPRPRHIVFMMLKKVYRAEQKQKHILKHFSIVRVV 420
QY 444 DPKKAAQIRSQVMTHLRYIYERNQSLSLLYNYPVAVAEIODEV 487
Db 421 DPKKAAQIRSQVMTHLRYIYERNQSLSLLYNYPVAVAEIODEV 464

RESULT 7
A:Accession: A49321
A:Title: amyloid beta (A4) homolog 2 precursor - human
N:Alternate names: CDE1-binding protein
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C:Accession: A49321; S34644; S40519
R:Spencer, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A:Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: c
A:Reference number: A49321; MUID:93250009; PMID:8485127
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: GB:S60099; NID:g300168; PID:AA60563.1; PID:g300169
A:Experimental source: placenta
A:Note: Sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P:131199)
A:Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R:von der Kammer, H.; Klaidiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL data library, April 1993
A:Description: The human homologue of the murine CDE1 binding protein is an amyloid prec
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <VON>
A:Cross-references: EMBL:Z22572; NID:g394763; PID:CAAG0295.1; PID:g394764
R:Masco, W.; Gurubhagavatula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, A.T.;
Nature Genet. 5, 95-99, 1993
A:Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94035131; PMID:8220435
A:Accession: S40519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:g450391; PID:AA41701.1; PID:g450392
C:Genetics:
A:Gene: GDB:APLP2; APLP2
A:Cross-references: GDB:139159; OMIM:104776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <RPI>

Query Match 47.2% Score 1723; DB 2; Length 763;
Best Local Similarity 47.0% Pred. No. 2.3e-83;
Matches 371; Conservative 112; Mismatches 166; Indels 140; Gaps 20;
QY 5 LALLLLAAWTARALEV-----PTDGNAG---LILAEFQIAFMFCGRLLNMHNVQNGKDSPP 56
Db 15 LLLLLLGGTAPALALAGY:EAALANAGTGFVAEPQIAMFCGKLMHVNIIQTGWEPDP 7;
QY 57 SGTKICIDTKEGILQVCOEYVPELQITNVVNEANOPTVQNWCKRGKCKTTPHFVYPR 116
Db 75 TGTKSCFETKEEVQLQVCOEYVPELQITNVVNEANOPTVQNWCKRGKCKTTPHFVYPR 132

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QY 117 CLVGEFVSALLVPDKCKFLHQRMDVGCETHLHMHTYAKETCSEKSTNLHDYGMLLPGCI 176
Db 133 CLVGEFVSALLVPDKCKFLHQRMDVGCETHLHMHTYAKETCSEKSTNLHDYGMLLPGCI 192
QY 177 DKFRGVFVCCPLADESDNVDSDAEEDSDVMWGGADTDYADGSEDKVVEVAEEVEAE 236
Db 193 DQFHGTETVCCPOTKLGVSVKFEEDDEE-----EEDEDEEEDYDVYKSEFPTEAD 245
QY 237 VEE--EEA--DDEDEDDGDEVEEBAEPY-----EEATERISINTTTTITTES 282
Db 246 LEDFTAAVDEDEDEEVEEDRDYDITFKGDDYNEENPTPEGSDGTMSDKETID 305
QY 283 VEEV-----VVPV 290
Db 306 KVAVCSQEAFTGFCRAVMPRWYFDLSKCKVFIYGGCGGNRNNEFESDYCMVACKAMIP 365
QY 291 TTAASTPDVADKYLETPTGDENEHAFQAKERLEAKHRRMSQVMEWEAEARQAKNPK 350
Db 366 PTPLPTND--VDYVPEFSADDNEHAFQAKERLEAKHRRMDRVKKEWEAEARQAKNPK 424
QY 351 ADKAVIOHFQKVESLEGEAEANERQQLVFETHMAREVAMLNDRRLALENYITALQAVPP 410
Db 425 AERQTLIGHFQAVKAKALEKAASEKQQLVFETHMAREVAMLNDRRLALENYITALQAVPP 484
QY 411 RPRHVNMLKKYVRAEQKDRHILKHFHVRVMDPKAAQIRSQVMTHLRYIYERNQSL 470
Db 485 RPRHILQALRYVRAENKDRHLIRHYOHVLAVDPEKAAQIRSQVMTHLRYIYERNQSL 544
QY 47: SLLYNVPAVEIEQDEVDLLOKEQNSDDVLAANNISEPRISYNDALMPSLTETKTIVE 530
Db 545 SLLYKVPYVAEQTEIDELLOEQR-----ADM-----DQFTASISTPTDVR 587
QY 531 LLPVNGESLUDLOQWHSFGADSVPAENTENEVEPVDARPAADRGLTTHKGSGLN----- 585
Db 588 ---VSSEES--EIPFPHPF--HPPALPENE---DTQPELYHPM--KKSGVGGEQDGL 635
QY 586 IKIEE---ISEVKMDAEPFRHDSGVGEVHOKLVFAEDVGS-----NKG 625
Db 636 IGAEKVINSKKNVDENNVIDETLDV--KEMFNARVGGLEERESVGLPDEFSJSS 693
QY 626 AIIGLMVGGVVIATVIFITLVMLKKQYTSIHGVVEVDAVATPEERHLSKMQONGYENP 685
Db 694 ALIGLGLVIAVATVIVISLVMLRKQYGTISHGIVEVDPLTPEERHLNKNQNHGYNP 753
QY 686 TYKFEQMQ 694
Db 754 TYKLEQMQ 762

RESULT 8
S42880
A:amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Mar-1999
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL data library, March 1994
A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid p;
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein

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C:Keywords: alternative splicing

F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.8%; Score 1711; DB 2; Length 765;
Best Local Similarity 46.1%; Pred. No. 9, 8e-83;
Matches 363; Conservative 122; Mismatches 157; Indels 136; Gaps 20;

QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPQIAMFCGRINMHNWVNGKWDSP 56
DB 15 LVLVLLGLTAPAAALAGYIEALANAGTGFVAEPQIAMFCGRINMHNWVNGKWDSP 74
QY 57 SGTKCIDTKEGILQYCCQVYPELQITNVVEANQPTVIONMCKRGKCKTHPHFVPIYR 116
DB 75 TGTKSLGTKEEVLYQYCCQVYPELQITNVVEANQPTVIONMCKRGKCKTHPHFVPIYR 132
QY 117 CLVGFVSDALLVPDKCKFLHQRMDYVCETHLHWHIVAKETCEKSTNLHDYGMLLPCGI 176
DB 133 CLVGFVSDVLLVPDNCQPFHQERMEVCEKHQRWHTLVKAECLTEGLTLYSYGMLLPCGI 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVMWGGADTDYA--DGSDDKVVVEAFEE 233
DB 193 DQFHGTGYCCPOTKVYDSSTMSKEEEEE-----DEEDYALDKSEFPTEAGLEDT 248
QY 234 VAEEVEEADDDDDGDEVEEAEPEYEE-----ATERTTISIATTTTTPESVEFVY 287
DB 249 EAAADEDEDEEEEGEEVVEDROYDYDFKGDYNEENPTPESSDGTISIKELAHGV 308
QY 288 R-----VPT 291
DB 309 KAVCSOEAMTGPCRAVPRWYFDSLKGKCVRFYIGCGGNRNFSEDCYMAVCKTMIP 368
QY 292 TAASTPDVADKYLETGCDENEHAFKAKERLEAKHPRMSQVNRWEEAFRCAKNLPA 353
DB 369 TPLPTND--VDVYFETSAADNEHARFQAKQEQLRIHRSDRVKKEWEAEALCAKNLPKA 427
QY 352 DKKAVIOHQFQEVESLFOFAANERQQLVETHMARVEAMLNDRRLALENYITAIQAVPPR 411
DB 428 EQTLILQHFQAMVKALEKAASEKQQLVETHLARVEAMLNDRRLALENYLAALQSDPPR 487
QY 412 PRHVENMLKYVRAEQDKRQHTLKHFEHVRMDPKKAAQIRSQVTHLRYIYERMGSL 471
DB 488 PHRIQLALRYVRAENKDLRIIRHYQHLAVDPEKAAQKSOVMTHLRYIYERMGSL 547
QY 472 LLYNPAVAEEIDQVDELLQKQNYSDVLANKISEPRISYGNDAIMPSTLTKTIVEL 531
DB 548 ELKVPYVAEGIEEIDELQEQR-----ADM-----DQTSISENPVDVR-- 589
QY 532 LPVNGEFLDLPQWHSFGADSVPAANTENEVEPVDARPAADRLTTPGSLTN----- 586
DB 590 --VSSEES-ELPPPHLPF--RPPFSLSENE---DQCPELYHPM--KKGSNAFQDQGL 638
QY 587 KTEE---ISEVKMDAEFRHDSGYEVHHQKLVFPAEDVGS-----NKG 626
DB 639 GAEEKVINSKNMKNMNNVIDETLDV--KEMIFNAERYGGLLEEPDSVGPLKEDFSLSSA 696
QY 627 IIGLMVGGVVIATVIFITLVMLKKQVYISHHGVVEVDAAVTPERHLSKMOONGYENPT 686
DB 697 LIGLLVIAVAIATVIVISLVMLKKRQGTISHGIVEVDPMLTPEERHLNMQNHGYE 756
QY 687 YKFEQMQ 694
DB 757 YKYLEQMQ 764

RESULT 9

A49974

beta-amyloid precursor protein 2 homolog APLP2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1993

C:Accession: A49974

R:Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.

J. Biol. Chem. 269, 2637-2644, 1994

A:Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid

A:Reference number: A49974; MUID:94132029; PMID:8300594

A:Accession: A49974

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-751 <SLD>

A:Cross-references: GB:U1557; NID:9558467; PID:AAA50603.1; P-D:9558468

A:Note: sequence extracted from NCBI backbone (NCBIP:144636)

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protei
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 46.5%; Score 1699; DB 2; Length 751;
Best Local Similarity 45.8%; Pred. No. 4, 1e-82;
Matches 362; Conservative 113; Mismatches 160; Indels 156; Gaps 20;

QY 5 LALLLLAANTARALEV-----PTDGNAG---LLAEPQIAMFCGRINMHNWVNGKWDSP 56
DB 15 LVLVLLGLTAPAAALAGYIEALANAGTGFVAEPQIAMFCGRINMHNWVNGKWDSP 74
QY 57 SGTKCIDTKEGILQYCCQVYPELQITNVVEANQPTVIONMCKRGKCKTHPHFVPIYR 116
DB 75 TGTKSLGTKEEVLYQYCCQVYPELQITNVVEANQPTVIONMCKRGKCKTHPHFVPIYR 132
QY 117 CLVGFVSDALLVPDKCKFLHQRMDYVCETHLHWHIVAKETCEKSTNLHDYGMLLPCGI 176
DB 133 CLVGFVSDVLLVPDNCQPFHQERMEVCEKHQRWHTLVKAECLTEGLTLYSYGMLLPCGI 192
QY 177 DKFRGVFVCCPLAE--ESDNVDSADAEEDSDVMWGGADTDYADGSEDKVVEAE--E 231
DB 193 DQFHGTGYCCPOTKVYDSSTMSKEEEEE-----DEDEEEDYDJKSEFPTE 243
QY 232 EVAEEVEEAD--DDEDDGDEVEE-----AEEPYEATERTTISIATT 276
DB 244 ADLEDFTEAADAEEDEEVEEDROYDYDFKGDYNEENPTPESSGTIS----- 298
QY 277 TTTTSEVEE----- 286
DB 299 --DKEIVHDKAVCSOEAMTGPCRAVPRWYFDSLKGKCVRFYIGCGGNRNFSEDCY 356
QY 287 -----VRVPTTAASIPDAVDKYLETGCDENEHAFKAKERLEAKHPRMSQVNRWEEA 341
DB 357 MAVCKAMIPPTPLPTND--VDVYFETSAADNEHARFQAKQEQLRIHRSDRVKKEWEA 415
QY 342 ERQAKNLPKADKAVTQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENY 401
DB 416 ELQAKNLPKTEROTLQHFQAMVKALEKAASEKQQLVETHLARVEAMLNDRRLALENY 475
QY 402 ITALQAVPPRPHRVFNMKKYVRAEQDKRQHTLKHFEHVRMDPKKAAQIRSQVTHLRY 461
DB 476 LAALQSDPPRPHRIQLALRYVRAENKDLRIIRHYQHLAVDPEKAAQKSOVMTHLHV 535
QY 462 IYERMGSLSLLYNPAVAEEIDQVDELLQKQNYSDVLANKISEPRISYGNDAIMP 521
DB 536 IERRNQSLLTKVPYVAEGIEEIDELQEQR-----ADM-----DQTS 578
QY 522 LTETKTIVELLPVNGEFLDLPQWHSFGADSVPAANTENEVEPVDARPAADRLTTPG 581
DB 579 ISENPDVVRVSSSE-ELPPPHLPF-----PSSLSENE-----GSCMAEQD- 621
QY 582 GLTNIKTEEL-SEVKMDAEFRHDSGYEVHHQKLVFPAEDVGS-----N 623
DB 622 GLIGAEKVINSKNMKNMNNVIDETLDV--KEMIFNAERYGGLLEEPDSVGPLKEDFSL 579
QY 624 KGALIGLMVGGVVIATVIFITLVMLKKQVYISHHGVVEVDAAVTPERHLSKMOONGY 683
DB 680 SNALIGLLVIAVAIATVIVISLVMLKKRQGTISHGIVEVDPMLTPEERHLNMQNHGY 739
QY 684 NPTYKFFEQMQ 694
DB 740 NPTYKYLEQMQ 750

RESULT 10

A46362

amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 C:Accession: A46362
 R:Wasco, W.; Bupp, K.; Magendantz, M.; Gusella, J.F.; Tanzi, R.E.; Solomon, F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A>Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer's disease amyloid beta protein.
 A:Reference number: A46362; MIMD:93066322; PMID:1279693
 A:Accession: A46362
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <WAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:118683, NCBI:118684)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kappa12-type proteinase
 C:Keywords: transmembrane protein

[illegible]

RESULT 11
JC1404

CDE1-box DNA-binding protein - mouse
C: Species: Mus musculus (house mouse)
C: Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C: Accession: JG1404
R: Vidal, F.; Blangy, A.; Rassoulzadegan, M.; Cuzin, F.
Biochim. Biophys. Res. Commun. 189, 1336-1341, 1992
A: Title: A murine sequence-specific DNA binding protein shows extensive local similarity to the human protein
A: Reference number: JG1404; MUID:93129193; PMID:1482349
A: Accession: JG1404
A: Molecule type: mRNA
A: Residues: 1-511 <VID>
C: Comment: This protein plays an important role in the early development of the mouse embryo
C: Keywords: DNA binding; transmembrane protein

Query Match 31.2% Score 1138; DB 2: Length 511:
Best Local Similarity 45.6%; Pred. No. 8.e+53;
Matches 252; Conservative 92; Mismatches 129; Indels 80; Gaps 16;

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Query Match      31.28; Score 1138; DB 2; Length 511;
Best Local Similarity 45.6%; Pred. No. 8,8e-53;
Matches 252; Conservative 92; Mismatches 129; Indels 80; Gaps 16;

QY 174 GQDKFRGVEVCCPLAE--ESDNVDSADAEEDSDVWVGADDTYAYGSDKDYVEAE- 230
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
6 CVDDQFHCTEYVCCPQTKTVDSDTMSKEESEE-----DEEDEDYDLDKSEF 56

QY 231 --EEEVAVEEEAD-DEDEDDGDEVEEAE-----EPYEAIERTTSIATTTTT 279
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
57 PTEADLEDFTEAADREEBEUEGEVEWEDROYDYPFGDDYNE--ENPTEPSEGTIS 114

QY 280 TESVEEVVPTTAASTPDADVXYLITPDGENSHAHFQAKERLEBAKHRRMSQVMEWE 339
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
115 DKEIVHDVKKVPTPLPTND-VDYVFTSADNDNEHARFQAKGLEIRHNKMDRYKKEWE 173

QY 340 EAEHQAKNIKPADKAVYIHFQKVEKSLFQEAANEHQQLVETHMAKVAMLNDRRRLALE 359
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
174 EAELOAKNLPTEKTLIQHQAWMKALEKAASEKQQLVETHLARVENMLNDRRTALE 233

QY 400 NYTALQAVPPRPBVTNMLKKVYAEQDKDKQHTLKHFEHVRMVDQKAAQIRSQVMTL 459
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
234 NYIALQSDPPRHRIILQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSOVMTHL 293

QY 460 RVIYERMQSLSLTYNPVAEESIQEVEDLQKEONYSDDVLANNIPEPSIYSGNALM 519
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
294 HWIEERRNQSLILYKPYVAQETQEEIDELQEQR-----ADM-----DOFT 336

QY 520 PSLTETKTVTELLPVNGEFLSDLOLQWHSGADSVPAENTENEVVPDAKPAADRGLTKRP 579
Db 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
337 SSISENPVDVNVSSSESE-EIIPFFHPLHP-----PSLSENE-----GSGMAEQD 380

QY 580 GSGLTINIKTEEI-SEVKMADEFRRHDSGYEVHHQKLVFFAEADVGS----- 622
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
381 G-GUJGAEEKVINSKNMNDENWVIDFLDV--KEMIFNAERYVGLGEEEPESVGLPREDFS 437

QY 623 --NKGAIGLWGGVVIATVIFITLVMKKQKXYSIHGVEVEADAATVEERHLKMKMOQG 681
Db 1 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111 1:1111
438 LSSNALIGLLVIAVAIATVIVISLVMKRNQYGTISHGIVEVDPMILTVEERHLKMKMHG 497

QY 682 YENPTYKFEQMQ 694
Db 11111111 1111

QY 498 YENPTYKYLEQMQ 510
Db 11111111 1111

```

RESULT 12
T15795

hypothetical protein C42D8.8 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C:Accession: F15795; A49414
R:Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of *C. elegans* cosmid C42D8.
A:Reference number: Z18405
A:Accession: F15795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <HAL>

520	QY	-----PSLTETKTVTELLPWNGBESLDLQPWHSFGADSVFANTENEVEVPDARPMADR	574
714	DB	VTAANPNLFETKS-----EKDLSUTE-----YGEATVSTTKVTLPTVDDOAVQRA	760
575	QY	LITRGSGLTNLKIEEISEVKADAEFRHDSOYEVHHQKIVF-----FAEDVGSNK-----GA	626
761	DB	VEDVAAA-----VAHQENQFOVHFTDZGHRRESSFLRRBFQAHHAAKSGRW	811
627	QY	IIGLWYGGVVIATVIFITLVKCKKQKVTSTH-HGWVFDVAATVP-----FFRRJLSKMQQ	679
812	DB	YFTTSPAGTALMAAEVGVAVAKWRISSKSPACGFIEDQNVITHPTVTEEKIIVPNMQI	871
680	QY	NGYENTPYKFFE	691
872	DB	NGYENTPYKFE	883

RESULT 14
 S38344
 CDEI-binding protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1995
 C:Accession: S38344
 R:Hanes, C.; von der Kammer, H.; Kristjansson, G.I.; Scheit, K.H.
 Biochim. Biophys. Acta 1216, 154-156, 1993
 A:Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
 A:Reference number: S38344; M0ID:94032480; PMID:6215408
 A:Accession: S38344
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-246 <HAN>
 A:Cross-references: EMBL:222592
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Knitz-type protease

[illegible]

RESULT 15
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993; sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.F.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
A:Reference number: PQ0438; MCID:93075180; PMID:1445331
A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657

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R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
  Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide ir
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 42-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal; Kunitz-type protein
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match      11.1%; Score 406; DB 2; Length 62;
Best Local Similarity 98.8%; Pred. No. 3, ie-15;
Matches 81; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 581 SGLTNKTEISEVKKMDAFRHDSDGYEVHQKLVFPAEDVGSNKGAIIGLAVGGVWV:ATV 640
DE 1 SGLTNKTEISEVKKMDAFRHDSDGYEVHQKLVFPAEDVGSNKGAIIGLAVGGVWV:ATV 60
QY 641 IFITLVMLKKKKQVTSIHHGWE 662
DB 61 IVITLVMLKKKKQVTSIHHGWE 82

Search completed: October 2, 2003, 14:00:36
Job time : 19.5667 secs

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A;Residues: 1-82 <DAV>
A;Cross-references: GB:M83558; GB:M83657

RL Gene 87:257-263(1990).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP751).
 RC TISSUE=Brain;
 RX MEDLINE-89346754; PubMed-2569763;
 RA de Sauvage F., Octave J.N.;
 RL "A novel mRNA of the A4 amyloid precursor gene coding for a possibly
 [6] secreted protein";
 RN Science 245:651-653(1989).
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM APP695).
 RC TISSUE=Brain;
 RX MEDLINE-87231971; PubMed-3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RL "Molecular cloning and characterization of a cDNA encoding the
 [7] cerebrovascular and the neuritic plaque amyloid peptides";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RP SEQUENCE OF 286-366 FROM N.A.
 RC MEDLINE-88122640; PubMed-2893290;
 RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,
 RL "Protease inhibitor domain encoded by an amyloid protein precursor
 [8] mRNA associated with Alzheimer's disease";
 RN Nature 331:528-530(1988).
 RP SEQUENCE OF 267-367 FROM N.A.
 RC MEDLINE-88122641; PubMed-2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RL "Novel precursor of Alzheimer's disease amyloid protein shows
 [9] protease inhibitory activity";
 RN Nature 331:530-532(1988).
 RP SEQUENCE OF 507-770 FROM N.A.
 RC TISSUE=Brain Cortex;
 RX MEDLINE-88124954; PubMed-2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RL Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 [10] disease brain: coding and noncoding regions of the fetal precursor
 [11] mRNA are expressed in the cortex";
 RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RP SEQUENCE OF 523-555, AND COLLAGEN-BINDING DOMAIN.
 RX MEDLINE-96139497; PubMed-8576160;
 RA Behr D., Hesse L., Masters C.L., Multhaup G.;
 RL "Regulation of amyloid protein precursor (APP) binding to collagen and
 [12] mapping of the binding sites on APP and collagen type I";
 RN J. Biol. Chem. 271:1613-1620(1996).
 RP SEQUENCE OF 656-737 FROM N.A.
 RC MEDLINE-89392030; PubMed-2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RL "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 [13] similarity to soybean trypsin inhibitor";
 RN Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RP SEQUENCE OF 672-681.
 RC TISSUE=Brain cortex;
 RX MEDLINE-88035004; PubMed-3312495;
 RA Pardridge W.M., Vinters H.V., Fang J., Eisenberg J., Choi T.B.,
 RL Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 [14] and partial sequence of a 4,200-dalton peptide isolated from cortical
 [15] microvessels";
 RN J. Neurochem. 49:1394-1401(1987).
 RP SEQUENCE OF 674-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE-87120328; PubMed-3810169;
 RA Goldsaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
 RL "Characterization and chromosomal localization of a cDNA encoding
 [16] brain amyloid of Alzheimer's disease";

RL Gene 87:257-263(1990).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM L-APP733).
 RC TISSUE=Leukocyte;
 RX MEDLINE-92288116; PubMed-1587857;
 RA Koenig G., Moening U., Czech C., Prior R., Banati R.,
 RL Schreier-Gasser U., Bauer J., Masters C.L., Beyreuther K.;
 RT "Identification and differential expression of a novel alternative
 [6] splice isoform of the beta A4 amyloid precursor protein (APP) mRNA in
 [7] leukocytes and brain microglial cells";
 RN J. Biol. Chem. 267:10804-10809(1992).
 RP SEQUENCE FROM N.A. (ISOFORM APP770).
 RC MEDLINE-97263807; PubMed-9108164;
 RA Hattori M., Tsukahara F., Furuhata Y., Tanahashi H., Hirose M.,
 RL Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 [8] sequencing of a 300 kb region of human APP locus";
 RN Nucleic Acids Res. 25:1802-1808(1997).
 RP SEQUENCE FROM N.A. (ISOFORM APP305).
 RC TISSUE=Pancreas;
 RX MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derue J.G.,
 RL Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang G., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loquellaro N.A., Peters G.J., Abramson R.D., Millaby S.C.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vialation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 [9] human and mouse cDNA sequences";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP SEQUENCE OF 1-10 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-89016647; PubMed-3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RL "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 [10] encodes a 95-kDa polypeptide";
 RN Nucleic Acids Res. 15:9351-9351(1988).
 RP ERRATUM, AND REVISIONS.
 RA Mita S., Sadlock J., Herbert J., Schon E.A.;
 RL Nucleic Acids Res. 16:11402-11402(1988).
 RP SEQUENCE OF 1-75 FROM N.A.
 RX MEDLINE-89165870; PubMed-2538123;
 RA La Fauce G., Lahiri D.K., Salton S.R., Robakis N.K.;
 RL "Characterization of the 5'-end region and the first two exons of the
 [11] beta-protein precursor gene";
 RN Biochem. Biophys. Res. Commun. 159:297-304(1989).
 RP SEQUENCE OF 18-50.
 RC TISSUE=Fibroblast;
 RX MEDLINE-87250462; PubMed-3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RL "Purification of protease nexin II from human fibroblasts";
 RN J. Biol. Chem. 262:8508-8514(1987).

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Query Match      98.2%  Score 3585.5;  EB 1;  Length 770;
Best Local Similarity 90.0%;  Pred. No. 1.7c-17c;
Matches 593;  Conservative 1;  Mismatches 1;  Indels 75;  Gaps 1;

QY 1  MLPLGLALLLAANTARALEVPTDGNAGLLAPQ*AMFCGRLNHMHVYONGKWDSPSGTK 60
DB 1  MLPLGLALLLAANTARALEVPTDGNAGLLAPQ*AMFCGRLNHMHVYONGKWDSPSGTK 60

QY 61  TCIDTKGILQYCEVYVPELQITNVVEANOPVTIQNCKKRGKCKTHPHFVLPYRCLVG 120
DB 61  TCIDTKGILQYCEVYVPELQITNVVEANOPVTIQNCKKRGKCKTHPHFVLPYRCLVG 120

QY 121  EFVSALLVPDKKFLHQERMDVCEHLLHHTVAKETCSEKSTKLHDYGMLLPGCLDKFR 180
DB 121  EFVSALLVPDKKFLHQERMDVCEHLLHHTVAKETCSEKSTKLHDYGMLLPGCLDKFR 180

QY 191  GVEFVCCPLAESONVSDADAEEDSDVWVGADIDVADGSEDKVYVAEEVAEVEE 240
DB 191  GVEFVCCPLAESONVSDADAEEDSDVWVGADIDVADGSEDKVYVAEEVAEVEE 240

QY 241  EADDDEDDDEDEVEEAEFEYEATERTTSIATITTTTTSVEVEVVR----- 288
DB 241  EADDDEDDDEDEVEEAEFEYEATERTTSIATITTTTTSVEVEVVR----- 288

QY 289  ----- 288
DB 289  ----- 288

QY 301  RAMISRWFVTEGKCAPFFYGGCGGNRNFDTEYCMVAGCSAMSOGLTKTQEP*AR 360
DB 301  RAMISRWFVTEGKCAPFFYGGCGGNRNFDTEYCMVAGCSAMSOGLTKTQEP*AR 360

QY 289  ---VPTTAASPDADVKYLETPGDENEHAHFQKAKERLEAKHRERMSQVHREAEERQA 345
DB 361  PVKLEPTTAASPDADVKYLETPGDENEHAHFQKAKERLEAKHRERMSQVHREAEERQA 420

QY 346  KNLPRADKKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITAL 405
DB 421  KNLPRADKKAVTQHFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITAL 460

QY 406  QAVPRPRHVENMLKKYRAEKDRQHTLKHFHVRVYDPKKAQIRSQVWTHLRVIYER 465
DB 481  QAVPRPRHVENMLKKYRAEKDRQHTLKHFHVRVYDPKKAQIRSQVWTHLRVIYER 540

QY 466  MNQSLSLYNPVAAVEE-QDEVELLQEQNYSDVLANMISEPRISYGNDAIMPSTET 525
DB 541  MNQSLSLYNPVAAVEEIQDEVELLQEQNYSDVLANMISEPRISYGNDAIMPSTET 600

QY 526  KTTVELLPVNGEFLSDLOPHHSTGADSVPAANTEVEFVPCARPAADRGLTTRFGSGLTN 585
DB 601  KTTVELLPVNGEFLSDLOPHHSTGADSVPAANTEVEFVPCARPAADRGLTTRFGSGLTN 660

QY 586  IKTEISEVKMDAEFRHDSGYEVHQQKLVFFAEDVGSNGKALIGLMVGGVVIATVIFITL 645
DB 661  IKTEISEVKMDAEFRHDSGYEVHQQKLVFFAEDVGSNGKALIGLMVGGVVIATVIVITL 720

QY 646  VMLKKKQVTSIHGGVVEVDAAVTPERHLSKMQQNGYENPTYKFFEQMOKN 695
DB 721  VMLKKKQVTSIHGGVVEVDAAVTPERHLSKMQQNGYENPTYKFFEQMOKN 770

RESULT 2
A4_MACFA
ID A4_MACFA STANDARD; PRT; 770 AA.
AC P53601; Q95KN7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40);
DE Gamma-Ctf(59) (Gamma-secretase C-terminal fragment 59); Gamma-Ctf(57)
DE (Gamma-secretase C-terminal fragment 57); Gamma-Ctf(50) (Gamma-
DE secretase C-terminal fragment 50); C31].
GN APP.
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OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS APP695 AND APP770).
RC TISSUE=Cerebellum;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlisny M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
CC -!- FUNCTION: Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell mobility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APBB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(O) and JIP (By
CC similarity). Inhibits G(O) alpha Arpase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction. In vitro, copper-metalated APP induces neuronal
CC death directly or is potentiated through Cu(II)-mediated low-
CC density lipoprotein oxidation (By similarity). Can regulate
CC neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPII domain
CC possess protease inhibitor activity (By similarity).
CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron (By similarity).
CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
CC peptides, including C31, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB family members, the APPA
CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
CC interacts with GPCR-like protein BPP, FRL1, APPB1, IBL, KNS2
CC (via its IPR domains) (By similarity), APPB2 (via BASS) and DBP1.
CC In vitro, it binds MAP7 via the MT-binding domains (By
CC similarity). Associates with microtubules in the presence of A-P
CC and in a kinesin-dependent manner (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated
CC pits. During maturation, the immature APP (N-glycosylated in the
CC endoplasmic reticulum) moves to the Golgi complex where complete
CC maturation occurs (O-glycosylated and sulfated). After alpha-
CC secretase cleavage, soluble APP is released into the extracellular
CC space and the C-terminal is internalized to endosomes and
CC lysosomes. Some APP accumulates in secretory transport vesicles
CC leaving the late Golgi compartment and returns to the cell
CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
CC nuclei of neurons (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=APP770;
CC IsoID=P53601-1; Sequence=Displayed;
CC Name=APP695;
CC IsoID=P53601-2; Sequence=VSP_000010; VSP_000011;
CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells (By similarity).
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
```

interaction. The PID domain-containing proteins which bind APP require the YENPTY motif for full interaction. These interactions are independent of phosphorylation on the terminal tyrosine residue. The NPXY site is also involved in clathrin-mediated endocytosis (By similarity).

-!- PTM: Proteolytically processed under normal cellular conditions. Cleavage by alpha-secretase or alternatively by beta-secretase leads to generation and extracellular release of soluble APP peptides, S-APP-alpha and S-APP-beta, respectively, and the retention of corresponding membrane-anchored C-terminal fragments, C83 and C99. Subsequent processing of C83 by gamma-secretase yields p3 peptides. This is the major secretory pathway and is nonamyloidogenic. Alternatively, presenilin/epsilon-catalyzed gamma-secretase processing of C99 releases the amyloid beta proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42). Major components of amyloid plaques, and the cytotoxic C-terminal fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By similarity).

-!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis (By similarity). Cleavage at Asp-739 by either caspase-3, -9 or -9 results in the production of the neurotoxic C31 peptide and the increased production of beta-amyloid peptides (By similarity).

-!- PTM: N- and C-linked glycosylated (By similarity).

-!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and serine residues is neuron-specific. Phosphorylation can affect APP processing, neuronal differentiation and interaction with other proteins (By similarity).

-!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and zinc, can induce histidine-bridging between beta-amyloid molecules resulting in beta-amyloid-metal aggregates (By similarity). Extracellular zinc-binding increases binding of heparin to APP and inhibits collagen-binding (By similarity).

-!- SIMILARITY: BELONGS TO THE APP FAMILY.

-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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FT CHAIN	712	770	GAMMA-CTF(59) (POTENTIAL).
FT CHAIN	714	770	GAMMA-CTF(57) (POTENTIAL).
FT CHAIN	721	770	GAMMA-CTF(50) (POTENTIAL).
FT CHAIN	740	770	C31 (POTENTIAL).
FT DOMAIN	18	699	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	700	723	POTENTIAL.
FT DOMAIN	724	770	CYTOPLASMIC (POTENTIAL).
FT DOMAIN	96	110	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	181	188	BPTI/KUNITZ INHIBITOR.
FT DOMAIN	291	341	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	391	423	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	491	522	HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN	523	540	COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN	732	751	INTERACTION WITH G(O)-ALPHA (BY SIMILARITY).
FT DOMAIN	230	260	ASP/GLO-RICH (ACIDIC).
FT DOMAIN	274	280	POLY-THR.
FT SITE	144	144	REQUIRED FOR COPPER(II) REDUCTION (BY SIMILARITY).
FT ACT_SITE	301	302	REACTIVE BOND (BY SIMILARITY).
FT SITE	671	672	CLEAVAGE (BY BETA-SECRETASE).
FT SITE	672	673	(BY SIMILARITY).
FT SITE	687	688	CLEAVAGE (BY CASPASE-6) (BY SIMILARITY).
FT SITE	704	704	CLEAVAGE (BY ALPHA-SECRETASE) (BY SIMILARITY).
FT SITE	706	706	IMPLICATED IN FREE RADICAL PROPAGATION (BY SIMILARITY).
FT SITE	711	712	INVOLVED IN OXIDATIVE REACTIONS (BY SIMILARITY).
FT SITE	713	714	CLEAVAGE (BY GAMMA-SECRETASE; SITE 1) (BY SIMILARITY).
FT SITE	720	721	CLEAVAGE (BY GAMMA-SECRETASE; SITE 2) (BY SIMILARITY).
FT SITE	724	734	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3) (BY SIMILARITY).
FT SITE	739	740	BASOLATERAL SORTING SIGNAL (BY SIMILARITY).
FT SITE	757	760	CLEAVAGE (BY CASPASES-3, -6, -8 OR -9) (BY SIMILARITY).
FT SITE	759	762	ENDOCYTOSIS SIGNAL.
FT SITE			NPXY MOTIF.

Query Match 98.2%; Score 3585.5; DB 1; Length 770;
 Best Local Similarity 90.0%; Pred. No. 1.7e-170;
 Matches 693; Conservative 1; Mismatches 1; Indels 75; Gaps 1;

QY	1	MLPGLALLLLA	AWTARALEVPTDGNAGLLAE	PTAMFCGR	LNMMHNVQNGK	WSDSPSTK	60
DB	1	MLPGLALLLLA	AWTARALEVPTDGNAGLLAE	PTAMFCGR	LNMMHNVQNGK	WSDSPSTK	60
QY	61	TCIDTKEGILQY	QCEVYPPELQITNV	VEANQPV	TONMCKRGR	KCKCKTHPRV	120
DB	61	TCIDTKEGILQY	QCEVYPPELQITNV	VEANQPV	TONMCKRGR	KCKCKTHPRV	120
QY	121	EFVSDALLVP	DKCKFLHQRMDVC	THLHWHTVAKET	CEKSTINLH	DYGMLLPG	180
DB	121	EFVSDALLVP	DKCKFLHQRMDVC	THLHWHTVAKET	CEKSTINLH	DYGMLLPG	180
QY	181	GVEFVCCPLAES	ONVSDADAEEDSD	OVWVGADTDY	ADGSEDKV	VEVAEEVEE	240
DB	181	GVEFVCCPLAES	ONVSDADAEEDSD	OVWVGADTDY	ADGSEDKV	VEVAEEVEE	240
QY	241	EADDDDEDD	DEVEEEAEPEE	ATEPTT	SIATTTT	TTTTSVEEVV	288
DB	241	EADDDDEDD	DEVEEEAEPEE	ATEPTT	SIATTTT	TTTTSVEEVV	288
QY	289						
DB	289						
QY	301	RAMISRWY	FDVTEGKCAPFF	YGGCGGN	NFNDETEY	CMVCGSVMS	350
DB	301	RAMISRWY	FDVTEGKCAPFF	YGGCGGN	NFNDETEY	CMVCGSVMS	350
QY	289	----	VPTTAAS	TPDAVDKYLE	TPGDENE	HAHFQKAKER	345
DB	289	----	VPTTAAS	TPDAVDKYLE	TPGDENE	HAHFQKAKER	345
QY	361	PVKLEPT	TAAS	TPDAVDKYLE	TPGDENE	HAHFQKAKER	420
DB	361	PVKLEPT	TAAS	TPDAVDKYLE	TPGDENE	HAHFQKAKER	420

QY 346 KNLPRADKKAVIQHFEQKVESLEQEAANEEOQLVETHMARVEAMLNDRKRLALENYIAL 405
 DB 421 KNLPRADKKAVIQHFEQKVESLEQEAANEEOQLVETHMARVEAMLNDRKRLALENYIAL 480
 QY 406 QAVPPRRHVNMLKKYVRAEQKQHQHTLKHFHVRMYDPKKAQIRSQVWTHLVYIVER 465
 DB 481 QAVPPRRHVNMLKKYVRAEQKQHQHTLKHFHVRMYDPKKAQIRSQVWTHLVYIVER 540
 QY 466 MNQSLSLYNNPAVAEFLQDEVELLOKEQNYSDOVLANMKSEPAISYGNDAIMPSTJET 525
 DB 541 MNQSLSLYNNPAVAEFLQDEVELLOKEQNYSDOVLANMKSEPAISYGNDAIMPSTJET 600
 QY 526 KTVIVLLPVGNGEFLDLOPHSFQADSVDPANTENEPVDPARPAADGLTTRGSGLTN 585
 DB 601 KTVIVLLPVGNGEFLDLOPHSFQADSVDPANTENEPVDPARPAADGLTTRGSGLTN 650
 QY 586 KTEIETSEVKMDAERHDSGVYEHVHQKLVFFAEDVGSNKGAIIGLVGVGVIAIVYVILL 645
 DB 661 KTEIETSEVKMDAERHDSGVYEHVHQKLVFFAEDVGSNKGAIIGLVGVGVIAIVYVILL 720
 QY 646 VMLKKKQYTSIHGVEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQKN 695
 DB 721 VMLKKKQYTSIHGVEVDAAVTPPEERHLSKMQQNGYENPTYKFFEQKN 770

RESULT 3
 AC_SAISC STANDARD: PRT: 751 AA.
 AC 095241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
 DE protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha); Soluble
 DE APP-beta (S-APP-beta); C59; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(40); Gamma-
 DE CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 GN APP
 OS *Saimiri sciureus* (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
 ON NCBI_TaxID=9521;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Liver;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Anorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with
 RT cerebral amyloid angiopathy.";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APB1/p160 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G10 and JIP (By
 CC similarity). Inhibits G10 alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction. In vitro, copper-metallated APP induces neuronal
 CC death directly or is potentiated through Cu(II)-mediated low-
 CC density lipoprotein oxidation (By similarity). Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I and IV (By
 CC similarity). The splice isoforms that contain the BPTI domain
 CC possess protease inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators

CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAP8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPP1, I81, KNS2
 CC (via its TPR domains) (By similarity). APPBP2 (via BaSS) and DBA.
 CC In vitro, it binds MAP2 via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized into endosomes and
 CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
 CC nuclei of neurons (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=APP770;
 CC IsoId=O95241-1; Sequence=Displayed;
 CC Name=APP695;
 CC IsoId=O95241-2; Sequence=Not described;
 CC -!- DOMAIN: The basolateral sorting signal (BaSS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/alpha-secretase
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-720 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-linked glycosylated (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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CC EMBL: S81024; AAD14347.1; ..
 DR HSSP: P05067; LAAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR001255; Beta_APP.
 DR InterPro: IPR002223; Kunitz_SF1.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF03494; Beta_APP; 1.
 DR Pfam: PF00014; Kunitz_SF1; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR PRODOM: PD00022; Kunitz_SF1; 1.
 DR SMART: SM00005; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
 KW Coated pits; Neutrons; Heparin-binding; Metal-binding; Copper; Iron;
 KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
 KW Proteoglycan; Amyloid; Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 751
 FT CHAIN 18 568
 FT CHAIN 18 552
 FT CHAIN 653 751
 FT CHAIN 653 694
 FT CHAIN 653 652
 FT CHAIN 659 751
 FT CHAIN 659 694
 FT CHAIN 669 692
 FT CHAIN 693 751
 FT CHAIN 695 751
 FT CHAIN 702 751
 FT CHAIN 721 751
 FT CHAIN 721 680
 FT DOMAIN 18 680
 FT TRANSMEM 681 704
 FT DOMAIN 705 751
 FT DOMAIN 96 110
 FT DOMAIN 181 188
 FT DOMAIN 291 341
 FT DOMAIN 316 344
 FT DOMAIN 363 428
 FT DOMAIN 504 521
 FT DOMAIN 713 732
 FT DOMAIN 230 260
 FT DOMAIN 274 280
 FT SITE 144 144
 FT ACT_SITE 301 302
 FT SITE 652 653
 FT SITE 653 654
 FT SITE 668 669
 FT SITE 685 685
 FT SITE 687 687
 FT SITE 692 693
 FT SITE 694 695
 FT SITE 695 695

FT	SITE	701	702	CLEAVAGE (BY GAMMA-SECRETASE; SITE 3)
FT	SITE	705	715	(BY SIMILARITY).
FT	SITE	720	721	BASOLATERAL SORTING SIGNAL
FT	SITE	738	741	(BY SIMILARITY).
FT	SITE	740	743	CLEAVAGE (BY CASPASES-3, -6, -8 OR -9)
FT	METAL	137	137	(BY SIMILARITY).
FT	METAL	137	137	ENDOCYTOSIS SIGNAL.
FT	METAL	137	137	NPXY MOTIF.
FT	METAL	137	137	COPPER (BY SIMILARITY).
Query Match	98.0%	Score 3579;	DB 1: Length 751;	
Best Local Similarity	91.9%	Pred No. 3.4e-170;		
Matches	690;	Conservative	2; Mismatches	3; Indels
56;	Gaps	1;		
QY	1	MLPGIALLLA	AWTARA	LEVPTDGNAGLAPQIAMFCGR
DB	1	MLPGIALLLA	AWTARA	LEVPTDGNAGLAPQIAMFCGR
QY	61	TCIDTKEG	ILQYCE	VYPELOIINVVEANQPVTONCKRGRKCKTHPHFVPRCLVG
DB	61	TCIDTKEG	ILQYCE	VYPELOIINVVEANQPVTONCKRGRKCKTHPHFVPRCLVG
QY	121	EFVSDALL	VPDKCF	LHOERMDVCETHLRHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR
DB	121	EFVSDALL	VPDKCF	LHOERMDVCETHLRHHTVAKETCSEKSTNLHDYGMLLPCGIDKFR
QY	181	GVEFVCCP	LAESD	SHVSDADAEEDSDVWVGADIDYADGSEDKVVVEAEVEEVEE
DB	181	GVEFVCCP	LAESD	SHVSDADAEEDSDVWVGADIDYADGSEDKVVVEAEVEEVEE
QY	241	EADDDDEDD	GDGEVEE	EAPEEATERTTSTATTTTTTSTESVEEVR
DB	241	EADDDDEDD	GDGEVEE	EAPEEATERTTSTATTTTTTSTESVEEVR
QY	289	-----	-----	-----VPTTAASIPDAVKYL
DB	301	RAHISRWY	FDVTGK	CAFPFFYGGCGGNRNEDTEYCGMAVCGSVIPTTAASTPDAVDKYL
QY	305	ETPGDENE	HAHFQK	AKERLEAKHREMSQVHWEAEERQAKNLPKADKAVIOHFQEKV
DB	361	ETPGDENE	HAHFQK	AKERLEAKHREMSQVHWEAEERQAKNLPKADKAVIOHFQEKV
QY	365	ESLEGEAAN	ERQCLV	ETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLKKYVR
DB	421	ESLEGEAAN	ERQCLV	ETHMARVEAMLNDRRLALENYITALQAVPPRPRHVNMLKKYVR
QY	425	AEQKORH	TLKHFE	HVMVDPKAAQIRSOVMTHLRYVERMNSLSLLYNVPAVEEIQ
DB	481	AEQKORH	TLKHFE	HVMVDPKAAQIRSOVMTHLRYVERMNSLSLLYNVPAVEEIQ
QY	485	DEVDELLQ	KEQNY	SDVVLANNMISEPRISYGNDAIMPSTETKTIVVELLPVNGEFLDQLQ
DB	541	DEVDELLQ	KEQNY	SDVVLANNMISEPRISYGNDAIMPSTETKTIVVELLPVNGEFLDQLQ
QY	545	PWHSFGAD	SVDPANTE	NEVEPVDARPAADRGTLTPRGSGLTNKTETEEISEVMKDAEFRHDS
DB	601	PWHSFGAD	SVDPANTE	NEVEPVDARPAADRGTLTPRGSGLTNKTETEEISEVMKDAEFRHDS
QY	605	GVEVHQK	LVFFAE	DVGSNKGAIIGLMVGGVVIATVITLVMKKKQYTSIHGGVVEVD
DB	661	GVEVHQK	LVFFAE	DVGSNKGAIIGLMVGGVVIATVITLVMKKKQYTSIHGGVVEVD
QY	665	AAVTPEER	HLSKMQQ	NGYENPTYKFFEQMON 695
DB	721	AAVTPEER	HLSKMQQ	NGYENPTYKFFEQMON 751

RESULT 4
 A4_PIG
 ID A4_PIG
 AC P79307; Q29023; Q9TU10;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)

DT 15-SEP-2003 (Rel. 42, last annotation update);
 DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
 DE amyloid protein homolog) [Contains: Soluble APP-alpha (S-APP-alpha);
 DE Soluble APP-beta (S-APP-beta); C99; Beta-amyloid protein 42 (Beta-
 DE APP42); Beta-amyloid protein 40 (Beta-APP40); C83; P3(42); P3(46);
 DE Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57)
 DE (Gamma-secretase C-terminal fragment 57); Gamma-CTF(50) (Gamma-
 DE secretase C-terminal fragment 50); C31].
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.;
 RT "Amyloid precursor protein 770.*";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-136 FROM N.A.
 RA TISSUE-Small intestine; N.A.
 RA Winteroe A.K., Fredholm M.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 667-723 FROM N.A.
 RA Johnson E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell motility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/Tip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and JIP (By
 CC similarity). Inhibits G(O) alpha ATPase activity (By similarity).
 CC Acts as a kinesin I membrane receptor, mediating the axonal
 CC transport of beta-secretase and presenilin 1 (By similarity). May
 CC be involved in copper homeostasis/oxidative stress through copper
 CC ion reduction (By similarity). In vitro, copper-metallated APP
 CC induces neuronal death directly or is potentiated through C-(31)-
 CC mediated low-density lipoprotein oxidation (By similarity). Can
 CC regulate neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen 2 and IV (By
 CC similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as
 CC copper, zinc and iron (By similarity).
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminus, to the PID domain of several
 CC cytoplasmic proteins, including APBB family members, the APBA
 CC family, MAPK8IP1, and SHC1. Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein APP, FPR1, APPBP1, I31, KMS2
 CC (via its TPR domains) (By similarity). APPBP2 (via Bass) and DDB1
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of A-P
 CC and in a kinesin-dependent manner (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC endoplasmic reticulum) moves to the Golgi complex where complete
 CC maturation occurs (O-glycosylated and sulfated). After alpha-
 CC secretase cleavage, soluble APP is released into the extracellular
 CC space and the C-terminal is internalized to endosomes and

CC lysosomes. Some APP accumulates in secretory transport vesicles
 CC leaving the late Golgi compartment and returns to the cell
 CC surface. GammaCTF(59) peptide is located to both the cytoplasm and
 CC nuclei of neurons (By similarity).
 CC -!- DOMAIN: The basolateral sorting signal (BASS) is required for
 CC sorting of membrane proteins to the basolateral surface of
 CC epithelial cells (By similarity).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The PID domain-containing proteins which bind APP
 CC require the YENPTY motif for full interaction. These interactions
 CC are independent of phosphorylation on the terminal tyrosine
 CC residue. The NPXY site is also involved in clathrin-mediated
 CC endocytosis (By similarity).
 CC -!- PTM: Proteolytically processed under normal cellular conditions.
 CC Cleavage by alpha-secretase or alternatively by beta-secretase
 CC leads to generation and extracellular release of soluble APP
 CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
 CC retention of corresponding membrane-anchored C-terminal fragments,
 CC C83 and C99. Subsequent processing of C83 by gamma-secretase
 CC yields P3 peptides. This is the major secretory pathway and is
 CC nonamyloidogenic. Alternatively, presenilin/nicastrin-mediated
 CC gamma-secretase processing of C99 releases the amyloid beta
 CC proteins, amyloid-beta 40 (Abeta40) and amyloid-beta 42 (Abeta42),
 CC major components of amyloid plaques, and the cytotoxic C-terminal
 CC fragments, gammaCTF(50), gammaCTF(57) and gammaCTF(59) (By
 CC similarity).
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal apoptosis
 CC (By similarity). Cleavage at Asp-739 by either caspase-3, -8 or -9
 CC results in the production of the neurotoxic C31 peptide and the
 CC increased production of beta-amyloid peptides (By similarity).
 CC -!- PTM: N- and O-linked glycosylation (By similarity).
 CC -!- PTM: Phosphorylation in the C-terminal on tyrosine, threonine and
 CC serine residues is neuron-specific. Phosphorylation can affect APP
 CC processing, neuronal differentiation and interaction with other
 CC proteins (By similarity).
 CC -!- PTM: Extracellular binding and reduction of copper, results in a
 CC corresponding oxidation of Cys-144 and Cys-158, and the formation
 CC of a disulfide bond (By similarity).
 CC -!- MISCELLANEOUS: Chelation of metal ions, notably copper, iron and
 CC zinc, can induce histidine-bridging between beta-amyloid molecules
 CC resulting in beta-amyloid-metal aggregates (By similarity).
 CC Extracellular zinc-binding increases binding of heparin to APP and
 CC inhibits collagen-binding (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: Contains 1 BPT1/kunitz inhibitor domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB032550; BAA84580.1; -
 CC EMBL; 284022; CAB06313.1; -
 CC EMBL; X56127; CAB39592.1; -
 CC HSSP; P03067; IAAP.
 CC InterPro: IPR008155; A4_APP.
 CC InterPro: IPR008154; A4_extra.
 CC InterPro: IPR001255; Beta-APP.
 CC InterPro: IPR002223; Kunitz_BPT1.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS: PR0203; AMYLOIDA4.
 CC PRINTS: PR00759; BASICTPASE.
 CC PRODOM: PD000222; Kunitz_BPT1; 1.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.

Dd	241	EADEDDDEDGDVEEAEPEEATERTTISIAITTTTTTSEVEEVKVEVCSQAETGPC	300
Qy	289	-----	288
Dd	301	RAMISRWYFDVTEGKCAPFFYGGCGGNRNFDTTEECVACGVSMSQSLLKTIQEHLPQD	360
Qy	289	----VPTTAASPDADVDKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEQA	345
Dd	361	PKVLPPTTAASPDADVDKYLETPGDENHAFQKAKERLEAKHREMSQVMREWEAEQA	420
Qy	346	KNLPKADKKAVTQHFQKRVESLEQEAANEQQQLVETHMARVEAMLNDRRLALENYITAL	405
Dd	421	KNLPKADKKAVTQHFQKRVESLEQEAANEQQQLVETHMARVEAMLNDRRLALENYITAL	480
Qy	406	QAVPPRPRIHVNMLKKYVRAEQKQRQHTLKHFEHVRWDPVKRAAQIRSOVMTHLVVIYER	465
Dd	481	QAVPPRPRIHVNMLKKYVRAEQKQRQHTLKHFEHVRWDPVKRAAQIRSOVMTHLVVIYER	540
Qy	466	MNQSLSLLYNPVAFAEEIQDEVDLQKEQNYSDGVLANMLSEPRISYGNDAIMPSTLET	525
Dd	541	MNQSLSLLYNPVAFAEEIQDEVDLQKEQNYSDGVLANMLSEPRISYGNDAIMPSTLET	600
Qy	526	KTIVELLPNVGEFSLDLPQWHSGCAGSVANTENEVEPVDARPAADRGITTRPGSGLTN	585
Dd	601	KTIVELLPNVGEFSLDLPQWHSGCAGSVANTENEVEPVDARPAADRGITTRPGSGLTN	660
Qy	586	IKTEEISEVKMDAEPFHDSGYEVHHQKLVLPFAEDVGSNKGAIIGLMVGSGVIATVIPITL	645
Dd	661	IKTEEISEVKMDAEPFHDSGYEVHHQKLVLPFAEDVGSNKGAIIGLMVGSGVIATVIPITL	720
Qy	646	VMLKKQVTSIHGGVVEVDAAVTPTEHRLSKMQQNGYENPTYKFFQMQON	695
Dd	721	VMLKKQVTSIHGGVVEVDAAVTPTEHRLSKMQQNGYENPTYKFFQMQON	770
RESULT 5			
AD	A4_CAVPO	STANDARD;	PRI: 770 AA.
ID	A4_CAVPO		
AC	O60495; Q60496;		
DT	15-SEP-2003 (Rel. 42, Created)		
DT	15-SEP-2003 (Rel. 42, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease		
DE	amyloid protein homolog) [Contents: Soluble APP-alpha (S-APP-alpha);		
DE	Soluble APP-beta (S-APP-beta); CTF-alpha; CTF-beta; Beta-amyloid		
DE	protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); P3(42);		
DE	P3(40); CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-		
DE	CTF(57) (Gamma-secretase C-terminal fragment 57); C31].		
GN	APP.		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.		
OX	NCBI_TaxID=10141;		
ON	[1]		
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.		
RC	TISSUE=Brain, and Liver;		
RX	MEDLINE=97236426; PubMed=916031;		
RA	Buck M., Mceller D., Rigl V.;		
RT	"Amyloid precursor protein in Guinea pigs - complete cDNA sequence and		
RT	alternative splicing."		
RL	Biochim. Biophys. Acta 1351:17-21(1997).		
RP	[2]		
RP	INTERACTION OF BETA-APP40 WITH APOE.		
RX	MEDLINE=98007700; PubMed=9349544;		
RA	Martel C.L., Mackic J.B., Matsubara E., Gervanale S., Miguel C.,		
RA	Miao W., McComb J.G., Frangione B., Giso J., Zlokovic B.V.;		
RT	"Isoform-specific effects of apolipoproteins E2, E3, and E4 on		
RT	cerebral capillary sequestration and blood-brain barrier transport of		
RT	circulating Alzheimer's amyloid beta."		
RL	J. Neurochem. 69:1993-2004(1997).		
RP	[3]		
RP	PROCESSING.		
RX	MEDLINE=20084499; PubMed=10619481;		

RA Beck M., Brueckner M.K., Holzer M., Kaap S., Pannicke T., Arendt T.,
RA Bigl V.,
RT "Guinea-pig primary cell cultures provide a model to study expression
RT of amyloidogenic processing of endogenous amyloid precursor
RL protein.";
RL Neuroscience 95:243-254(2000).
RN [4]

RP GAMMA-SECRETASE PROCESSING;
RX MEDLINE-20576391; PubMed=11035007;
RA Pinnix I., Musunuru U., Tun H., Sridharan A., Golde T., Eckman C.,
RA Ziani-Cherif C., Onstead L., Sambamurti K.,
RT "A novel gamma-secretase assay based on detection of the putative
RT C-terminal fragment-gamma of amyloid beta protein precursor.";
RL J. Biol. Chem. 276:431-487(2001).
CC

CC **!- FUNCTION:** Functions as a cell surface receptor and performs
CC physiological functions on the surface of neurons relevant to
CC neurite growth, neuronal adhesion and axonogenesis. Involved in
CC cell motility and transcription regulation through protein-protein
CC interactions (By similarity). Can promote transcription activation
CC through binding to APPB1/Tip60 and inhibit Notch signaling through
CC interaction with Numb (By similarity). Couples to apoptosis-
CC inducing pathways such as those mediated by G(C) and JIP (By
CC similarity). Inhibits G(0) alpha Arpase activity (By similarity).
CC Acts as a kinesin I membrane receptor, mediating the axonal
CC transport of beta-secretase and presenilin 1 (By similarity). May
CC be involved in copper homeostasis/oxidative stress through copper
CC ion reduction (By similarity). In vitro, copper-metallated APP
CC induces neuronal death directly or is potentiated through Cu(II)-
CC mediated low-density lipoprotein oxidation (By similarity). Can
CC regulate neurite outgrowth through binding to components of the
CC extracellular matrix such as heparin and collagen I and IV (By
CC similarity). The splice isoforms that contain the BPTI domain
CC possess protease inhibitor activity (By similarity).
CC

CC **!- FUNCTION:** Beta-amyloid peptides are lipophilic metal chelators
CC with metal-reducing activity. Bind transient metals such as
CC copper, zinc and iron. Beta-amyloid peptides bind to lipoproteins
CC and apolipoproteins E and J in the CSF and to HDL particles in
CC plasma, inhibiting metal-catalyzed oxidation of lipoproteins.
CC

CC **!- FUNCTION:** Apicaps elicit adhesion of neural cells to the
CC extracellular matrix and may regulate neurite outgrowth in the
CC brain (By similarity).
CC

CC **!- FUNCTION:** The gamma-C9 peptides as well as the caspase-cleaved
CC peptides, including C3i, are potent enhancers of neuronal
CC apoptosis (By similarity).
CC

CC **!- SUBUNIT:** Birds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APPB family members, the APBA
CC family, MAPK8IP1, SHC1 and Numb and Dab1 (By similarity). Also
CC interacts with GPCR-like protein Bp, EPRL1, APPBPI, IBI, KNS2
CC (via its TPR domains). APPB2 (via BASS) and DDB1 (By similarity).
CC Associates with microtubules in the presence of ATP and in a
CC kinesin-dependent manner (By similarity). Soluble Abeta40 binds
CC all three isoforms of APOE, in vitro and in vivo. When lipidated,
CC the apoE4 isoform-beta-APP40 complex is capable of being
CC transported across the blood-brain barrier.
CC

CC **!- SUBCELLULAR LOCATION:** Type I membrane protein. Cell surface
CC protein that rapidly becomes internalized via clathrin-coated pits
CC (By similarity). During maturation, the immature APP (N-
CC glycosylated in the endoplasmic reticulum) moves to the Golgi
CC complex where complete maturation occurs (O-glycosylated and
CC sulfated) (By similarity). After alpha-secretase cleavage, soluble
CC APP is released into the extracellular space and the C-terminal is
CC internalized to endosomes and lysosomes (By similarity). Some APP
CC accumulates in secretory transport vesicles leaving the late Golgi
CC compartment and returns to the cell surface (By similarity). APP
CC sorts to the basolateral surface in epithelial cells (By
CC similarity).
CC

CC **!- ALTERNATIVE PRODUCTS:**
CC Event-Alternative splicing; Named isoforms=2;
CC Comment-Additional isoforms, missing exons 7,8 and 15, seem to
CC exist. The L-isoforms, missing exon 15, are referred to as
CC appicaps;
CC Name=APP770;
CC

CC IsoId=O60495-1; Sequence=Displayed;
CC Name=APP695;
CC IsoId=O60495-2; Sequence=VSP_007221, VSP_007222;
CC **TISSUE SPECIFICITY:** Isoform APP695 is the major isoform found in
CC brain. The longer isoforms containing the BPTI domain are
CC predominantly expressed in peripheral organs such as muscle and
CC liver.
CC

CC **!- INDUCTION:** Increased levels during neuronal differentiation.
CC **!- DOMAIN:** The basolateral sorting signal (BASS) is required for
CC sorting of membrane proteins to the basolateral surface of
CC epithelial cells.
CC

CC **!- DOMAIN:** The NPYX sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPYX motif are often required for complete
CC interaction. The PID domain-containing proteins which bind APP
CC require the YENPTY motif for full interaction. These interactions
CC are independent of phosphorylation on the terminal tyrosine
CC residue (By similarity). The NPYX site is also involved in
CC clathrin-mediated endocytosis.
CC

CC **!- PTM:** Proteolytically processed under normal cellular conditions.
CC Cleavage by alpha-secretase or alternatively by beta-secretase
CC leads to generation and extracellular release of soluble APP
CC peptides, S-APP-alpha and S-APP-beta, respectively, and the
CC retention of corresponding membrane-anchored C-terminal fragments,
CC CTF-alpha and CTF-beta. Subsequent processing of CTF-alpha by
CC gamma-secretase yields P3 peptides. This is the major secretory
CC pathway and is non-amyloidogenic. Alternatively,
CC presenilin/nicastrin-mediated gamma-secretase processing of CTF-
CC beta releases the amyloid beta proteins, amyloid-beta 40 (Abeta40)
CC and amyloid-beta 42 (Abeta42), major components of amyloid
CC plaques, and the corresponding cytotoxic C-terminal fragments
CC (CTFs).
CC

CC **!- PTM:** Proteolytically cleaved by caspase-3 during neuronal
CC apoptosis (By similarity).
CC

CC **!- PTM:** N- and O-linked glycosylated. O-linkage of chondroitin
CC sulfate to the L-APP isoforms produces the APP proteoglycan core
CC proteins, the apicaps (By similarity).
CC

CC **!- PTM:** Phosphorylation in the C-terminal on tyrosine, threonine and
CC serine residues is neuron-specific (By similarity).
CC Phosphorylation can affect APP processing, neuronal
CC differentiation and interaction with other proteins.
CC

CC **!- PTM:** Extracellular binding and reduction of copper, results in a
CC corresponding oxidation of Cys-144 and Cys-158, and the formation
CC of a disulfide bond (By similarity).
CC

CC **!- MISCELLANEOUS:** Chelation of metal ions, notably copper, iron and
CC zinc, can induce histidine-bridging between beta-amyloid molecules
CC resulting in beta-amyloid-metal aggregates.
CC

CC **!- SIMILARITY:** BELONGS TO THE APP FAMILY.
CC

CC **!- SIMILARITY:** Contains 1 BPTI/Kunitz inhibitor domain.
CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC

CC EMBL: X97631; CAA56230.1; -;
CC EMBL: X99198; CAA67589.1; -;
CC HSSP: P05C67; 1BA4.
CC InterPro: IPR008155; A4_APP.
CC InterPro: IPR008154; A4_extra.
CC InterPro: IPR001255; Beta-APP.
CC Pfam: PF00014; Kunitz_BPTI; 1.
CC PRINTS: PR00203; AMYLOIDA4.
CC ProDom: PD000222; Kunitz_BPTI; 1.
CC SMART: SM00006; A4_EXTRA; 1.
CC SMART: SM00131; KU; 1.
CC PROSITE: PS00319; A4_EXTRA; 1.
CC PROSITE: PS00320; A4_INTRA; 1.
CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
CC

DR PROSITE: P550279; BPTI_KUNITZ.2; 1.
KW Apoptosis; Endocytosis; Cell adhesion; Serine protease inhibitor;
KW Coated pits; Neutone; Heparin-binding; Metal-binding; Copper; Iron;
KW Zinc; Signal; Transmembrane; Glycoprotein; Phosphorylation;
KW Proteoglycan; Alternative splicing; Amyloid.
FT SIGNAL 1 17
FT CHAIN 18 770
FT CHAIN 18 687
FT CHAIN 18 671
FT CHAIN 672 770
FT CHAIN 672 713
FT CHAIN 672 711
FT CHAIN 688 710
FT CHAIN 688 713
FT CHAIN 688 711
FT CHAIN 712 770
FT CHAIN 714 770
FT CHAIN 740 770

Query Match 96.3%; Score 3517.5; DB 1; Length 770;
Best Local Similarity 88.1%; Pred. No. 3.9e-157; Gaps 1;
Matches 678; Conservative 7; Mismatches 10; Indels 75;

QY 1 MLPGLALLIARATARA-EVPTDGNAGLLAEFO-AMFGRLNMHNQNGKNSDFSGIK 60
DB 1 MLPGLALLIITWTARA-EVPTDGNAGLLAEFO-AMFGRLNMHNQNGKNSDFSGIK 60

QY 61 TCIDTKEGILQYCGEYVPELQITNVVEANQVPTONWCKRKRCKTHPHFVPIYKCLVS 120
DB 61 TCIGSKEGILQYCGEYVPELQITNVVEANQVPTONWCKRKRCKTHPHFVPIYKCLVS 120

QY 121 EFVSDALLVPDKCKFLQERMDVCEVTHLWHTVAKETCEKSTNLHLYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLQERMDVCEVTHLWHTVAKETCEKSTNLHLYGMLLPGIDKFR 180

QY 181 GVEFVCCPLAESDNDSDAEEDSDVWVGGAUTDYADGSEDKVVEAEFEVVEFE 240
DB 181 GVEFVCCPLAESDNDSDAEEDSDVWVGGAUTDYADGSEDKVVEAEFEVVEFE 240

QY 241 EADDSDDDGDEVEEAEPEEATERTTSIATTTTITTSVSEVYV----- 265
DB 241 EADDSDDDGDEVEEAEPEEATERTTSIATTTTITTSVSEVYV----- 265

QY 289 ----- 289
DB 289 ----- 289

QY 301 RSMISRWYFDVTEGKCAPFFYGGCGGNRNFDESYCHAVCGSVMSQKLLTSGEPVSQ 360
DB 289 ---VPTTAASTPDADVCKYLETPGDENEHAFQKAKERLEAKHRMSQVMEWEAEKQA 345

QY 361 PVKLPTAASTPDADVCKYLETPGDENEHAFQKAKERLEAKHRMSQVMEWEAEKQA 420
DB 346 KNLPAKDKKAVIOHFOEKVESLEQPAANERQOLVETHMARVEAMLNDRRLALENYIAL 405

QY 421 KNLPAKDKKAVIOHFOEKVESLEQPAANERQOLVETHMARVEAMLNDRRLALENYIAL 480
DB 406 QAVPPRPRHFNMLKYYVRAEOKDQHTLKHFEHVRMVDPKKAOIRSOVMTHLRVYER 465

QY 481 QAVPPRPRHFNMLKYYVRAEOKDQHTLKHFEHVRMVDPKKAOIRSOVMTHLRVYER 540
DB 466 MNGSLSLNVPAAVEEIODEYDELLQKEQNYSDSVLANMISEPRIISYGNDAKPSLTET 525

QY 541 MNGSLSLNVPAAVEEIODEYDELLQKEQNYSDSVLANMISEPRIISYGNDAKPSLTET 600
DB 526 KTTVELLPVNGEFLDDIQPHSFAGDASVPANTENEVEVDARPAADRLTTRFGSGLTN 585

QY 601 KTTVELLPVNGEFLDDIQPHSFAGDASVPANTENEVEVDARPAADRLTTRFGSGLTN 660
DB 586 IKTEEISEVKMAEPHDSGYEVHOKLVFFAEEDVCGSNKGATIGLWGVGVVAPVPIETI 645

QY 661 IKTEEISEVKMAEPHDSGYEVHOKLVFFAEEDVCGSNKGATIGLWGVGVVAPVPIETI 720
DB 646 VMLKKQYQY:SIHHGVVEYDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 695

DB 721 VMLKKQYQY:SIHHGVVEYDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN 770

RESULT 6
A4_MOUSE
ID A4_MOUSE STANDARD: PRT: 770 AA.
AC P12023; P97487; P97942; Q99K32;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid beta A4 protein precursor (APP) (ABPP) (Alzheimer's disease
DE Soluble APP-alpha (SAPP-alpha); Amyloidogenic glycoprotein (AG) [Contains:
DE Soluble APP-beta (SAPP-beta); Soluble APP-beta (SAPP-beta); C99
DE (APP-C99); Beta-amyloid protein 42 (Beta-Ap42); Beta-amyloid protein
DE 40 (Beta-Ap40); C83; P3(42); P3(40); Gamma-Ctf(59) (Gamma-secretase
DE C-terminal fragment 59) (Amyloid intracellular domain 59) (AID(59))
DE (APP-C59); Gamma-Ctf(57) (Gamma-secretase C-terminal fragment 57)
DE (Amyloid intracellular domain 57) (AID(57)) (APP-C57); Gamma-Ctf(50)
DE (Gamma-secretase C-terminal fragment 50) (Amyloid intracellular domain:
DE 50) (AID(50)); C31].
GN APP.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sakaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
R1 "Complementary DNA for the mouse homolog of the human amyloid beta
R1 protein precursor.";
R2 Biochem. Biophys. Res. Commun. 149:665-671(1987).
R3
R4 REVISIONS.
RA Yamada T.;
R3 Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RP
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
R1 "The amyloid beta protein precursor or proteinase nexin II from mouse
R1 is closer related to its human homolog than previously reported.";
R2 Biochem. Biophys. Acta 1129:141-143(1991).
R3
R4 SEQUENCE FROM N.A. (ISOFORM APP695).
RC STRAIN=SAMP8; TISSUE=Hippocampus;
RX PubMed=11235921;
RA Kumar V.B., Vyas K., Franko M., Choudhary V., Buddhiraju C.,
R1 Alvarez J., Morley J.E.;
R1 "Molecular cloning, expression, and regulation of hippocampal amyloid
R1 precursor protein of senescence accelerated mouse (SAMP8).";
R2 Biochem. Cell Biol. 79:57-67(2001).
R3
R4 SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
R1 Sakai Y.;
R1 "Positive and negative regulatory elements for the expression of the
R1 Alzheimer's disease amyloid precursor-encoding gene in mouse.";
R2 Gene 112:189-195(1992).
R3
R4 PARTIAL SEQUENCE FROM N.A. (ISOFORM APP770).
RP TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.C.,
RA A.Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshyuki S., Carninci P., Prange C.,

RA Raha S.S., Loqueillado N.A., Peters G.J., Abramson R.D., Miliady S.J., Bosak S.A., McEwan P.J., McKernan K.J., Maick J.A., Gumaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Young A.C., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein C.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903(2002).

RL [7]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING. TISSUE=Brain, and Kidney; MEDLINE=89149813; PubMed=2493250;

RX Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.; "Structure and expression of the alternatively-spliced forms of mRNA for the mouse homolog of Alzheimer's disease amyloid beta protein precursor"; Biochem. Biophys. Res. Commun. 158:906-912(1989).

RL [8]

RP SEQUENCE OF 289-364 FROM N.A. STRAIN=CD-1; TISSUE=Placenta; MEDLINE=89345111; PubMed=2569710;

RX Fukuchi K., Martin G.M., Deeb S.S.; "Sequence of the protease inhibitor domain of the A4 amyloid protein precursor of Mus domesticus"; Nucleic Acids Res. 17:5396-5396(1989).

RL [9]

RP SEQUENCE OF 656-737 FROM N.A. STRAIN=129/Sv; Wraag M.A., Busfield F., Duff K., Korenblat K., Capecechi M., Loring J.F., Goate A.M.; "Introduction of six mutations into the mouse genome using 'Hit and Run' gene-targeting: introduction of familial Alzheimer's disease mutations into the mouse amyloid precursor protein gene and humanization of the A-beta fragment"; Submitted (DEC-1996) to the ENBL/GenBank/DBJ databases.

RL [10]

RP TISSUE SPECIFICITY OF ALTERNATIVE SPLICED FORMS. PubMed=8510506; RX Sola C., Mengod G., Ghetti B., Palacios J.M., Triarhou L.C.; "Regional distribution of the alternatively spliced isoforms of beta APP RNA transcript in the brain of normal, heterozygous and homozygous weaver mutant mice as revealed by in situ hybridization histochemistry"; Brain Res. Mol. Brain Res. 17:340-346(1993).

RL [11]

RP INTERACTION WITH KNS2. PubMed=1114335; RX Kamal A., Stokin G.B., Yang Z., Xia C.-H., Goldstein L.S.; "Axonal transport of amyloid precursor protein is mediated by direct binding to the kinesin light chain subunit of kinesin II"; Neuron 28:449-459(2000).

RL [12]

RP C-TERMINAL PROTEIN-PROTEIN INTERACTIONS, AND MUTAGENESIS OF TYR-726; THR-743; TYR-757; ASN-759 AND TYR-762. MEDLINE=21408156; PubMed=11517249; RX Matsuda S., Yasukawa T., Homma Y., Ito Y., Nishikura T., Hiraki T., Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T., Kyriakis J.M., Nishimoto T.; "C-Jun N-terminal kinase (JNK)-interacting protein-1b/islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK."; J. Neurosci. 21:6597-6607(2001).

RL [13]

RP INTERACTION WITH MAPK8IP1, AND PHOSPHORYLATION. MEDLINE=22028091; PubMed=15912189; RX Taru H., Iijima K.-I., Hase M., Kirino Y., Yagi Y., Suzuki T.; "Interaction of Alzheimer's beta-amyloid precursor family proteins with scaffold proteins of the JNK signaling cascade."; J. Biol. Chem. 277:20070-20078(2002).

RA Raha S.S., Loqueillado N.A., Peters G.J., Abramson R.D., Miliady S.J., Bosak S.A., McEwan P.J., McKernan K.J., Maick J.A., Gumaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Young A.C., Rodrigues S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein C.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16893-16903(2002).

RL [14]

RP INTERACTION OF CTF PEPTIDES WITH NUMB. PubMed=12011466; RX Roncarati R., Sestan N., Scheinfeld M.H., Berechid B.E., Lopez P.A., Meucci O., McGrade J.C., Rakic P., Adamio L.; "The gamma-secretase-generated intracellular domain of beta-amyloid precursor protein binds Numb and inhibits Notch signaling."; Proc. Natl. Acad. Sci. U.S.A. 99:7102-7107(2002).

RL [15]

RP GAMMA-SECRETASE PROCESSING, AND INTERACTION WITH APBB1. PubMed=11553691; RX Cupers P., Orlans I., Craessaerts K., Annaert W., De Strooper B.; "The amyloid precursor protein (APP)-cytoplasmic fragment generated by gamma-secretase is rapidly degraded but distributes partially in a nuclear fraction of neurons in culture."; Neurochem. 78:1168-1178(2001).

CC -1- FUNCTION: Functions as a cell surface receptor and performs physiological functions on the surface of neurons relevant to neurite growth, neuronal adhesion and axonogenesis. Involved in cell mobility and transcription regulation through protein-protein interactions. Can promote transcription activation through binding to APPB1/Tip60 and inhibit Notch signaling pathways such as those mediated by G(O) and JIP. Inhibits G(O) alpha ATPase activity (By similarity). Acts as a kinesin I membrane receptor, mediating the axonal transport of beta-secretase and presenilin 1. May be involved in copper homeostasis/oxidative stress through copper ion reduction. Can regulate neurite outgrowth through binding to components of the extracellular matrix such as heparin and collagen I and IV (By similarity). The splice isoforms that contain the BPTI domain possess protease inhibitor activity (By similarity).

CC -1- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators with metal-reducing activity. Bind transient metals such as copper, zinc and iron. Rat and mouse beta-amyloid peptides bind only weakly transient metals and have little reducing activity due to substitutions of transient metal chelating residues. Beta-APP42 may activate mononuclear phagocytes in the brain and elicit inflammatory responses. Promotes both tau aggregation and TPK II-mediated phosphorylation (By similarity).

CC -1- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved peptides, including C31, are potent enhancers of neuronal apoptosis.

CC -1- SUBUNIT: Binds, via its C-terminal, to the PID domain of several cytoplasmic proteins, including APBB family members, the APBA family, MAPK8IP1, SHC1, Numb and Dab1. Binding to Dab1 inhibits its serine phosphorylation. Also interacts with GPCR-like protein BPP, FPR1, APPB1, Ibl, KNS2 (via its TPR domains), APPB2 (via BASS) and DDB1 (By similarity). In vitro, it binds MAPT via the MT-binding domains (By similarity). Associates with microtubules in the presence of ATP and in a kinesin-dependent manner (By similarity). Interacts, through a C-terminal domain, with GNAO1 (By similarity). Amyloid beta-42 binds CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid associates with HADH2 (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface protein that rapidly becomes internalized via clathrin-coated pits. During maturation, the immature APP (N-glycosylated in the endoplasmic reticulum) moves to the Golgi complex where complete

Query Match 95.5%; Score 3488.5; DB 1; Length 770;
Best Local Similarity 87.7%; Pred. No. 1,1e-165;
Matches 675; Conservative 6; Mismatches 14; Indels 75; Gaps 1;

QY 1 MLFLGALLLJAATARALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNKWSDSPGK 60
DQ 1 MLPSLALLLAAWTVRALEVPTDGNAGLLAEPOIAMFCGRLNMHMVQNKWSDSPGK 60
QY 61 TCIDTREGILQYCEVPELQITNVVEANQPTVQNKGRKQCKTHPRFVTPYCLVG 120
DB 61 TCIGTREGILQYCEVPELQITNVVEANQPTVQNKGRKQCKTHPRFVTPYCLVG 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEHLHMHVTVAKETCEKSTNLHNDYGHLLPCGIDKFR 180


```
Db 121 EFVSDALLVPDKCKFLHQRMDVCEETHLHWHTYAKETCSKSTNLNHDYGMLLPGGDKFR 180
Qy 181 GVEFVCCPLAESDNVSDAEDDDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEFE 240
Db 181 GVEFVCCPLAESDSVSDAEDDDSDVWVGADTDYADGSEDKVVEAEVEEVAEVEFE 240
Qy 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVEVR----- 288
Db 241 EADDDDEDDGDEVEEAEPEEATERTTSIATTTTTTIESVEEVEVRVCSFOAETGPC 300
Qy 289 ----- 288
Db 301 RAMISRNYFDVTEGCKV2FFVGGCGGNRNFDTREYCMVCGSVSTQSLKTTSEPLPD 360
Qy 289 ---VPTTAASTPDVAYKYLETGPDENEHAHFQAKERLEAKHRFRMSQVMRWEAEARQA 345
Db 361 PDKLPTTAASTPDVAYKYLETGPDENEHAHFQAKERLEAKHRFRMSQVMRWEAEARQA 420
Qy 346 KNLPRADKAVIQHFQCKVESLECEAANERQQLVETHWAEVAMLDNRRLALENVITAL 475
Db 421 KNLPRADKAVIQHFQCKVESLECEAANERQQLVETHWAEVAMLDNRRLALENVITAL 480
Qy 406 QAVPPRPFRHFNMLKKYVRAEQKDQHTLKHFEHVRVMDPKKAAQIRSQVMTHLRVIYER 455
Db 481 QAVPPRPFRHFNMLKKYVRAEQKDQHTLKHFEHVRVMDPKKAAQIRSQVMTHLRVIYER 540
Qy 466 MNQSLSLYNNVPAVAEETQDEVDELQEQNYSDVLANMISEPRISYGNDAIMPSJET 525
Db 541 MNQSLSLYNNVPAVAEETQDEVDELQEQNYSDVLANMISEPRISYGNDAIMPSJET 600
Qy 526 KTTVELLPVNGEFSDDIQQWHSFGADSVPAANTFNEVEPVDAKPAADRGLTTPGSGLTN 585
Db 601 KTTVELLPVNGEFSDDIQQWHSFGADSVPAANTFNEVEPVDAKPAADRGLTTPGSGLTN 660
Qy 586 IKTEISEVMKDAEFRHDSGVYEHQKLVFAEDVGSNGKGAIIIGLMVGGVZATVIFITL 645
Db 661 IKTEISEVMKDAEFRHDSGVYEHQKLVFAEDVGSNGKGAIIIGLMVGGVZATVIFITL 720
Qy 546 VMLKKKQYTSIHHGVVEVDAATVPEERHLSKMQCGYENPTYKFFEQMON 695
Db 721 VMLKKKQYTSIHHGVVEVDAATVPEERHLSKMQCGYENPTYKFFEQMON 770

RESULT 7
A4_RAT
AC P05592; STANDARD; PRT: 770 AA.
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Amyloid beta A4 protein precursor (APP) (Alzheimer's disease amyloid
DE protein homolog) (Amyloidogenic glycoprotein) (AG) (Contains: Soluble
DE APP-alpha (S-APP-alpha); Soluble APP-beta (S-APP-beta); C95; Beta-
DE amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40);
DE C83; P3(42); P3(40); Gamma-Ctf(59) (Gamma-secretase C-terminal
DE fragment 59); Gamma-Ctf(57) (Gamma-secretase C-terminal fragment 57);
DE Gamma-Ctf(50) (Gamma-secretase C-terminal fragment 50); C31].
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM APP695).
RC TISSUE=Brain;
RX MEDLINE=88312533; PubMed=200758;
RA Shivers B.D., Hilbich C., Multhaup G., Salbaum G.M., Beyreuther K.,
RA Seeburg P.H.;
RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
RL in rat brain suggests a role in cell contact.";
RN [2]
```

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RP SEQUENCE OF 289-364 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kung J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
RN [3]
RP SEQUENCE OF 720-730, AND MASS SPECTROMETRY.
RX PubMed=11483588;
RA Gu Y., Misonou H., Sato T., Dohmae N., Takio K., Ihara Y.;
RT "Distinct intramembrane cleavage of the beta-amyloid precursor protein
RT family resembling gamma-secretase-like cleavage of Notch.";
RL J. Biol. Chem. 276:35235-35238(2001).
RN [4]
RP ALTERNATIVE SPLICING.
RX PubMed=8624099;
RA Sandbrink R., Masters C.L., Beyreuther K.;
RT "APP gene family. Alternative splicing generates functionally related
RT isoforms.";
RL Ann. N.Y. Acad. Sci. 777:281-287(1996).
RN [5]
RP TISSUE SPECIFICITY OF APPICAN.
RX PubMed=7744833;
RA Shioi J., Pangalos M.N., Ripellino J.A., Vassilacopoulou D.,
RA Mytilinou C., Margolis R.W., Robakis N.K.;
RT "The Alzheimer amyloid precursor proteoglycan (appican) is present in
RT brain and is produced by astrocytes but not by neurons in primary
RT neural cultures.";
RL J. Biol. Chem. 270:11839-11844(1995).
RN [6]
RP TISSUE SPECIFICITY OF ISOFORMS.
RX PubMed=8996834;
RA Sandbrink R., Monning U., Masters C.L., Beyreuther K.;
RT "Expression of the APP gene family in brain cells, brain development
RT and aging.";
RL Gerontology 43:119-131(1997).
RN [7]
RP INTERACTION WITH DDB1, AND MUTAGENESIS OF TYR-757; ASN-759 AND
RP TYR-762.
RX PubMed=9930726;
RA Katanabe T., Sukegawa J., Tomita S., Iijima K.-I., Oguchi S.,
RA Suzuki T., Nairn A.C., Greengard P.;
RT "A 127-kDa protein (UV-DB) binds to the cytoplasmic domain of the
RT Alzheimer's amyloid precursor protein.";
RL J. Neurochem. 72:549-556(1999).
RN [8]
RP INTERACTION WITH GNAO1, AND MUTAGENESIS OF HIS-732 AND HIS-733.
RX PubMed=10024358;
RA Brouillet E., Tremblay A., Galanaud D., Volovitch M., Bouillot C.,
RA Valenza C., Prochiantz A., Allinquant B.;
RT "The amyloid precursor protein interacts with Gq heterotrimeric
RT protein within a cell compartment specialized in signal
RT transduction.";
RL J. Neurosci. 19:1717-1727(1999).
RN [9]
RP CHARACTERISTICS OF APPICAN, AND MUTAGENESIS OF SER-656.
RX MEDLINE=95256193; PubMed=7737970;
RA Pangalos M.N., Efthymiopoulos S., Shioi J., Robakis N.K.;
RT "The chondroitin sulfate attachment site of appican is formed by
RT splicing out exon 15 of the amyloid precursor gene.";
RL J. Biol. Chem. 270:10388-10391(1995).
RN [10]
RP BETA-AMYLOID METAL-BINDING.
RX PubMed=10386999;
RA Huang X., Atwood C.S., Hartshorn M.A., Multhaup G., Goldstein L.E.,
RA Scarpa R.C., CuaJungco M.P., Gray D.N., Lim J., Moir R.D., Tanzi R.E.,
RA Bush A.I.;
RT "The A beta peptide of Alzheimer's disease directly produces hydrogen
RT peroxide through metal ion reduction.";
RL Biochemistry 38:7609-7616(1999).
RN [11]
RP BETA-AMYLOID ZINC BINDING.
RX MEDLINE=99343552; PubMed=10413512;
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RA Liu S.T., Howlett G., Barrow C.J.;
 RT "Histidine-13 is a crucial residue in the zinc ion-induced aggregation
 of the A beta peptide of Alzheimer's disease.";
 RL Biochemistry 38:9373-9378(1999).
 RN [12]
 RP IMPORTANCE OF GLY-704 IN FREE RADICAL PROPAGATION, AND MUTAGENESIS OF
 RP GLY-704.
 RX PubMed:11959460;
 RA Kanski J., Varadarajan S., Aksanova M., Butterfield D.A.;
 RI "Role of glycine-33 and methionine-35 in Alzheimer's amyloid beta-
 RI peptide 1-42-associated oxidative stress and neurotoxicity.";
 RL Biochim. Biophys. Acta 1586:190-198(2001).
 RN [13]
 RP PHOSPHORYLATION.
 RX PubMed:9085254;
 RA Oishi M., Nairn A.C., Czernik A.J., Lim G.S., Isohara T., Candy S.E.,
 RA Greengard P., Suzuki T.;
 RI "The cytoplasmic domain of Alzheimer's amyloid precursor protein is
 RI phosphorylated at Thr654, Ser655, and Thr668 in adult rat brain and
 RT cultured cells.";
 RL Mol. Med. 3:111-123(1997).
 RN [14]
 RP PHOSPHORYLATION ON SER-730.
 RX PubMed:10329382;
 RA Isohara T., Horuchi A., Watanabe T., Ando K., Czernik A.J., Uno I.,
 RA Greengard P., Nairn A.C., Suzuki T.;
 RI "Phosphorylation of the cytoplasmic domain of Alzheimer's beta-amyloid
 RI precursor protein at Ser655 by a novel protein kinase.";
 RL Biochem. Biophys. Res. Commun. 258:300-305(1999).
 RN [15]
 RP PHOSPHORYLATION, INDUCTION, SUBCELLULAR LOCATION, AND MUTAGENESIS OF
 RP THR-743.
 RX MEDLINE:99274744; PubMed:10341243;
 RA Ando K., Oishi M., Takeda S., Iijima K.-I., Isohara T., Nairn A.C.,
 RA Kirino Y., Greengard P., Suzuki T.;
 RI "Role of phosphorylation of Alzheimer's amyloid precursor protein
 RI during neuronal differentiation.";
 RL J. Neurosci. 19:4421-4427(1999).
 RN [16]
 RP PHOSPHORYLATION ON THR-743.
 RX PubMed:10936190;
 RA Iijima K.-I., Ando K., Takeda S., Satoh Y., Seki T., Isohara S.,
 RA Greengard P., Kirino Y., Nairn A.C., Suzuki T.;
 RI "Neuron-specific phosphorylation of Alzheimer's beta-amyloid precursor
 RI protein by cyclin-dependent kinase 5.";
 RL J. Neurochem. 75:1085-1091(2000).
 RN [17]
 RP CARBOHYDRATE STRUCTURE OF APPICAN.
 RX PubMed:11479316;
 RA Tsuchida K., Shioi J., Yamada S., Boghosian G., Wu A., Cai H.,
 RA Sugahara K., Robakis N.K.;
 RI "Appican, the proteoglycan form of the amyloid precursor protein,
 RI contains chondroitin sulfate F in the repeating disaccharide region
 RI and 4-O-sulfated galactose in the linkage region.";
 RL J. Biol. Chem. 276:37155-37160(2001).
 CC -!- FUNCTION: Functions as a cell surface receptor and performs
 CC physiological functions on the surface of neurons relevant to
 CC neurite growth, neuronal adhesion and axonogenesis. Involved in
 CC cell mobility and transcription regulation through protein-protein
 CC interactions (By similarity). Can promote transcription activation
 CC through binding to APBB1/rip60 and inhibit Notch signaling through
 CC interaction with Numb (By similarity). Couples to apoptosis-
 CC inducing pathways such as those mediated by G(O) and Jip. Inhibits
 CC G(O) alpha ATPase activity. Acts as a kinesin I membrane receptor,
 CC mediating the axonal transport of beta-secretase and presenilin 1
 CC (By similarity). May be involved in copper homeostasis/oxidative
 CC stress through copper ion reduction. Can regulate neurite
 CC outgrowth through binding to components of the extracellular
 CC matrix such as heparin and collagen I and IV (By similarity). The
 CC splice isoforms that contain the BPTI domain possess protease
 CC inhibitor activity (By similarity).
 CC -!- FUNCTION: Beta-amyloid peptides are lipophilic metal chelators
 CC with metal-reducing activity. Bind transient metals such as

CC copper, zinc and iron. Rat and mouse beta-amyloid peptides bind
 CC only weakly transient metals and have little reducing activity due
 CC to substitutions of transient metal chelating residues. Beta-Ap42
 CC may activate mononuclear phagocytes in the brain and elicit
 CC inflammatory responses. Promotes both tau aggregation and TPX II-
 CC mediated phosphorylation (By similarity).
 CC -!- FUNCTION: Appicans elicit adhesion of neural cells to the
 CC extracellular matrix and may regulate neurite outgrowth in the
 CC brain.
 CC -!- FUNCTION: The gamma-CTF peptides as well as the caspase-cleaved
 CC peptides, including C31, are potent enhancers of neuronal
 CC apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPB family members, the APPA
 CC family, MAPK3ip1, SHC1 and Numb and Dab1 (By similarity). Binding
 CC to Dab1 inhibits its serine phosphorylation (By similarity). Also
 CC interacts with GPCR-like protein BPP, FPR1, APPBp1, IBL, KNS2
 CC (via its TPR domains), APPBp2 (via BASS) (By similarity) and DDB1.
 CC In vitro, it binds MAPT via the MT-binding domains (By
 CC similarity). Associates with microtubules in the presence of ATP
 CC and in a kinesin-dependent manner (By similarity). Interacts,
 CC through a C-terminal domain, with GNAO1. Amyloid beta-42 binds
 CC CHRNA7 in hippocampal neurons (By similarity). Beta-amyloid
 CC associates with HADH2 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC protein that rapidly becomes internalized via clathrin-coated
 CC pits. During maturation, the immature APP (N-glycosylated in the
 CC Query Match 95.5%; Score 3488.5; DB 1; Length 770;
 CC Best Local Similarity 87.5%; Pred. No. 1.1e-165;
 CC Matches 674; Conservative 8; Mismatches 13; Indels 75; Gaps 1;
 CC
 CC QY 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNNHNMVONCKWDSOPSGTK 60
 CC DB 1 MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIAMFCGRLNNHNMVONCKWDSOPSGTK 60
 CC QY 61 TCIDTREGILQYCEVYPELQITNVVYEAQPVTIQNMCKRGKQCKTHPHFVPIYRCLVG 120
 CC DB 61 TCIDTREGILQYCEVYPELQITNVVYEAQPVTIQNMCKRGKQCKTHPHFVPIYRCLVG 120
 CC QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 CC DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 CC QY 181 GVEFVCCPLAESDNDVSDADEDDSDVWVGADTDYADGSEDKVVEVEEVAEEVEE 240
 CC DB 181 GVEFVCCPLAESDSDSADAEEDSDVWVGADTDYADGSEDKVVEVEEVAEEVEE 240
 CC QY 241 EADDEDEDDGDEVEEEAEPEYEEATERTSTATTITTTTITTESVEEVYR----- 288
 CC DB 241 EADDEDEDDGDEVEEEAEPEYEEATERTSTATTITTTTITTESVEEVYR----- 288
 CC QY 289 ----- 288
 CC DB 301 RAMISRWYFDVTGKCAPFFYGGCGGNRNNDTEYCNVAVCGSVSSQLKTTSEPLPD 360
 CC QY 289 ---VPTIAASTPDAVDKYLETPODENEHAHFQKAKERLEAKHRMSQVMEWEAEARA 345
 CC DB 361 PVKLPTTAATPDAVDKYLETPODENEHAHFQKAKERLEAKHRMSQVMEWEAEARA 420
 CC QY 346 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEALNDRRLALENYITAL 405
 CC DB 421 KNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEALNDRRLALENYITAL 480
 CC QY 406 QAVPPRPRIHVNMLKKYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRIYIER 465
 CC DB 481 QAVPPRPRIHVNMLKKYVRAEQKDRQHTLKHFEHVRWDPKKAQIRSQVMTLRIYIER 540
 CC QY 466 MNQSLLLYNPVAAEEIQDEVDLLQKQNSDDVLANWISPRISYNDALMPSLTET 525
 CC DB 541 MNQSLLLYNPVAAEEIQDEVDLLQKQNSDDVLANWISPRISYNDALMPSLTET 600
 CC QY 526 KTTVELLPVNGEFLDQLQPHWSFGADSVPAENTENEVEPVDARPAADRGLTTPGSGLTN 585

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|||||
601 KTTVELLPVNGFSDJOLQWHPFGVDSVPANTENEVEVDARPAADRLT-RPGSGLTN 660
Qy IKTEISEVKMDAEFRHDSGYEVHHOKLVFFAEDVGSNKGAIIGLMVGGWIAIVIFIL 645
|||||
661 IKTEISEVKMDAEFGHDSGFVYRHOKLVFFAEDVGSNKGAIIGLMVGGWV-ATV-VIIL 720
Qy VMLKKKQYTSIHGGVVEVDAAVTPESRHLKMKQONQYENPTYKFFEQMON 695
|||||
721 VMLKKKQYTSIHGGVVEVDAAVTPESRHLKMKQONQYENPTYKFFEQMON 770

RESULT 8
APP2_MOUSE
ID APP2_MOUSE STANDARD: PRT: 695 AA.
AC Q06335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (CDEI-box binding protein); (CDEBP).
GN APLP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=Fetal brain;
RC TISSUE=Fetal brain;
RA von der Kammer H.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE OF 1-245 FROM N.A.
MEDLINE=94032480; PubMed=2218408;
Hanes J., von der Kammer H., Kristiansson G.I., Scheit K.H.;
"the complete cDNA coding sequence for the mouse CDEI binding
protein.";
RL Biochim. Biophys. Acta 1216:154-156(1993).
[3]
SEQUENCE OF 185-695 FROM N.A.
MEDLINE=93129193; PubMed=1482349;
Vidal F., Blangy A., Rassoulzadegan K., Cuzin F.;
"A murine sequence-specific DNA binding protein shows extensive local
 similarities to the amyloid precursor protein.";
RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
[4]
SEQUENCE OF 1-35 FROM N.A.
STRAIN=129/Sv;
MEDLINE=96029629; PubMed=7592716;
von Koch C.S., Lahiri D.K., Mammen A.L., Copeland N.G.,
Gilbert D.J., Jenkins N.A., Sisodia S.S.;
"The mouse APLP2 gene. Chromosomal localization and promoter
 characterization.";
RL J. Biol. Chem. 270:25475-25480(1995).
CC -!- FUNCTION: BINDS TO THE DNA 5'-GTCAATG-3' (CDEI BOX) WHICH PLAYS
CC AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
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CC -----
DR EMBL; Z22592; CAA80306.1; -
DR EMBL; M97216; AAC20039.1; -
DR EMBL; U34291; AAC52318.1; -
DR PIR; S38344; S38344.
DR HSSP; P05067; LMPV.
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DR MGI:88047; APLP2.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Transmembrane; DNA-binding; Signal; Nuclear protein.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 695 AMYLOID-LIKE PROTEIN 2.
FT DOMAIN 30 624 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 625 648 POTENTIAL.
FT DOMAIN 649 695 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 218 294 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DOMAIN 218 231 POLY-GLU.
FT DOMAIN 256 266 POLY-GLU.
FT CARBOHYD 485 485 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 185 189 GMLLP -> MACCC (IN REF. 3).
SQ SEQUENCE 695 AA: 78944 MW: 8944 B95AAB2A0311 CRC64;
Query Match 47.4%; Score 1730; DB 1; Length 695;
Best Local Similarity 49.2%; Pred. No. 9.6e-79;
Matches 359; Conservative 118; Mismatches 163; Indels 90; Gaps 19;
Qy 5 LALLLLAAWTARALEV-----PTDGNAG---LLAEPQIAMEFCGRNLNMHMVQNGKWDSDP 56
Db 15 LVLVLLIIGLTAPAAALAGYIEALAAANAGTGFVAEPQIAMLGKGLNMHVNIQTCKWEPDP 74
Qy 57 SGTKCIDTKGIIQYQYVPELQITNVVEANQPTIQLNWKCKRGRKQCKTHPHFVLPYR 116
Db 75 TGTSCGLTKKEVLYQYCOEYPELQITNVMEANQFVNIDSNCRRDKRCKCS--HIVPFK 132
Qy 117 CLVGEFVSALMLVPCKCKFLHORMDVCETHLHVAKETCSKSNLNDYGLMPCGI 176
Db 133 CLVGEFVSQVILVVDNCOFFHQERMEVCEKQRHHTLVKEACLTGLTYSYGLMLPGCV 192
Qy 177 DKFRGVEFVCCPLAE--ESDNVDSADAPEDSDVMVGADTDYADGSEDKVVEVAE---E 231
Db 133 DQFHGIEYVCCPQTKTVDSSTMSKEFEFEFE-----DEEDEDYDLKDSRPT 243
Qy 232 FEVAEVEERAD-DDEDDGDEVEEAE-----EPYEEA-ERTTSIATTTTTTIES 282
Db 244 ADLEDTFAADEDEEEVEEVEDDYDYPFGKDDYNE--ENTEPSSSEGTISDK 301
Qy 283 VEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQAKERLEAKHRMSQVMREWEAE 342
Db 302 IVHDVKVPPIPLPTND-VDVYLETSAQDNEHARFQAKQLEIRHRNMRDVRKKEWEAE 360
Qy 343 RQAKNLPKADKKAVIQHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRLALENYI 402
Db 361 LQAKNLPKIEROTLIQHFQAMVKALEKAAEKKQQLVETHLARVEAMLNDRRLALENYL 420
Qy 403 TALQAVPPRPHRVFNMKKYVRQKQRHTLKHFEHVRVMDPKKAAQIRSQVTHLRVI 462
Db 421 AALQSDPPRPHRILOALRRYVRAENKDRLHTRHQHVLAVDPEKAAQMSQVMTLHRVI 480
Qy 463 YERNQSLLYNPVAAVEETQDEVDLQEQNYSDVLANMISEPRISYGNDAIPLSL 522
Db 481 EERNQSLTLYKVPYVAQEQIEIDELLQEQR-----ADM-----DQFTSSI 523
Qy 523 TETKTVTELLPVNGEFLDDLOPWHSFGADSVPAANTENEVEPVDARPAADRLTTRPGSG 582
Db 524 SENPVDVVRVSSESE-ELPPFPHLPHPF-----PSLSENE-----GSGMAEQDG-G 566
Qy 583 LTNIKTEEI-SEVKMDAEFRHDSGYEVHHOKLVFFAEDVGS-----NK 624
Db 567 LIGAEKVINSKNKNMKNWIDETLDV--KEMIFNAERVVGLEEEEPESVGPLREDFSLSS 624
Qy 625 GAIIGLMVGGWVIAIVITILVMLKKKQYTSIHGGVVEVDAAVTPESRHLKMKQONQYEN 684
Db 625 NALIGLLVIAVIAIVVISLVMLKRYQYTSIHGGVVEVDAAVTPESRHLKMKQONQYEN 684
Qy 685 PTYKFFEQMQ 694
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DB 685 PTYKYL.FQM 694
|||||
RESULT 9
ID APP2_HUMAN STANDARD: PRT; 763 AA.
AC Q06481.1
DI 01-JUN-1994 (Rel. 29, Created)
DI 02-OCT-1996 (Rel. 34, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
DE (CDEI-box binding protein) (CDEB2).
GN APLP2 OR APLP2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93250009; PubMed=8485127;
RA Norris K., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
RA "Molecular cloning of the cDNA for a human amyloid precursor protein
RA homolog: evidence for a multigene family.";
RL Biochemistry 32:4481-4486(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=95217334; PubMed=7702756;
RA von der Kammer H., Hancs J., Klaidiny J., Scheit K.H.;
RT "A human amyloid precursor-like protein is highly homologous to a
RT mouse sequence-specific DNA-binding protein.";
RL DNA Cell Biol. 13:1137-1143(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94035131; PubMed=8220435;
RA Wasco W., Gurubhagavatula S., Paradis M., Romano D.M., Sisodia S.S.,
RA Hyman B.T., Neve R.L., Tanzi R.E.;
RT "Isolation and characterization of APLP2 encoding a homologue of the
RT Alzheimer's associated amyloid beta protein precursor.";
RL Nat. Genet. 5:95-99(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Lung;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Udell I.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bcsak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hsieh S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Stevchenko Y., Bouffard G.G.,
RA Alakesley R.C., Touchwood J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.F.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length-h
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
CC MAY BIND TO THE DNA 5'-GTCCATG-3' (CDEI BOX).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
```

(POTENTIAL).
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=3;
Comment-Additional isoforms seem to exist:
Name=1;
IsoId=Q06481-1; Sequence=Displayed;
Name=2;
IsoId=Q06481-2; Sequence=VSP_000016;
Name=3;
IsoId=Q06481-3; Sequence=VSP_000019;
-!- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
AND ENDOTHELIAL TISSUES
-!- SIMILARITY: BELONGS TO THE APP FAMILY
-!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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EMBL; S60099; AAC60589.1;
EMBL; L09209; AAA35526.1;
EMBL; 222572; CAA80295.1;
EMBL; L27631; AAC41701.1;
EMBL; BC000373; AAH00373.1;
PIR; A49321; A49321.
HSSP; P05067; IAMP.
Genew; HGNC:598; APLP2.
MIM; 104776;
GO; GO:0016021; C: integral to membrane; NAS.
GO; GO:0005634; C: nucleus; IDA.
GO; GO:0003677; F: DNA binding activity; NAS.
GO; GO:0007186; P: G-protein coupled receptor protein signaling.; NAS.
InterPro; IPR001868; A4_APP.
InterPro; IPR002223; Kunitz_BPTI.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
ProDom; PD000222; Kunitz_BPTI; 1.
SMART; SM00006; A4_EXTRA; 1.
SMART; SM00331; KU; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS0279; BPTI_KUNITZ_2; 1.
Transmembrane; Signal; Alternative splicing; DNA-binding;
Nuclear protein; Serine protease inhibitor.
SIGNAL 1 29 POTENTIAL.
CHAIN 30 763 AMYLOID-LIKE PROTEIN 2.
DOMAIN 30 692 EXTRACELLULAR (POTENTIAL).
TRANSMEM 693 716 POTENTIAL.
DOMAIN 717 763 CYTOPLASMIC (POTENTIAL).
DOMAIN 215 280 ASP/GLU-RICH (HIGHLY ACIDIC).
DOMAIN 306 364 BPTI/KUNITZ INHIBITOR.
DOMAIN 215 231 POLY-GLU.
ACT_SITE 320 321 REACTIVE BOND (BY SIMILARITY).
FT DISULFID 310 360 BY SIMILARITY.
FT DISULFID 319 343 BY SIMILARITY.
FT DISULFID 335 356 BY SIMILARITY.
FT VARSPPLIC 308 363 Missing (in isoform 2).
FT VARSPPLIC 613 624 /FTID=VSP_000018.
FT VARSPPLIC 543 543 Missing (in isoform 3).
FT CONFLICT 543 543 S -> I (IN REF. 1).
SQ SEQUENCE 763 AA; 86955 MW; CA3A7D6DDB8A28D0 CRC64;
Query Match 47.2%; Score 1723; DS 1; Length 763;
Best Local Similarity 47.0%; Pred. No. 2.4e-78;
Matches 371; Conservative 112; Mismatches 166; Indels 140; Gaps 20;


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FI  CONFLICT 575 577 /FTID=VSP_000021.
PT  SEQUENCE 765 AA; 86982 MW; CFS1FCCE305AUCF CRC84;
SQ  Query Match 46.8%; Score 1711; DB 1; Length 765;
    Best Local Similarity 46.1%; Pred. No. 9,4e-78;
    Matches 363; Conservative 122; Mismatches 167; Indels 136; Gaps 20;

Oy 5 LALLLLAAWTAARALEV-----PTDGNAG---LAAEPOIAFMFCGRNNMHWQNGKVEDSP 56
Db 15 LVLVLLGLTAPAAALAA3YIEALANAGTGFVAEPQIAFMFCGLNHNWNIQIGKEPDP 74
Oy 57 SGTCTCIDTREGILQYCOEYVPELOITNVVEANQVITQWCKHGRKCKCHREHFLPYR 116
Db 75 TGTSCSLCTKEVLYCOEYIPESQITNVEANQVWDSWCRKRKKCKCHS--HIVTIPFK 132
Oy 117 CLVGEFVSDALLVPDKCFILHOERMDYCETHLHWHTIVAKETCFSEKSTNLHDYGMLLPCGI 176
Db 133 CLVGEFVSDVLLVPENCQFFQHERMEVCEKHQRHHTVVKAECLTEGNTLYSYGNLLPCGV 192
Oy 177 DKFGVFEVCCPLAE--ESQNVDSADAEDDSQVWVGADIDYA-DGSEDKVVEVAEEZE 233
Db 193 DQFHCTGYVCCPQTKVYVDSSTNSKESEEEFE-----DEFEDYALDKSEFTEACLDFT 248
Oy 234 VAEVEEEDADDDEDDGDEVEEAESEPYEE-----ATERITSIATTTT--ESVEEVV 287
Db 249 EAAADEDEDEEEEGEEVVEDRDYYSDFKGDYNEENPTESPSSDGTISDKETIAND 308
Oy 288 R-----VPT 291
Db 309 KAVCSQEAMTGPCRAVMPRYFDLSKGVKCYRFTYGGCGGNRNFESEDCYMAVCKTMIPP 368
Oy 292 TAASTPDVADKYLETGDENEHAHFQAKERLEAKHRSQVYRENEEAEQAKNLPKA 351
Db 369 TPLPTND-VDYFETSADDNEHAFQAKESQLEIRHSRMDRVKKEWAELOAKNLPKA 427
Oy 352 DKKAVIOHFQEKVESLEQEAANERQQLVETHMARVEAMLNDRRRLALENYITALQVAPPR 411
Db 428 EROTLIHFQAMVKALEKEAASEKQQLVETHLARVEANLNDRRRTALENYLAALQSDPPR 487
Oy 412 PRHVENMLKYYVRAEQKROHTLKHFEHVRMDPKKAAQIRSQVTHLRVYIERMKOSLS 471
Db 488 PHRLQALRYVRAENKDRLHTIRHYQHVLAVDPEKAAQKSKQVYTHLRVIEERKOSLS 547
Oy 472 ILVYVPAVAFIQDEVDLQKQENYSDVLANMISSEPRISYGNALMPSLTETKTIVEL 531
Db 548 LIYKVPVAGIEQIEIDELQEQR-----ACM-----DQFTSSISENPVQVR- 589
Oy 532 LPVNGEFSJDDLPQWHSFGADSVPAANTENEVEPYDARPAADRGTLTPGSGLTN-----I 586
Db 590 --VSSEES-ERFPFHPF--HPFPLSENE-----DIQPFILYHPN--KKGSGMAEQDQGL 638
Oy 587 KTEP--ZSEVKMDAEFRHDSGYEVHVKLVFEPAEDYGS-----NKGAE 626
Db 639 GAEEKVINSKNKMDENNVVIDETLDV--KEMIFNRRVGGLEEEPPDSVGLREDFSISSSA 636
Oy 627 IIGLVGSGVVIATVIFITLYMLKKQYTSIHGHVVEVCAAVTPERHLSKMQCGYHNPT 696
Db 697 LIGLLVIAVATATVIVSLYMLKKQYCTISHGIVEVHPMLTPEERHLSKMQCGYHNPT 736
Oy 687 YKFEQMQ 694
Db 757 YKYLEQMQ 764

RESULT 11
APPL_HUMAN STANDARD: PRT: 650 AA.
AC P51693; O00113; Q96A92;
DI 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].

GN OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CN NCBI_TaxID=9606;
RX [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=98088960; PubMed=9428684;
RA Falla K., Peraus G., Kreger S., Puwirwang U., Hesse L., Multaup G.,
RA Masters C.L., Beyreuther K., Wiedemann A.;
RT "Human amyloid precursor-like protein 1 -- cDNA cloning, ectopic
RT expression in COS-7 cells and identification of soluble forms in the
RT cerebrospinal fluid.";
RI Eur. J. Biochem. 250:354-363(1997).
RX [2]
RX SEQUENCE FROM N.A.
RX MEDLINE=98180887; PubMed=9521588;
RA Leckkeri U., Kestila M., Lamerdin J., McCready P., Adamson A.,
RA Olsen A., Tryggvason K.;
RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT 19q13.1.";
RI Hum. Genet. 102:192-196(1998).
RX [3]
RX SEQUENCE FROM N.A.
RX TISSUE=Ovary;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madar A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RX [4]
RX POSSIBLE FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=96115107; PubMed=7494461;
RA Kim T.-W., Wu K., Xu J.-L., McAuliffe G., Tanzi R.E., Wasco W.,
RA Black I.B.;
RT "Selective localization of amyloid precursor-like protein 1 in the
RT cerebral cortex postsynaptic density.";
RI Brain Res. 32:36-44(1995).
RX [5]
RX HEPARIN AND ZINC BINDING.
RX MEDLINE=95014513; PubMed=7929392;
RA Bush A.I., Pettigrell W.H. Jr., de Paradis M., Tanzi R.E., Wasco W.;
RT "The amyloid beta-protein precursor and its mammalian homologues.
RT Evidence for a zinc-modulated heparin-binding superfamily.";
RI J. Biol. Chem. 269:26618-26621(1994).
RX [6]
RX INTERACTION WITH APBA2.
RX MEDLINE=99107877; PubMed=9890987;
RA Tomita S., Ozaki T., Taru H., Oguchi S., Takeda S., Yagi Y.,
RA Sakiyama S., Kirino Y., Suzuki T.;
RT "Interaction of a neuron-specific protein containing PDZ domains with
RT Alzheimer's amyloid precursor protein.";
RI J. Biol. Chem. 274:2243-2254(1999).
RX [7]
RX EXTRACELLULAR COPPER-BINDING.
RX MEDLINE=22130992; PubMed=12135352;
RA Simons A., Ruppert T., Schmidt C., Schlicksupp A., Pipkorn R.,

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RA Read J., Masters C.L., White A.R., Cappai R., Beyreuther K.,
 RA Bayer T.A., Multhaup G.,
 RT "Evidence for a copper-binding superfamily of the amyloid precursor
 RT protein.";
 RL Biochemistry 41:9310-9320(2000).
 CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
 CC gamma-secretase processed fragment, Aβ(1-42), activates transcription
 CC activation through APBβ1 (Fe65) binding (By similarity). Couples
 CC to JIP signal transduction through C-terminal binding. May
 CC interact with cellular G-protein signaling pathways. Can regulate
 CC neurite outgrowth through binding to components of the
 CC extracellular matrix such as heparin and collagen I.
 CC -!- FUNCTION: The gamma-CIF peptide, C30, is a potent enhancer of
 CC neuronal apoptosis (By similarity).
 CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
 CC cytoplasmic proteins, including APPβ and AβA family members,
 CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
 CC serine phosphorylation (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
 CC processed in the Golgi complex.
 CC -!- TISSUE SPECIFICITY: Expressed in the cerebral cortex where it is
 CC localized to the postsynaptic density (PSD).
 CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
 CC phosphorylated proteins is required for the specific binding of
 CC the PID domain. However additional amino acids either N- or C-
 CC terminal to the NPXY motif are often required for complete
 CC interaction. The NPXY site is also involved in clathrin-mediated
 CC endocytosis.
 CC -!- PTM: Proteolytically cleaved by caspases during neuronal
 CC apoptosis. Cleaved, in vitro, at Asp-620 by caspase-3 (By
 CC similarity).
 CC -!- PTM: N-glycosylated.
 CC -!- PTM: O-glycosylated.
 CC -!- MISCCELLANEOUS: Binds zinc and copper in the extracellular domain.
 CC Zinc-binding increases heparin binding. No Cu(II) reducing
 CC activity with copper-binding.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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 CC
 CC EMBL: U48437; AAB96331.1;
 CC EMBL: AD000864; AAB50173.1;
 CC EMBL: BC012889; AAB12889.1;
 CC HSP: P05067; LMWP.
 CC Genbank: HGNC:597; APLP1.
 CC MW: 104775;
 CC GO: GO:0005604; C:basement membrane; TAS.
 CC GO: GO:0005208; F:amyloid protein; TAS.
 CC GO: GO:0007397; P:histogenesis and organogenesis; TAS.
 CC GO: GO:0007399; P:neurogenesis; TAS.
 CC InterPro: IPR001868; A4_APP.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC PRINTS: P00203; AMYLOIDA4.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC Apoptosis: Endocytosis; Cell adhesion; Coated pits; Neurone;
 KW Heparin-binding; Metal-binding; Copper; zinc; Signal; Transmembrane;
 KW Glycoprotein.
 FT SIGNAL 1 38
 FT CHAIN 39 650
 FT CHAIN 621 650
 FT DOMAIN 39 580
 FT TRANSMEM 581 603
 FT DOMAIN 604 650
 FT DOMAIN 158 178
 FT DOMAIN 204 211

FI	DOMAIN	310	342	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	410	441	HEPARIN-BINDING (BY SIMILARITY).
FT	DOMAIN	442	459	COLLAGEN-BINDING (BY SIMILARITY).
FT	DOMAIN	640	643	CLATHRIN-BINDING (POTENTIAL).
FT	DOMAIN	241	247	POLY-GLU.
FT	DOMAIN	264	268	REQUIRED FOR COPPER(II) REDUCTION (BY
FT	SITE	167	167	SIMILARITY).
FT	SITE	604	615	RASOLATERAL SORTING SIGNAL (BY
FT	SITE	620	621	SIMILARITY).
FT	SITE	638	641	CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
FT	SITE	640	643	ENDOCYTOSIS SIGNAL (BY SIMILARITY).
FT	CARBOHYD	337	337	NPXY MOTIF.
FT	CARBOHYD	461	461	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	551	551	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	48	48	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CONFLICT	48	48	A -> P (IN REF. 1).
SO	SEQUENCE	650 AA	72176 MW	B95F0F4DIC5BAC7 CRC64;

Query Match 32.4%; Score 1185; DB 1; Length 650;
 Best Local Similarity 38.7%; Pred. No. 8.2e-52;
 Matches 271; Conservative 115; Mismatches 231; Indels 84; Gaps 16;

QY	1	MLPGLALLLAAWTARALEVPTDGNAGLLAEPOIATMFCGRLLNMYNQVNGKWDSPGSK	60
DB	23	LPPLLLLRAPAGTSLAGSGAAEAPGSAQVAGLCGRLLTLDRTGRWEPDQSR	82
QY	61	TCIDTKEGILQYCEVYPELOITNVVANQVPIIQQMCKRKCKOCKTHPHF-VLPYRCLV	119
DB	83	RCLRPQVRLEYCYROMYPELOIARVEQATQAIPIERMCGSGSRSCARPHQVVPFCLP	142
QY	120	GEFVSALLVPDKKFLHQRMDVCETHLHWHTVAKETCTSEKSLNLDYGMGLPCGIDKF	179
DB	143	GEFVSALLVPDKKFLHQRMDVCETHLHWHTVAKETCTSEKSLNLDYGMGLPCGIDKF	202
QY	180	RGVEVCCPLAEESQNVDSADAEEDSDVWNGADIDYADGSEDKVVEVAEEVEEVEE	239
DB	203	RGVEVCCPLAEESQNVDSADAEEDSDVWNGADIDYADGSEDKVVEVAEEVEEVEE	246
QY	240	EDADDUEDC--EDGSEVEEAEFPEYEATERITTSATTTTTSVEEVEVPTTAATP	297
DB	247	ESFPQVDYFVEPQAEES--ETVPPSSHLAVGKVTTPR-----PT-----	291
QY	298	DAVDKLTTPDENEHAFQAKERLEAKHRMSQVMREWEAEAKNLPKADKAVI	357
DB	292	DGVDIYFCMPGEISEHGEFLRAKMDLEERRMRQINEVREWAMADNOSKNLPKADQALN	351
QY	358	QHFQEKVESLEBOEAANRQQLVETHMARVEAMLNDRGRALLENVITLQAVPPRPHVEN	417
DB	352	EHFQSILOTLEQVSGERQRLVETHATRVIALINDQRAALEGFLAALQADPPQAEVLL	411
QY	418	MLKKYVRAEQDKROHTLKHFEHVRMVDPKAAQIRSOVMTHLRVIERMNCGLSLIYNVP	477
DB	412	ALRRYLRAEQEQHRLRIYHQVAAVDPDEKAQMRQFVHTLQVIEERVNOSGLLDQNP	471
QY	478	AVAEIODEVDELQKEQNYSDVDLANMISEPRISYGNALMPSLTETKTVELLVNGE	537
DB	472	HLAQELRFQIQLHSEH-----LGPSELEA-----PAPG	502
QY	538	FSLD--DLQPWHSFCADSVPAANTENEVEPVDARPAADRLTRFGSGLTNKTETSEVSK	595
DB	503	SSEDKGGLQPPDS--KDOTPM-----TLPGSTEQDAAASPEKEMKPLSQYE	547
QY	596	MDAEFRHDSQYEVHH---QKLVFFAEADVGSNKGALIGLVGGVVIATVITLVMK-KKK	651
DB	548	RKVNASVPRGFPFFHSSEIQDELAPAGTGVGREAVSGLLIMGAGGSLVLSMLLRKK	607
QY	652	OYTSIHGQVVEVDAVATPEERHLSKMQQNGENPTYKFEQ	692
DB	608	PYGALSHGVVEVDPMLTLEEQQLRELQKHGYENTYRFLFE	648

RESULT 12

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APPI_MOUSE
IC APPI_MOUSE STANDARD: PRT: 653 AA.
AC Q03157; Q8VC38;
DT 01-OCT-1993 (Rel. 27, Created)
DI 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
GN APLP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93066322; PubMed=1279593;
RA Wasco W., Bupp K., Magendanz M., Gusella J.F., Tanzi R.E.,
RA Solomon F.;
RA "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=Retina;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Plakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.C.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN [3]
RP COLLAGEN-BINDING.
RX MEDLINE=96139497; PubMed=8576160;
RA Behr D., Hesse L., Masters C.L., Multhaup G.;
RT "Regulation of amyloid protein precursor (APP) binding to collagen and
RI mapping of the binding sites on APP and collagen type I.";
RL J. Biol. Chem. 271:1613-1620(1996).
RN [4]
RP INTERACTION WITH DAB1.
RX MEDLINE=99389880; PubMed=10460257;
RA Homayouni R., Rice D.S., Sheldon M., Curran T.;
RT "Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
RT protein 1.";
RL J. Neurosci. 19:7507-7515(1999).
RN [5]
RP INTERACTION WITH MAPK8IP1.
RX MEDLINE=21408156; PubMed=11517249;
RA Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T.,
RA Hirai S., Ohno S., Kita Y., Kawasumi M., Koyama K., Yamamoto T.,
RA Kyriakis J.M., Nishimoto I.;
RT "C-Jun N-terminal kinase (JNK)-interacting protein-1b/1slet-brain-1
RT scaffolds Alzheimer's amyloid precursor protein with JNK.";
RL J. Neurosci. 21:6597-6607(2001).
RN [6]
RP GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS OF
RP TYR-641.
RX MEDLINE=22313598; PubMed=12228233;
RA Scheinfeld M.H., Gheris E., Laky K., Fowlkes B.J., D'Adamo L.;

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RT "Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-
RT secretase regulates transcription.";
RL J. Biol. Chem. 277:44195-44201(2002).
CC -!- FUNCTION: May play a role in postsynaptic function. The C-terminal
CC gamma-secretase processed fragment, ALD1, activates transcription
CC activation through APBB1 (Fe65) binding. Couples to JIP signal
CC transduction through APBB1 (Fe65) binding. May interact with
CC cellular G-protein signaling pathways. Can regulate neurite
CC outgrowth through binding to components of the extracellular
CC matrix such as heparin and collagen I.
CC -!- FUNCTION: The gamma-CTF peptide, C30, is a potent enhancer of
CC neuronal apoptosis (By similarity).
CC -!- SUBUNIT: Binds, via its C-terminal, to the PID domain of several
CC cytoplasmic proteins, including APBB and APA family members,
CC MAPK8IP1 and Dab1 (By similarity). Binding to Dab1 inhibits its
CC serine phosphorylation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. C-terminally
CC processed in the Golgi complex.
CC -!- DOMAIN: The NPXY sequence motif found in many tyrosine-
CC phosphorylated proteins is required for the specific binding of
CC the PID domain. However additional amino acids either N- or C-
CC terminal to the NPXY motif are often required for complete
CC interaction. The NPXY site is also involved in clathrin-mediated
CC endocytosis.
CC -!- PTM: Proteolytically cleaved by caspases during neuronal
CC apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
CC similarity).
CC -!- PTM: N-glycosylated.
CC -!- PTM: O-glycosylated.
CC -!- MISCELLANEOUS: Binds zinc and copper in the extracellular domain.
CC Zinc-binding increases heparin binding. No Cu(II) reducing
CC activity with copper-binding.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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DR EMBL; L04538; AAA37247.1; -
DR EMBL; BC021877; AAH21877.1; -
DR PIR; A46362; A46362.
DR HSP; P05066; LMWP.
DR MGD; MG188046; Appl1.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMVLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR KX Apoptosis; Endocytosis; Cell adhesion; Coated pits; Neurone;
DR KW Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
DR Glycoprotein.
FT SIGNAL 1 37 POTENTIAL
FT CHAIN 38 653 AMYLOID-LIKE PROTEIN 1.
FT CHAIN 624 653 C30 (BY SIMILARITY).
FT DOMAIN 38 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 606 POTENTIAL.
FT DOMAIN 607 653 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 157 177 COPPER-BINDING.
FT DOMAIN 203 210 ZINC-BINDING (BY SIMILARITY).
FT DOMAIN 313 345 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 413 444 HEPARIN-BINDING (BY SIMILARITY).
FT DOMAIN 445 462 COLLAGEN-BINDING (BY SIMILARITY).
FT DOMAIN 263 271 POLY-GLU.
FT DOMAIN 535 538 POLY-SER.
FT DOMAIN 601 606 POLY-LEU.
FT SITE 166 166 REQUIRED FOR COPPER(II) REDUCTION (BY
FT SITE 607 618 SIMILARITY).
FT SITE 607 618 BASOLATERAL SORTING SIGNAL (BY

```



```
D5      6 LMIGLLIPILVA-TVYAGSPAGSKRHEKTPMVAFCGYRQYX-TEEGSNKIDDERYA 63
QY      61 TCIDTKSGILQYCEVYPPELOQIINVVEANQVPTWIONWCKRGRKCKTHPHFVIFPCIVAG 120
DB      64 2CFSGKDLKCYKRAYSMITNIVEYSHVSDWCREGSPCK-WHSVRVYHCTDG 122
QY      121 EFVSDALLVPDPKAFLEHQRMDVCFTHLEHWHITVAKETCSRSKSN-LEEDYGMILLPC 174
DB      123 EFHEALQVPHDCQFQSHVNSRQCNQNDYOHKQDEAGCKCTKSKGNKMDMYRSFAVLEFC 192
QY      175 GIDKFRGVEFYCCPLAEESUNVDSADAEEDSDVMWGGADTDYADGSEDKVVEVAEEFV 234
DB      183 ALDMFTGVFEVCCP-----NDQINKTDVQIK----- 209
QY      235 AEVVEEEADDEDEDGDEVEEAEAEPEEATERITISATITITTTTSVEEVVRPTAA 294
DB      210 ---EDDDDDDDDAYEDDYSEEDKDEE----- 236
QY      295 STPDVAVKYLETGPDENEHAHFOKAKERLEAKHREMSOVWREEA-----ERCANLP 349
DB      237 -EPSQDPYFKIANWINEHDDFKAEEMDEKHKKVDYKWKEGCJLETRYNEQAKAD-P 294
QY      350 KADKAVTQ---HFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL- 405
DB      295 KGAEEKFSOMNARFQKTVSSLEEEHKKRKEIEAVHEERVQAMLNKKRCDATHDYQALA 354
QY      406 -QAVPPRPRHVENMLKKYVRAEQDROHTJKHFEHVRVMDPKKAAQIRSQWTHLRYIE 464
DB      355 THVKNPKHVSQSLKATIRAEKDRMHLNRYRELKADSKAEAAAYKPTVIHLRYIDC 414
QY      465 RMNOSLSLLYNP-----AVA--EEIQDEVDLELQKQNTYSDQVLNMISEPRISY 513
DB      415 RINGTLAMLRDPDLKRYVPIATYKDYRDEYSPDISVE-----DSELTPIIHDDPEFK 470
QY      514 GN--DALMPSLT-----EKTTVVELLPVNGESLDDQLPWHFSGADSPANT---ENEVEP 564
DB      471 NAKLDVKAPTTTAKPVKETDNKVLPTDASDEEAEDEYDEDEQVKKTPDKKKVKYV 530
QY      565 VDARE-----AADRLITRPGSLNLIKTEE-----ISEVKMDA 598
DB      531 VDIPKEIKVTEIEKAPKPIVETSVQTDDEDEDESSSTSSSEDEDEKNIKELRVDI 590
QY      599 E-----FRHDSGYEVHHQKLVFFAEADYGSNKGATIGLWGVGVVIATVIFITIVMLK 649
DB      591 EPIIDEPASEYRHD-----KLQISPEVERSSAVFPQVVLASANKFITAICIIAT 642
QY      650 KKQYTSIHGVVEYDAVTPPERILSNQOQNGYENPTYKFE 691
DB      643 NARRRRMRGFIQVD-VYTPPEERHVGQVNGVYENPTYSEFD 693

RESULT 14
A4_DROME
ID A4_DROME STANDARD: PRT; 887 AA.
AC P14599; Q9TVVG; Q9U4H3; Q9W5F.;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-amyloid-like protein precursor
GN APPL OR VND OR BCDNA:GH04413 OR EG:65F1.5 OR CG7727.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89184650; PubMed=2494667;
RA Rosen D.R., Martin-Morris L., Luo L., White K.;
RT "A Drosophila gene encoding a protein resembling the human
beta-amyloid protein precursor."
RL Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA War K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Baliew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Fertaz C., Fertiera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT *The genome sequence of Drosophila melanogaster.*
RL Science 287:2185-2195(2000).
RN [3]
RN REVISIONS.
RP STRAIN=Berkeley;
RX MEDLINE=22436069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.C.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT *Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.*
RN Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RN SEQUENCE FROM N.A.
RP STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=107311137;
RA Henos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaecle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT *from sequence to chromosome: the tip of the X chromosome of D.
melanogaster.*
RL Science 287:2220-2222(2000).
RN [5]
```

RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley; TISSUE=Ovary;
RX MEDLINE=20196012; PubMed=10731138;
RA Rubin G.M., Hong L., Brokstein P., Evans-Holm M., Frise E.,
RA Stapleton M., Harvey D.A.;
RT "A Drosophila complementary DNA resource";
RN Science 287:2222-2224(2000).
[61]
RP SEQUENCE OF 1-83 FROM N.A.
RX MEDLINE=91184006; PubMed=2127912;
RA Martin-Morris L.E., White K.;
RT "The Drosophila transcript encoded by the beta-amyloid protein
precursor-like gene is restricted to the nervous system";
RL Development 110:185-193(1990).
CC !- FUNCTION: Probably corresponds to the protein encoded by the
essential locus vnd, a gene required for embryonic nervous system
development.
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- TISSUE SPECIFICITY: Expressed in post-mitotic neurons in the
central and peripheral nervous systems. Within the nervous system
transcripts are not observed in neuroblasts, newly generated
neurons and at least one class of presumed glial cells.
CC !- DEVELOPMENTAL STAGE: Expressed in all developmental stages.
CC !- DOMAIN: The clathrin-binding site is essential for its association
with α -tubulin, β -tubulin, and γ -tubulin. The sequence specific
recognition extends to peptide residues that are C-terminal to the
NPXY motif. This interaction appears to be independent of
phosphorylation (By similarity).
CC !- SIMILARITY: BELONGS TO THE APP FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch>)
or send an email to license@sib-sib.ch.
CC
DR EMBL: J04516; AAA28874.1; .
DR EMBL: AE003418; AAF45520.2; .
DR EMBL: AL031883; CAA21409.1; .
DR EMBL: AL022139; CAA21409.1; JOINED.
DR EMBL: AL022139; CAA18093.1; .
DR EMBL: AL031883; CAA18093.1; JOINED.
DR EMBL: AF181628; AAD55414.1; .
DR EMBL: X55774; CAA39294.1; .
DR EMBL: X55775; CAA39294.1; JOINED.
DR PIR: A32758; A32758.
DR HSP: P05067; IHRP.
DR FlyBase: FBgn000108; Appl.
DR GO: GO:0005576; C:extracellular; IDA.
DR GO: GO:0005886; C:plasma membrane; IDA.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW Signal; Transmembrane; Amyloid; Neurogenesis.
FT SIGNAL 1 27
FT CHAIN 28 887
FT DOMAIN 28 813
FT TRANSHEM 814 834
FT DOMAIN 835 887
FT DOMAIN 877 880
FT CARBOHYD 150 150
FT CARBOHYD 161 161
FT CARBOHYD 237 237
FT CARBOHYD 240 240
FT CARBOHYD 574 574
FT CONFLICT 177 177
FT CONFLICT 229 229
FT CONFLICT 332 332
FT CONFLICT 743 743

SQ	SEQUENCE	887 AA: 98332 MW: F0F0855AD65A5275 CRC64:
	Query Match	20.7%; Score 755.5; DB 1; Length 887;
	Best Local Similarity	25.6%; Pred. No. 2.1e-30;
	Matches	234; Conservative 128; Mismatches 286; Indels 265; Gaps 29;
QY	7	LLLLAANTARALEVPTDGNAGLLA-----EFOIAMFC--GRLNHMHVY-QNGKNDSDPSG 58
DB	9	LLLSRLVVLAI-----GTAQQAASPRWEPQIAVLCEAGQIQPYLSSEGRWVTLDSK 63
QY	59	T---KTCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONKCKRG---RROCKTHPEVF 112
DB	64	KTGTPTCLRDKMLLDYCKKAYPNRDIINIVESSHYKICGCRQGALNAAKCKGSRWI 123
QY	113	IPYRCLVGEFSDALLVPDKCKFLHQMEDVCETHLHWHVTYAKETCSKSTNLHDYGMLL 172
DB	124	KPFRCL-GPFSODALLVPEGCLFDHINASHKWPVRWNOTGAAACQERGOMRSPFAMLL 182
QY	173	PGCIDKFCRQVFCPCP-----LAEESDNDV---S 198
DB	183	PGCISVFGSEVFCPCPKFKTDEIHVKTTDLVMPAAOINSADELVMNDEDSNDNSYS 242
QY	199	ADAEDDDSDVMGCGADTDYADGSEDKVVEVAEEV-----AE 236
DB	243	KDANEDDL3-----DEDDLMGDDDEDDWADAAATAGGSPNTSSGDSNSGLDD:NAE 296
QY	237	VEE-EEACDDEDEDCDEVEEEAEFY-----EATER 268
DB	297	YDSGEEDNYEEDGAGSEAEVEASWDQSGAKVYSLKSSSPSSAPVAPAEKAPVK 356
QY	269	TTSIATTTTTTSEVEV-----RVPTTAASTPDVAKYLETPTDENEHAHEQ 317
DB	357	SESVTSTPOLSASAAFAVAANSNGSGTGAGAPPSTAQTS---DPYTFHDPHYEQSYK 413
QY	318	KAKERLEAKHREMSQVHREVEEAERQAKNLPKADKKA-----VIOHFEKVESELEQ 370
DB	414	VSOKLESHREKTRVYMKDSDLEEKYODMRADPKAAQSFQKQRTARFOTISQVALLDEE 473
QY	371	AAANEQQLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMLKRYVRAEQKDR 430
DB	474	GNAEKHOLAAMHQORVLAHINORKREAMTCYTQALTQPPNAHHVEKCLQKLLRALJHKDR 533
QY	431	QHTLKHFEH-VRMVP---KKAQIRSQVMTHLRVYERMNQSLSLINVPVAVAEI---- 483
DB	534	AHALAHYRHLNNGGGPGGLEAAASERPTLERLIIDRAVNSQMTMLKRYPELSAKIAQL 593
QY	484	-----QDEV----- 487
DB	594	MNDYTLALRSKDDIPGSSLGMSSEAEAGILDKYRVELERKVAEKERLRLAEKQKQRAA 653
QY	488	-----DELLQKEQNYSDVLANMISE-----PRISYGNDAI 518
DB	654	EREKLEEKLRLEAKKVDMDLMSQVAAQSOQTSQTSOSQAQQQOQKSLPCKELGPDA 713
QY	519	M-----PSLTETKTIVELLVPNGEFSLDLOPHWFSFGADSVPAENTENEVEVDARPA 773
DB	714	LVTAAPNLETTS-----FKDLSDE-----YGEATVSSTKVQTVLITVDDDAVQR 760
QY	574	GLTTRPGSGLTNLTKEIESEVKMDAEFRHDSGYEVHOKLVF-----FAEDVGSNK--- 625
DB	761	AVEDVAAA-----VAHQEAEPQVOHFMTDHLGHRSSFSLRREFAQHAHAKEGRN 811
QY	626	AIIGLMVGWVIATVIFITLMLKKQVTSIH-HGVVEVDAAVTP-----EERHLSKMQ 678
DB	812	VYFTLSFAGIALMAAVFVGAVAKWRTSRSPHAQFIEVDQNVVTHHPHIVREKIVPNMQ 871
QY	679	QNGYENPTYKFE 691
DB	872	INGYENPTYKFE 884

RESULT 15
A4_BOVIN

GenCore version 5.1.6
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QM protein: - protein search, using sw model

Run on: October 2, 2003, 13:55:24 ; Search time 39 Seconds

(without alignments)
4611.863 Million cell updates/sec

Title: US-09-806-194-20

Perfect score: 3653
Sequence: 1 MLPGLALLLAWTARALEV.....QQNGYENPTYKFFEQMKNKK 697

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvrius:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3568	97.7	695	11	O60496 cavia sp. p
2	3535	96.8	695	11	P97487 mus musculus
3	3530.5	96.6	770	6	Q9TUD0 sus scrofa
4	3423	93.7	695	13	Q9DGJ8 gallus gall
5	3382	92.6	751	13	Q9DGJ7 gallus gall
6	3209	87.8	693	13	Q98SG0 xenopus lae
7	3185	87.2	695	13	Q98SF9 xenopus lae
8	3098	84.8	747	13	Q91963 xenopus lae
9	2959.5	81.0	699	13	Q57394 narke japon
10	2762.5	75.6	569	13	Q9PVL1 gallus gall
11	2630.5	72.0	607	11	Q99K32 mus musculus
12	2608	71.4	534	13	Q93296 gallus gall
13	2568	70.3	780	13	Q73683 tetraodon f
14	2524	69.1	738	13	Q90W28 brachydanio
15	2482.5	68.0	694	13	Q8UUR9 brachydanio
16	2443.5	66.9	737	13	Q93279 fugu rubrip

ALIGNMENTS

RESULT 1

O60496 PRELIMINARY; PRT: 695 AA.

AC O60496; (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-NOV-2002 (TREMURel. 22, Last annotation update)
 DE Putative amyloid precursor protein.
 OS Cavia sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_TaxID=10143;
 RN 11
 PP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX NEDLINE=97236426; PubMed=9116031;
 RA Beck M., Mueller D., Bigl V.;
 RT Amyloid precursor protein in Guinea pigs - complete cDNA sequence and alternative splicing.
 RL Biochim. Biophys. Acta 1351:17-21(1997).
 DR EMBL; X97631; CAA66230.1; .
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 SO SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match: 97.7%; Score 3568; DB 11; Length 695;

Best Local Similarity 97.7%; Pred. No. 6.1e-208;
 Matches 679; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Oy 1 MLPGLALLLAWTARALEVPTDGNAGLLAEPOIAMFCGRLLNNHNVQNGKWDSPSGTK 60

Db 1 MLPGLALLLAWTARALEVPTDGNAGLLAEPOIAMFCGRLLNNHNVQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYYPPELQITNVVEANOPVTIQNMCKRGKCKKTHPHFVTPYRCVLS 120
DB 61 TCIGSGEGILQYCOEYYPPELQITNVVEANOPVTIQNMCKRSKCKKTHPHFVTPYRCVLS 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVEAEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTITTTESVEEVVVRPTTAASPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTITTTESVEEVVVRPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEGEAANERQQLVETHMARVEAMNDRRRLALENYTALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEGEAANERQQLVETHMARVEAMNDRRRLALENYTALQAVPPRPHVFNMLK 420
QY 421 KYVRAQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
DB 421 KYVRAQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
QY 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTLTKTTVELLPVNGEFSL 540
DB 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTLTKTTVELLPVNGEFSL 540
QY 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGTLTRPGSGLTNLKTEEISEVKMDAEF 600
DB 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGTLTRPGSGLTNLKTEEISEVKMDAEF 600
QY 601 RHDSCYEVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660
DB 601 RHDSCYEVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660

RESULT 2

P97487 ID P97487 PRELIMINARY: PRT: 695 AA.
AC P97487; P97942;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hippocampal amyloid protein.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RC STRAIN=29SV;
RC STRAIN=129SV;
RA Wragg M.A., Busfield F., Duff K., Koronblat K., Capeocchi M.,
RA Loring J.F., Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U84012; AAB41502.1; -;
DR EMBL: U82624; AAB40919.1; -;
DR HSSP: P05067; IMWP.

MG: 88059; App.
InterPro: IPR001968; A4_APP.
InterPro: IPR001255; Beta-APP.
Pfam: PFC2177; A4_EXTRA; 1.
Pfam: PFC3494; Beta-APP; 1.
PRINTS: PR00203; AMYLOIDA4.
SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2E261236E CRC64;
Query Match Best Local Similarity 96.8%; Score 3535; DB 11; Length 695;
Matches 675; Conservative 5; Mismatches 15; Indels 0; Gaps 0;
QY 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPQIAFMFCGRLLNMHNMVNGKWDSPSGTK 60
DB 1 MLPGLALLLLAAWTAARALEVPTDGNAGLLAEPQIAFMFCGRLLNMHNMVNGKWDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYYPPELQITNVVEANOPVTIQNMCKRGKCKKTHPHFVTPYRCVLS 120
DB 61 TCIGSGEGILQYCOEYYPPELQITNVVEANOPVTIQNMCKRGKCKKTHPHFVTPYRCVLS 120
QY 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHQERMDVCEITHLWHTVAKETCEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVEAEVEEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVWVGADTDYADGSEDKVVEVEAEVEEVEE 240
QY 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTITTTESVEEVVVRPTTAASPDVAV 300
DB 241 EADDDDEDDGDEVEEAEPEYEATERTTSTATTITTTESVEEVVVRPTTAASPDVAV 300
QY 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
DB 301 DKYLETPGDENEHAHFQKAKERLEAKHRERMSQVMREWEAEERQAKNLPKADKAVIQHF 360
QY 361 QEKVESLEGEAANERQQLVETHMARVEAMNDRRRLALENYTALQAVPPRPHVFNMLK 420
DB 361 QEKVESLEGEAANERQQLVETHMARVEAMNDRRRLALENYTALQAVPPRPHVFNMLK 420
QY 421 KYVRAQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
DB 421 KYVRAQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVYERMNOSLSLLYNPVA 480
QY 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTLTKTTVELLPVNGEFSL 540
DB 481 ERIQDEVDLLOKEQNSDDVLANNMISEPRISYGNDAIMPSTLTKTTVELLPVNGEFSL 540
QY 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGTLTRPGSGLTNLKTEEISEVKMDAEF 600
DB 541 DDLQPMHFGVDSVPANTENEVEPVDARPAADRGTLTRPGSGLTNLKTEEISEVKMDAEF 600
QY 601 RHDSCYEVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660
DB 601 RHDSCYEVHHOKLVFFAEEDVGSNGKGAIGLVGGVVIATVITLVMKKKQYTSIHGGV 660
QY 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQM 695
DB 661 VEVDAAVTPEERHLSKMOONGYENPTYKFFEQM 695
RESULT 3
Q9TUI0 ID Q9TUI0 PRELIMINARY: PRT: 770 AA.
AC Q9TUI0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Amyloid precursor protein.
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN NCBI_TaxID=9823;
R [1]

RA KINURA A., Takahashi, T.;
RT "Amyloid Precursor Protein 770";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB032550; BAA84580.1;
DR HSP; P05067; IAAIP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00305; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BCC583E CRC64;

Query Match 96.6%; Score 3530.5; DB 6; Length 770;
Best Local Similarity 88.3%; Pred. No. 1.1e-205;
Matches 680; Conservative 8; Mismatches 7; Indels 75; Gaps 1;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHNQNGKWDSPSGTK 60

DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHNQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKGRKQCKTHPHFVYRCLVG 120

DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKGRKQCKTHPHFVYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNMLJPCGIDKFR 180

DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNMLJPCGIDKFR 180

QY 181 GFVEVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKVKVEVAEVEE 240

DB 181 GFVEVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKVKVEVAEVEE 240

QY 241 FAEDDEDEDGDEVEEAEPYEATERTTSIATTTTTTIESVEEYVR----- 288

DB 241 FAEDDEDEDGDEVEEAEPYEATERTTSIATTTTTTIESVEEYVR----- 288

QY 289 ----- 286

DB 301 RAMISRWFVDTGKCAFFYGGCGGNRNFTDEYCMAYCGSVMSQLKTTFQHLPOD 360

QY 289 ---VPTTAATPDPAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 345

DB 361 PVKLPTTAATPDPAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQA 420

QY 346 KNLPKADKAVIQHFOEKVESLEGEAANERQQLVETHARVEAMLDNRRLALENYITAL 405

DB 421 KNLPKADKAVIQHFOEKVESLEGEAANERQQLVETHARVEAMLDNRRLALENYITAL 460

QY 406 QAVPPRHVFNMLKYYRAEQDKRQHTLKHFEHVRMVDPKAAQIRSQVMTLRLVIYER 465

DB 481 QAVPPRHVFNMLKYYRAEQDKRQHTLKHFEHVRMVDPKAAQIRSQVMTLRLVIYER 540

QY 466 MNQSLSLLYNPVAAEEIQDEVDLLOKEONYSDVLANNISPRISYGNDAIMPSTLET 525

DB 541 MNQSLSLLYNPVAAEEIQDEVDLLOKEONYSDVLANNISPRISYGNDAIMPSTLET 600

QY 526 KTIIVELLPVNGEFLDDIOPWHSPGADSVDPANTENEVEPVDARPAADRGLTIRFGSLTN 585

DB 601 KTIIVELLPVNGEFLDDIOPWHSPGADSVDPANTENEVEPVDARPAADRGLTIRFGSLTN 660

QY 586 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEYVGSNKGAIIGLVKGWVIATVIFITL 645

DB 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFFAEYVGSNKGAIIGLVKGWVIATVIVITL 720

QY 646 VMLKKKQYTSIHGGVVVVDAAVTPERHLKSMQONGYENPTYKFEQMN 595

DB 721 VMLKKKQYTSIHGGVVVVDAAVTPERHLKSMQONGYENPTYKFEQMN 770

RESULT 4

Q9DQ38

ID Q9DQ38 PRELIMINARY; PRT; 695 AA.

AC Q9DQ38;

DI 01-MAR-2001 (TREMBLrel. 16, Created)

DI 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Beta-amyloid precursor protein 695 isoform.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA Sarasa M., Rodoloso A., Sorribas V.;

RT "Cloning of full-length chicken beta-amyloid precursor protein

RT isoforms";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF289218; AAG00593.1; -

DR HSP; P05067; IBA4.

DR InterPro: IPR001868; A4_APP.

DR InterPro: IPR001255; Beta_APP.

DR Pfam: PF02177; A4_EXTRA; 1.

DR Pfam: PF03494; Beta_APP; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 93.7%; Score 3423; DB 13; Length 695;

Best Local Similarity 93.8%; Pred. No. 3.7e-199;

Matches 654; Conservative 17; Mismatches 22; Indels 4; Gaps 3;

QY 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHNQNGKWDSPSGTK 60

DB 1 MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNMHNQNGKWDSPSGTK 60

QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKGRKQCKTHPHFVYRCLVG 120

DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVIONWCKGRKQCKTHPHFVYRCLVG 120

QY 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNMLJPCGIDKFR 180

DB 121 EFVSDALLVPDKCKFLHQRMDVCETHLHWHIVAKETSEKSTNLHDYGNMLJPCGIDKFR 180

QY 181 GFVEVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKVKVE--VAEEVEAEVE 238

DB 181 GFVEVCCPLAESDNVDSADAEEDSDVWVGADTDYADGSEKVKVEEPEDEELTVVE 240

QY 239 EEEACDDEDEDGDEVEEAEPYEATERTTSIATTTTTTIESVEEYVYVPTTAASPD 298

DB 241 DEADDD--DODDGDDEI--EETEEYEATERTTSIATTTTTTIESVEEYVYVPTTAASPD 298

QY 299 AYDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIQ 358

DB 299 AYDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIQ 358

QY 359 HFOEKVESLEGEAANERQQLVETHARVEAMLDNRRLALENYITALQAVPPRHVFN 418

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Db 359 HFQKVESLEGEAANERQOLVETHMARVEAMINDEBRIALENVITALQTVPPRRIVFNM 418
QY 419 LKKYVRABQKDRQHTLKHFEHVRMVDPKKAAQISQVMTHLRVIERMNSO:SLLYNVPA 478
Db 419 LKKYVRABQKDRQHTLKHFEHVRMVDPKKAAQISQVMTHLRVIERMNSO:SLLYNVPA 478
QY 479 VAEETODEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGE 538
Db 479 VAEETODEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGE 538
QY 539 SDDLOPHSFGADSVAPANTENEPVDARPAADRGLTTRPGSLTNIKTEISEVKMDA 598
Db 539 SDDLOPHSFGADSVAPANTENEPVDARPAADRGLTTRPGSLTNIKTEISEVKMDA 598
QY 599 EFRHDSGYEVHOKLVFFAEVDSGSKGAILGLMVGGVYIAIV:PIILVLMKKCYTSIHH 658
Db 599 EFRHDSGYEVHOKLVFFAEVDSGSKGAILGLMVGGVYIAIV:PIILVLMKKCYTSIHH 658
QY 659 GVVEVDAVTPPERHLSKMOQNGYENPTYKFEQMON 695
Db 659 GVVEVDAVTPPERHLSKMOQNGYENPTYKFEQMON 695

RESULT 5
Q9DGT7
ID Q9DGT7 PRELIMINARY; PRI: 751 AA.
AC Q9DGT7;
DT 0: -MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein 751 isoform.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sardas M., Rodolose A., Serribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1;
DR HSSP; P05067; LB84
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Kunitz_BP1.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPT1; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR Prodom; PD000222; Kunitz_BP1; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; K3; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE; PS00279; BPT1_KUNITZ_2; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 92.68; Score 3382; DB 13; Length 751;
Best Local Similarity 86.78; Pred. No. 1.2e-196;
Matches 653; Conservative 18; Mismatches 22; Indels 60; Gaps 4;

QY 1 MFLPGALLLAAWTARALEVPTDGNAGLLAEPOIAFMFCGRINMHVYONGKWDSDPSGTX 60
Db 1 MFLPGALLLAAGAALEVPAADGNAGLLAEPOIAFMFCGRINMHVYONGKWDSDPSGTX 60
QY 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVQNWCKKCKCKCKTHPFIPIYRCLVG 120
Db 61 TCIDTKEGILQYCOEYVPELQITNVVEANQPTVQNWCKKCKCKCKTHPFIPIYRCLVG 120

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QY 121 EFVSDALLVPCKKFLQICRMDCVCEHLHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EFVSDALLVPCKKFLQICRMDCVCEHLHWHITVAKETCSKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNYSDADEDDSDVMWGADTDYADGSDKQVVE--VAEEEEVAEVE 238
Db 181 GVEFVCCPLAESDNYSDADEDDSDVMWGADTDYADGSDKQVVE--VAEEEEVAEVE 238
QY 239 EEEADDDDEDDGDEVEEAEPEYEATEKRTTSIATTTTTTSVEEVEWR----- 288
Db 241 DEDADD--DDDDGDEI-BETEEYEATEKRTTSIATTTTTTSVEEVEVEVSEQEATG 298
QY 289 -----VPTTAASTPDAVOK 302
Db 299 PCRAMISRWYEDVAGKCAPFFYGGCGGNRNFDSEYCMVAGSVLPTTAASTPDAVOK 358
QY 303 YLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIQHFQE 362
Db 359 YLETPGDENEHAHFQKAKERLEAKHREMSQVMREWEAEERQAKNLPKADKAVIQHFQE 418
QY 363 KVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKKY 422
Db 419 KVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRRHVFNMKKY 478
QY 423 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSO:SLLYNVPAVAEE 482
Db 479 VRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIERMNSO:SLLYNVPAVAEE 538
QY 483 QDEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGEFLSD 542
Db 539 IQDEVELLOKEQNSDDVLNMTSEPRISYGNDAIMPS:JETKTTVELLPVNGEFLSD 598
QY 543 LQPHSFGADSVAPANTENEPVDARPAADRGLTTRPGSLTNIKTEI1SEVKMDAEFRH 602
Db 599 LQPHSFGADSVAPANTENEPVDARPAADRGLTTRPGSLTNIKTEI1SEVKMDAEFRH 658
QY 603 DSGYEVHOKLVFFAEVDSGSKGAILGLMVGGVYIAIVIFITLVMKKKQYTSIHQWVE 662
Db 659 DSGYEVHOKLVFFAEVDSGSKGAILGLMVGGVYIAIVIFITLVMKKKQYTSIHQWVE 718
QY 663 VDAAVTPPERHLSKMOQNGYENPTYKFEQMON 695
Db 719 VDAAVTPPERHLSKMOQNGYENPTYKFEQMON 751

RESULT 6
Q98SGO
ID Q98SGO PRELIMINARY; PRI: 693 AA.
AC Q98SGO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Beta-amyloid precursor protein A.
GN APP.
CS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
CC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1;
DR HSSP; P05067; 1H23.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.

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DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match      87.8%; Score 3209; DB 13; Length 695;
Best Local Similarity 87.7%; Pred. No. 3,4e-186;
Matches 61; Conservative 36; Mismatches 44; Indels 5; Gaps 4;

QY 1 MLPGLALLAAWTAARALEVPTDGNAGLLAEPOIAFCGRLNMMHNVQNGKWDSDPSGK 60
DB 1 MLPHITLLVLTVA-GALALEVPADCGLLAEPOIAFCGRLNMMHNVQNGKWEIDVSGK 59

QY 61 TCIDTKGILQYQCEVYPELOITNVVEANQPVITONMCKGRKCKOCHPHFVPIYRCLVG 120
DB 60 GCITGKGIQYQCEVYPELOITNVVEANQPVITONMCKGRKCKOCHPHFVPIYRCLVG 119

QY 121 EFVSDALLVPDKCFHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMGLPCGIDKFR 180
DB 120 EFVSDALLVPDKCFHQRMDVCETHLHWHTVAKETCSKSTNLHDYGMGLPCGIDKFR 179

QY 181 GVEFVCCPAAEEDSNVSDADAEEDSDVWVGADIDYADGSEDKVVEA--EEFEVAAVE 238
DB 180 GVEFVCCPAAEEDSNVSDADAEEDSDVWVGADIDYADGSEDKVVEA--EEFEVAAVE 238

QY 239 EEEADDDDDGDEVEEAEPEYEATERTTSIATTTTTTSTESVEEVVVPVTAASIPD 298
DB 239 EEEADDDDDGDEVEEAEPEYEATERTTSIATTTTTTSTESVEEVVVPVTAASIPD 296

QY 299 AVDKYLETPGDNEHAHFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKKAVI 358
DB 297 AVDKYLETPGDNEHAHFQKAKERLEAKHREMSQVMREWEAEARQAKNLPKADKKAVI 356

QY 359 HFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVEN 418
DB 357 HFQEKVESLEQEAANEERQOLVETHMARVEAMLNDRRLALENYITALQAVPPRPRHVEN 416

QY 419 LKKYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVA 476
DB 417 LKKYVRAEQDKROHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIERMNSLSLLYNVA 476

QY 479 VAEETQDEVDLLOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEF 538
DB 477 VAEETQDEVDLFOKEQNSDDVLANMISEPRISYGNDAIMPSTETKTVELLPVNGEF 535

QY 539 SLDDIQLPWHISFGADSVPAANTENEVEPVDARPAARGLTTRPGSLTNIKTEEISEVKMD 598
DB 537 NIEDLQPHISFGADSVPAANTENEVEPVDARPAARGLTTRPGSLTNIKTEEISEVKMD 595

QY 599 EFRHDSGVEVHHQKLVFFAEVGSNGKGAIGLMVGGVVIATVITLVMKKKCYTIIH 659
DB 597 EYRHTAYEVHHQKLVFFAEVGSNGKGAIGLMVGGVVIATVITLVMKKKCYTIIH 656

QY 659 GVEVDAAVTPEERHLSKMQONGYENPTYKFFEQMQN 695
DB 657 GWEVDAAVTPEERHLTKMQONGYENPTYKFFEQMQN 693

RESULT 7
Q98SF9
AC Q98SF9; PRELIMINARY; PRT; 695 AA.
DT 01-JUN-2001 (TReMBLrel. 17. Created)
DT 01-JUN-2001 (TReMBLrel. 17. Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22. Last annotation update)
DE Beta-amyloid precursor pro-ein B.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

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RESULT 8


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091963
ID Q91963 PRELIMINARY: PRT: 747 AA.
AC Q91963:
DT 01-NOV-1995 (TrEMBLrel. 0.; Created)
DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23; Last annotation update)
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xeropodinae.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93129227; PubMed-1282805;
RA Okada H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL: S52417; AAB24853.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_RPT1.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPT1; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00759; BASICPTASE.
DR PRODOM: PS000222; Kunitz_BPT1; 1.
DR SMART: SM00131; Kunitz; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE: PS0279; BPT1_KUNITZ_2; 1.
KW protease inhibitor; Serine protease inhibitor;
SQ SEQUENCE 747 AA; 84893 MW; A7598185681D948 CRC64;

Query Match 84.5%; Score 3098; DB 13; Length 747;
Best Local Similarity 80.9%; Pred. No. 1.9e-179;
Matches 597; Conservative 35; Mismatches 42; Indels 64; Gaps 5;

QY 17 ALEVPTDGNAGLLAEPOIANP-CGRLNHNMVNQKNDSPSGTKTKIDTKEGILQYQCE 75
DB 15 ALEVLGNGLLAEPOIANPVSARLNHNMVNQKNETDVSQ---CIGTKEGILQYQCE 71
QY 76 VYPELQITNVVEANQPTVIONWCKGRKQCKTRPHFVPIYRCLVGERVSDALVPOKCKF 135
DB 72 VYPELQITNVVEANQPTVIONWCKGRKQCKSRTHIVPYRCLVGERVSDALLVPDKCKF 13;
QY 136 LHOQEMDVCEHLHWHHTVAKETCEKSTNLDYGMLLPCCGIDKFRGVFFVCCPLAESDN 195
DB 132 LHOQEMDVCETHLHWHHTVAKESCKSMLEHYGMLPCCGIDKFRGVFFVCCPSABESES 191
QY 196 VDSADAEEDSDVMWGADTDYADGSDQKVVVEA--EEERVAEVEEAEADDEDGQGV 253
DB 192 FDSADAEEDCDVMWGADADYDVRSDKAVEAQPDREEEVEVEEBEDDDGDD--DGDE 249
QY 254 VEZAEPEYERATERITSIATITTTTTTSEVVEVVR----- 288
DB 250 AEPEPEPEYERATERITSIATITTTTTTSEVVEVVR----- 309
QY 289 -----VPTTAASTPDVDKYLETPGDENEHAFQ 317
DB 310 SKCAQFIYGGCGGNRNFFESDQYCHAVGSGVIPATAASTPDVDKYLENPDNENEHDFL 369
QY 318 KAKERLEAKHRERMSQVMEERAEERAKNLPKADKKAIVQHTQEKVESLEQEAAERQO 377
DB 370 KAKERLECKHEKKESEVYKWEERAEERAKNLPKADKKAIVQHTQEKVESLEQEAAERQO 429
QY 378 LVETIHARVEAMLNDRRRLALENYITALQAVPPRPHVNMKKYVRAEQDKRQHTLKHF 437
DB 378 LVETIHARVEAMLNDRRRLALENYITALQADPPRPHVNMKKYVRAEQDKRQHTLKHF 439
QY 438 EHVWMDPKKAQIRSQVNTHLRVLYERNMOSLSLLYNYPVPAVEIQDEVDLLOKEQNY 497
DB 490 EHVWMDPKKAQIRSQVNTHLRVLYERNMOSLSLLYNYPVPAVEIQDEVDLLOKEQNY 545
QY 498 SDDVLANNISUPRISYGNDALMPSLTKTTVELLPVNGEFSLDDLOPWHSGFADSVPA 557
DB 550 SDDVMNMVSDHRVSYGNDALMPSLTKTTVELLPVNGEFSLDDLOPWHSGFADSVPA 609
QY 558 TENEVPEVDARPAADRGLTIRPGSLTNIKTEEISEVVKMDAEFRHDSGYEVHHQKLVFFA 617
DB 610 TENEVPEVDARPAADRGLTIRPGSLTNIKTEEISEVVKMDSEYRHDATAYEVHHQKLVFFA 669
QY 618 EDVGSNKGAIGLVGGVVVATVITVLMLKKKYTSIHHGVVEVDAAVTPERHLISKM 677
DB 670 EEVGSNKGAIGLVGGVVVATVITVLMLKKKYTTIHHGVVEVDAAVTPERHLISKM 729
QY 678 QONGYENPTYKFFEQMON 695
DB 730 QONGYENPTYKFFEQMON 747

RESULT 9
Q57394 PRELIMINARY: PRT: 699 AA.
AC Q57394;
DT 01-JUN-1998 (TrEMBLrel. 06; Created)
DT 01-JUN-1998 (TrEMBLrel. 06; Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE EU amyloid precursor protein 699.
GN EU APP699.
OS Närke Japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualia; Pristiogadidae; Batoidae;
OC Torpediniformes; Narcinoidae; Narkidae; Närke.
OX NCBI_TaxID=62965;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Electric lobe;
RX MEDLINE-98129705; PubMed=9461486;
RA Tijiima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,
RA Suzuki T.;
RT "CDNA isolation of Alzheimer's amyloid precursor protein from
RT cholinergic nerve terminals of the electric organ of the electric
RT ray.";
RL Biochem. J. 330:29-33(1998).
DR EMBL: AB005544; BAA24230.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 81.0%; Score 2959.5; DB 13; Length 699;
Best Local Similarity 80.7%; Pred. No. 4.4e-171;
Matches 568; Conservative 58; Mismatches 59; Indels 19; Gaps 8;

QY 2 LRG-LALLLLAANTA-----RALEVPTDGNAGLL-NEPOIANPFCGRLNHNMVNQK 52
DB 5 LRGRLGMLLLAALAAALVLAFLRALEVPTDGGAGLLAAEPQIANPFCGRLNHNMVNQK 64
QY 53 DSDPSGCTKIDTKEGILQYQCEVPELQITNVVEANQPTVIONWCKGRKQCKTRPHFV 112
DB 65 VSDPSGNTCTGEGILRYLQYQCEVPELQITNVVEANQPTVIONWCKGRKQCKTRPHFV 124
QY 113 IPRCLVGEFVSDALLVPKCKFLHQRMDVCETHLHWHHTVAKETCEKSTNLDYGM 172
DB 113 IPRCLVGEFVSDALLVPKCKFLHQRMDVCETHLHWHHTVAKETCEKSTNLDYGM 172

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D0 125 VPKYCLVGEFVSALVYPKCKFLHREKMDTCESHLWETVAKETGDKIMNLDYGMLL 184
QY 173 PCGIDKRGVEFVCCPLAESDMMVDSADAEDSDVMWGGADTDYADGSDKVEVAFEE 232
DB 185 PCGIDFPRGVFVCCPIPEENDKIDS-DMDESDVMWGGDDADYADGG-DKTV---EE 236
QY 233 EVAEEEDDDDDDEGDEVEE-EEEPYEATERITISATITTTTSSVEEVVRVPT 291
DB 239 KPIEEEDDESIDDEWDCDDDEVVDDQYFPTETIS--SITTTTSA:BEVVRVPT 295
QY 292 TAASPTPAVKYLETGCDENEHAFQAKERLEAKHREMSQVWREAEFROAKNLPKA 351
DB 296 TAASPTPAVKYLETGCDENEHAFQAKERLEAKHREMSKIMREWEAEFROAKNLPKA 355
QY 352 DKKAVIQHFOEKVESLEGEAANERQQLVETIMARVEAMLNDRRRLALENYITALQAVPPK 411
DB 356 DKKAVIORFOMVESLEGEAASERQQLVETIMARVEAMLNDRRRLALENYTAALQADPPR 415
QY 412 PRHVENMLKYYVRAEQDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLS 471
DB 416 PRHVLNALKKYSRAEQDRQHTLKHFDHVRADVPEKAAQIKSOVMTHLRVIDERMNQSLS 475
QY 472 LLNVPAVAZEIDDEVDELLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTVEEL 531
DB 476 LLKVPVSAEEQDEVELLQRESYMDMMANSVSUTRISYNDALVPSLSIEKTTIEL 535
QY 532 LPVNGEFLDDLPWHSFGADSPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEI 591
DB 536 LPDGEFILLDLPWHPFVIESIPANTENEVEPVDARPAADRGLTTRPGSGLTGKTEEI 595
QY 592 SEYKMDAEFRHDSYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITVLMKKK 651
DB 596 AELKMETEFQDSDYEVHHOKLVFFPKDVGSKNGKAIIGLMVGGVVIATVITVLMKKK 655
QY 652 QYTSIHGGVVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMN 695
DB 656 QYTSIHGGVVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMN 699

RESULT 10
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RI "tells us about the evolution of the amyloid protein precursor supergene family"
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; PG5067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; A4_APP; 1.
DR PRINTS; PS00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA: 64753 MW: 0AB8BB581563A19D CRC64:
Query Match: 75.6%; Score 2762.5; DB 13; Length 569;
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Best Local Similarity 93.4%; Pred. No. 2.8e-159;
Matches 534; Conservative 14; Mismatches 19; Indels 5; Gaps 4:
QY 126 ALLVPDKCKFLHREKMDVCETHLHWHHTVAKETCSEKSTNLDHYGMLPCGIDKRGVEFV 185
DB 1 ALLVPDKCKLLHREKMDVCETHLHWHHTVAKESSEKSNLHDYGMLLSGCIDKRGVEFV 60
QY 186 CCPLAESDMMVDSADAEDSDVMWGGADTDYADGSDKVE--VAEEVEAEVEEEDAD 243
DB 61 CCPLAESDNLDSADAEDSDVMWGGADYADGSDKVEEQPEDEBELTWEDEAD 120
QY 244 DDEDDDCGVEEAEAEPEEATERITISATITTTTSSVEEVVRVPTAASPTPAVKY 303
DB 121 DD-DDDDGDEI-EETEEYEAEATERITISATITTTTSSVEEVVRVPTAASPTPAVKY 178
QY 304 LETPGDENEHAFQAKERLEAKHREMSQVWREAEFROAKNLPKADKKAVIQHFOEK 363
DB 179 LETPGDENEHAFQAKERLEAKHREMSQVWREAEFROAKNLPKADKKAVIQHFOEK 238
QY 364 VESLEGEAANERQQLVETIMARVEAMLNDRRRLALENY:TALQAVPPRPRHVFNMKKYV 423
DB 239 VESLEGEAANERQQLVETIMARVEAMLNDRRRLALENY:TALQAVPPRPRHVFNMKKYV 298
QY 424 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSLLYVPAVAEEI 483
DB 299 RAEQKDRQHTLKHFEHVRMVDPKKAAQIRSOVMTHLRVIYERMNQSLSFLYVPAVAEEI 358
QY 484 QDEVDDELLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTVEELPVNGEFLDD 543
DB 359 QDEVDDELLOKEQNSDDVLANNMISPRISYNDALMPSLTETKTVEELPVNGEFLDD 418
QY 544 QPWHSGADSPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFRHD 603
DB 419 QPWHFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNVKTTEESEVKMDAEFRHD 478
QY 604 SYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVIFITVLMKKKQYTSIHGGVVEV 663
DB 479 SYEVHHOKLVFFAEDVGSNGKAIIGLMVGGVVIATVITVLMKKKQYTSIHGGVVEV 538
QY 664 DAAVTPPEERHLSKMOONGYENPTYKFFEQMN 695
DB 539 DAAVTP-ERHLSKMOONGYENPTYKFFEQMN 569

RESULT 11
Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 68.4 kDa protein (fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AAH05490.1; -.
DR HSSP; P05067; 2AAP.
DR MGI; MGI:88059; App.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR001255; Beta_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta_APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 1.
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DR SMART: SMO0131: KU: 1
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
DR Hypothetical protein; protease inhibitor; serine protease inhibitor.
DR NON_TER 1
FT
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 72.0%; Score 2630.5; DB 11; Length 607;
Best Local Similarity 85.5%; Pred. No. 3e-151;
Matches 519; Conservative 4; Mismatches 9; Indels 75; Gaps 1;

QY 164 NLHDYGMLLPGGIDKFGVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSD 223
DB 1 NLHDYGMLLPGGIDKFGVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSD 62
QY 224 KVEVEAEVEAEVEAEADDEDGDEVEEAEPEEATERTTSIATTTTTSV 283
DB 61 KVEVEAEVEAEVEAEADDEDGDEVEEAEPEEATERTTSIATTTTTSV 120
QY 284 EEVVR----- 288
DB 121 EEVVRVCSQAETGPCRAMISRWYFDVTEGKCVPEFYGGCGGNRNNEFTEHYCMVACS 180
QY 289 -----VPTTAASIPDAVDKY-ETPGDENEHAFQKAKERLEAKHR 328
DB 181 VSTQSLKLTSEPLQDFDKLPTTAASIPDAVDKY-ETPGDENEHAFQKAKERLEAKHR 240
QY 329 ERMQVNRWEAEAEQAKNLPKADKKAVIOHFQEKVFSLEGEAANERQQLVEHMARVEA 386
DB 241 ERMQVNRWEAEAEQAKNLPKADKKAVIOHFQEKVFSLEGEAANERQQLVEHMARVEA 300
QY 389 MLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKA 448
DB 301 MLNDRRLALENYITALQAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKA 360
QY 449 AQISQVMTLRLVIERKNSLSLLYNVPVAVEIODEVDELQEQNSDDVIANKISE 506
DB 361 AQISQVMTLRLVIERKNSLSLLYNVPVAVEIODEVDELQEQNSDDVIANKISE 420
QY 509 PRISYGNDAIMPSTETIKITVELLPVNGEFLSDLOQWHSEFGADSVDPANTENEVEPDAK 569
DB 421 PRISYGNDAIMPSTETIKITVELLPVNGEFLSDLOQWHSEFGADSVDPANTENEVEPDAK 480
QY 569 PAADRGTLTRPGSLTNKTEEISEVKMDAEFRHDSQYEVHHQKLVFFAEADVCSNKGAT 628
DB 481 PAADRGTLTRPGSLTNKTEEISEVKMDAEFRHDSQYEVHHQKLVFFAEADVCSNKGAT 540
QY 629 GLMVGGVVIATVITILVLMKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYK 588
DB 541 GLMVGGVVIATVITILVLMKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYK 600
QY 689 FFEOMQN 695
DB 601 FFEOMQN 507

RESULT 12
O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE Amyloid protein (Fragment).
DE Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
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PX MEDLINE-98337885; PubMed-9671674;
RA Barnes N.Y.; Li L.; Yoshikawa K.; Schwartz L.M.; Oppenheim R.W.;
RA Milligan C.E.;
RI "Increased production of amyloid precursor protein provides a
K: substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1;
DR WSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 71.4%; Score 2608; DB 13; Length 534;
Best Local Similarity 94.6%; Pred. No. 5.9e-150;
Matches 505; Conservative 13; Mismatches 12; Indels 3;

QY 164 NLHDYGMLLPGGIDKFGVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSD 223
DB 3 NLHDYGMLLPGGIDKFGVCCPLAEESDNVDSADAEEDSDVWVGADTDYADGSD 62
QY 224 KVEVEAEVEAEVEAEADDEDGDEVEEAEPEEATERTTSIATTTTTSV 281
DB 63 KVEVEAEVEAEVEAEADDEDGDEVEEAEPEEATERTTSIATTTTTSV 120
QY 282 SYEEVVRVPTTAASIPDAVDKY-ETPGDENEHAFQKAKERLEAKHRMSQVNRWEAE 341
DB 121 SYEEVVRVPTTAASIPDAVDKY-ETPGDENEHAFQKAKERLEAKHRMSQVNRWEAE 180
QY 342 ERQAKNLPKADKKAVIOHFQEKVFSLEGEAANERQQLVEHMARVEAMLNDRRLALENY 401
DB 181 ERQAKNLPKADKKAVIOHFQEKVFSLEGEAANERQQLVEHMARVEAMLNDRRLALENY 240
QY 402 ITALQAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKAQIRSQVMTLRLV 461
DB 241 ITALQAVPPRPHVFNMLKKYVRAEQKDRQHTLKHFHVRMVDPKKAQIRSQVMTLRLV 300
QY 462 IYERNQSLSLLYNVPVAVEIODEVDELQEQNSDDVLANMISEPRISYGNDAIMP 521
DB 301 IYERNQSLSLLYNVPVAVEIODEVDELQEQNSDDVLANMISEPRISYGNDAIMP 360
QY 522 TETKTITVELLPVNGEFLSDLOQWHSEFGADSVDPANTENEVEPVDARPAADRGTLTRPG 581
DB 361 TETKTITVELLPVNGEFLSDLOQWHSEFGADSVDPANTENEVEPVDARPAADRGTLTRPG 420
QY 582 GLTNKTEEISEVKMDAEFRHDSQYEVHHQKLVFFAEADVCSNKGALIGLVGGVVIATVI 641
DB 421 GLTNKTEEISEVKMDAEFRHDSQYEVHHQKLVFFAEADVCSNKGALIGLVGGVVIATVI 480
QY 642 FTLVLMKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYKFFEQMN 695
DB 481 FTLVLMKKQYTSIHGGVVEVDAVTPERHLSKMQONGYENPTYKFFEQMN 534

RESULT 13
O73683 PRELIMINARY; PRT; 780 AA.
AC O73683;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE Alzheimer's disease amyloid A4 protein homolog precursor [Contains:
DE beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Tetraodon fluviatilis (Puffer fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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OC Tetradontoidae; Tetradontidae; Tetradontom.
OX NCBI_TaxID=47145;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98252138; PubMed=9599080;
RT Villard L., Tassone P., Chromograc-Jurcevic T., Clancy K., Gordiner K.:
RA Analysis of pufferfish chromogracins of the AT-rich human APP gene.
RL Gene 210:17-24(1998).
CC CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH XII-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC CC -!- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
CC BPTI/KUNITZ FAMILY OF INHIBITORS.
DR EMBL: AF018165; AAC41275.1; -.
DR HSSP: P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00759; BASICPTASE.
DR PRODOM: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; FALSE_NFG.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
FW Serine protease inhibitor.
FT SIGNAL 1 18
FT CHAIN 19 780
FT CHAIN 682 724
FT DOMAIN 719 711
FT TRANSMEM 712 732
FT DOMAIN 733 780
FT DOMAIN 323 382
FT SITE 769 772
FT DISULFID 327 378
FT DISULFID 336 361
FT CARBOHYD 563 560
FT SEQUENCE 780 AA; 89238 MW; 60071BE94520191D CRC64;
Query Match 70.3%; Score 2568; DB 13; Length 780;
Best Local Similarity 65.3%; Pred. No. 2,6e-147;
Matches 512; Conservative 71; Mismatches 95; Indels 106; Gaps 10;
QY 7 LLLLAANTRALEVPIDNAGLLAPQIAMFCGRLLMNTYQNGKWDSPSGTKTCIDIK 66
DB 8 LLLLAANSTLAAEVPIDVSMGLAEPVAFMFCGKINMHINVOGKWEPEPSCSKCIGK 67
QY 67 EGILCYCGEYVPELOITNVVEANQVPTIQNCKCRKCKTHPHVPIYRCINGEFVSDA 126
DB 68 EGILQICQYVPELOITNVVEANQVPTIQNCKCRKCKTHPHVPIYRCINGEFVSDA 127
QY 127 LLVPDKCFELHQRMDVCFTHLRKHHTVAKETCSKSTNLHDYGMLLPGCIDKFRGVEVC 186
DB 128 LLVPDKCFELHQRMNQCESHLHHTVAKESCGDRAMNLEDYGMLLPGCIDRFRGVEVC 187
QY 187 CPLAESDNVDGADEEDSVWNGAGTDYADGS-----EKKVVEVAEE 232
DB 188 CP-AEAERMDSTEDADSDSVWNGADNDYSDNSMVRPEPAEQOEETRPVSVVEEEEG 246
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233 EVARVEEE-----ADDEDDEGDGEVEEBEAEPEEATERTTSTA 273
247 EVAQEDDEEEVLDTDQGDGEDEHAADEEEVDIDAFGESDDVDADDEPTNVA 306
274 ---TTTTTSEEVEEYV----- 288
307 MTITTTTTTSEEVEEYVFMFCMAHADTGPCIASMPSWYDAVDGRTMYELMYGCGGNMN 366
289 -----VPTTAASPTDAVDKYLETFGDENEHAHFQKAKERLEAKHRMSQ 333
367 NFSEEEYCLSVCSVVPTDMPSSPDADVHYLETADENEHAHFQKAKERLEAKHRMSQ 426
334 VMRENEBAERQAKNLKADKKAVIQHFOEKVESLEGEAANERQQLVETHMARVEAMLNDR 393
427 VMRENEBAERQAKNLPRADKKIVIQHFOEKVESLEGEAASERQQLVETHMARVEALJNDR 486
394 RRLALENYITALGAVPPRPHVFNMLKKYVRAEQKDRHTLKHFEHVRMVDPKKAAQJRS 453
487 RRLALENYITALGQDPPRPHVFNMLKKYVRAEQKDRHTLKHFEHVRMVDPKKAAQJRS 546
454 QVMTHLRVIYERMNOSLSLYNPVABEIQDEVDLQKEQNYSDVLANMISEPRISY 513
547 QVTLHLKAVIEERMNOSLSLYNPVABEIQDEVDLQKEQNYSDVLANMISEPRISY 605
514 GNDALMPSLTETKTITVELLPVNGEFSLDLQCPNH--SFGADSVPAENTENEVEVDARPA 571
606 GNDALMPSLTETKTITVELLPVNGEFSLDLQCPNH--SFGADSVPAENTENEVEVDARPA 659
572 DGLTTRPGSLTNIKTEISEVKMDAEFRDGSYEVHVKLVFFAEADVGSNKGAIIGLM 631
660 ERGVPTP---VTCKSMEAVPELMEDETRQSTYEYEVHVKLVFFAEADVGSNKGAIIGLM 716
632 VGVVIATVITLVLMLKKQYTSIHGGVVEVDAVTPPEERHLSKMOONGYENPTYKFFE 691
717 VGVVIATVITLVLMLKKQYTSIHGGVVEVDAVTPPEERHLSKMOONGYENPTYKFFE 776
692 QMON 695
777 QMON 780
RESULT 14
Q90W28 PRELIMINARY; PRG: 738 AA.
AC Q90W28:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Amyloid precursor protein.
GN APPA OR APP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Groth C., Lardelli M.;
RT "Expression analysis of zebrafish app.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF389401; AAK64495.1; -.
DR ZFIN: ZDB-GENE-000616-13; appa.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta_APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00759; BASICPTASE.
DR PRODOM: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
```


QY 653 YTSIHGVEYDAAVTPERHLSKMQONGYENPTYKFFEQMON 695
 ||| |||:|||| |||||:||||:||||:||||:||||:||||
DE 652 YTS-IHGVIEYDAAVTPERHLAKMQONGYENPTYKFFEOMON 694

Search completed: October 2, 2003, 14:02:40
Job time : 41 secs